



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:47 AM UTC

PDB ID : 1BSP / pdb_00001bsp
Title : THERMOSTABLE THYMIDYLATE SYNTHASE A FROM BACILLUS SUBTILIS
Authors : Stout, T.J.; Schellenberger, U.; Santi, D.V.; Stroud, R.M.
Deposited on : 1998-07-09
Resolution : 2.50 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 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)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

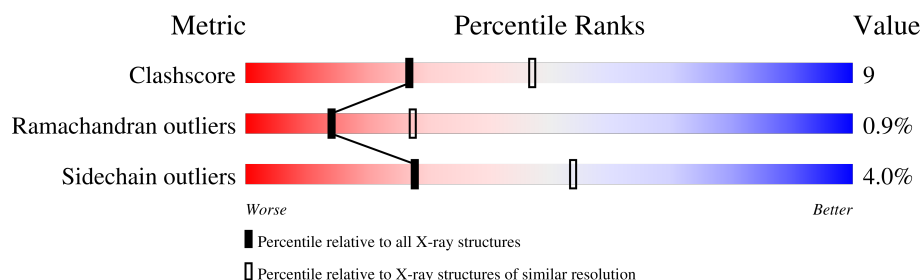
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	278	
1	B	278	

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	PO4	A	300	-	X	-	-
2	PO4	A	301	-	X	-	-

2 Entry composition [i](#)

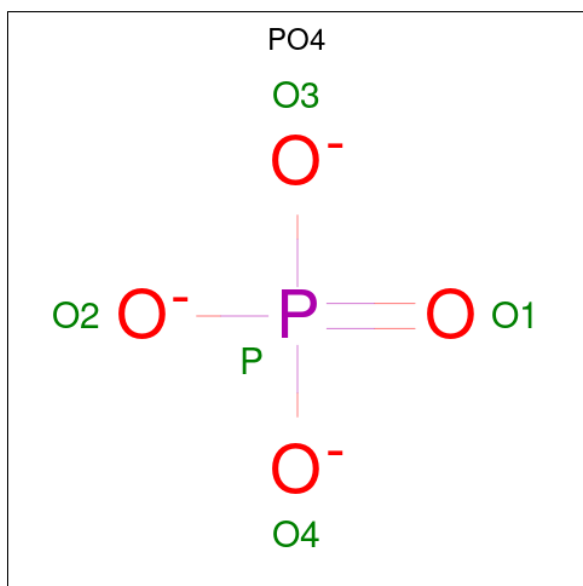
There are 3 unique types of molecules in this entry. The entry contains 4841 atoms, of which 43 are hydrogens and 0 are deuteriums.

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 THYMIDYLATE SYNTHASE A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	277	Total	C	H	N	O	S	25	0	0
			2341	1469	43	392	427	10			
1	B	278	Total	C	N	O	S		0	0	0
			2307	1474	393	430	10				

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 3 is water.

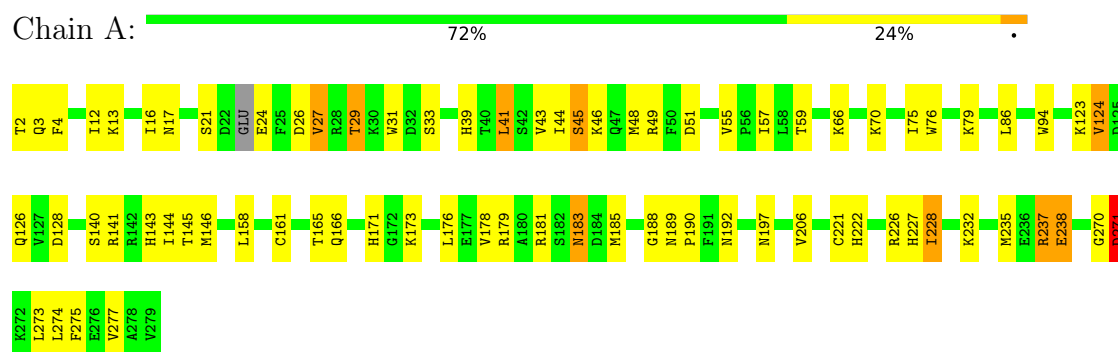
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	92	Total 92	O 92	0	0
3	B	91	Total 91	O 91	0	0

3 Residue-property plots

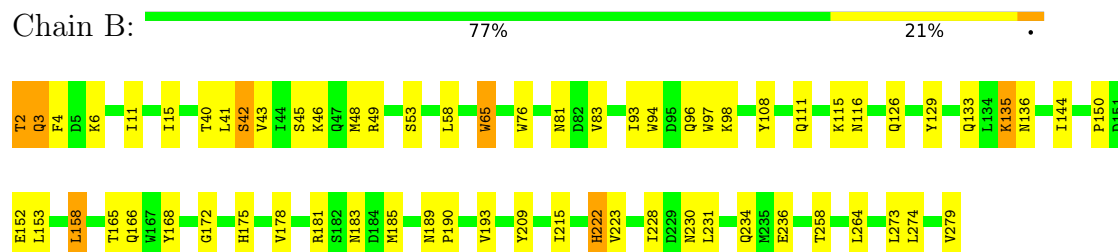
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: THYMIDYLATE SYNTHASE A



• Molecule 1: THYMIDYLATE SYNTHASE A



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.22Å 97.44Å 118.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50	Depositor
% Data completeness (in resolution range)	87.4 (50.00-2.50)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.181 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4841	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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: 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	0.44	0/2355	0.93	10/3188 (0.3%)
1	B	0.42	0/2365	0.96	10/3203 (0.3%)
All	All	0.43	0/4720	0.94	20/6391 (0.3%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	42	SER	N-CA-C	8.44	121.99	109.24
1	B	228	ILE	N-CA-C	8.26	119.04	110.62
1	A	41	LEU	N-CA-C	-6.99	97.56	109.24
1	A	188	GLY	N-CA-C	6.02	120.47	112.77
1	A	228	ILE	N-CA-C	6.02	117.48	110.62
1	A	27	VAL	N-CA-C	6.00	116.56	108.17
1	A	76	TRP	N-CA-C	5.90	118.95	111.69
1	B	222	HIS	N-CA-C	5.86	117.69	108.96
1	A	192	ASN	N-CA-C	5.86	117.75	111.36
1	B	76	TRP	N-CA-C	5.85	118.79	111.24
1	B	65	TRP	N-CA-C	5.71	117.51	111.28
1	B	53	SER	N-CA-C	-5.54	106.48	113.18
1	B	136	ASN	N-CA-C	5.47	117.32	111.36
1	A	222	HIS	N-CA-C	5.33	118.28	109.85
1	A	161	CYS	N-CA-C	-5.31	104.39	111.24
1	A	197	ASN	N-CA-C	-5.20	105.70	111.36
1	B	41	LEU	N-CA-C	-5.14	99.91	108.34
1	A	144	ILE	N-CA-C	5.13	115.51	108.12
1	B	81	ASN	N-CA-C	-5.08	105.99	113.61
1	B	258	THR	N-CA-C	-5.04	101.63	109.24

There are no chirality outliers.

There are no planarity outliers.

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	2298	43	2230	50	0
1	B	2307	0	2237	41	0
2	A	10	0	0	0	0
3	A	92	0	0	10	0
3	B	91	0	0	2	0
All	All	4798	43	4467	83	0

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 9.

All (83) 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:165:THR:HG22	1:A:178:VAL:HG12	1.69	0.74
1:A:13:LYS:HB2	1:A:235:MET:HE1	1.73	0.70
1:B:42:SER:HB3	1:B:222:HIS:HB3	1.77	0.67
1:A:45:SER:HB3	1:B:49:ARG:HH12	1.60	0.67
1:B:165:THR:HG22	1:B:178:VAL:HG12	1.77	0.65
1:B:166:GLN:HG2	1:B:168:TYR:CZ	2.35	0.61
1:A:189:ASN:HB3	1:A:190:PRO:HD3	1.82	0.60
1:A:2:THR:HG22	3:A:377:HOH:O	2.02	0.60
1:A:13:LYS:O	1:A:16:ILE:HG13	2.02	0.59
1:B:43:VAL:HG11	1:B:46:LYS:HE2	1.83	0.59
1:A:238:GLU:H	1:A:238:GLU:CD	2.10	0.57
1:A:24:GLU:C	1:A:26:ASP:H	2.14	0.56
1:B:15:ILE:HG21	1:B:223:VAL:HG22	1.87	0.56
1:B:83:VAL:HG21	1:B:98:LYS:HB3	1.88	0.56
1:A:57:ILE:HA	3:A:328:HOH:O	2.07	0.55
1:A:146:MET:HB3	1:B:150:PRO:HG3	1.88	0.55
1:B:2:THR:O	1:B:3:GLN:HB2	2.07	0.54
1:A:43:VAL:HG11	1:A:46:LYS:HE2	1.90	0.54
1:B:234:GLN:HB2	1:B:273:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:TYR:O	1:B:133:GLN:HG2	2.09	0.52
1:A:75:ILE:O	1:A:79:LYS:HA	2.10	0.52
1:B:126:GLN:HG3	3:B:293:HOH:O	2.08	0.52
1:A:2:THR:HG21	1:A:51:ASP:OD1	2.10	0.51
1:A:165:THR:HB	1:A:176:LEU:HD11	1.93	0.51
1:A:4:PHE:HE1	1:A:48:MET:SD	2.34	0.50
1:A:126:GLN:HG3	3:A:334:HOH:O	2.11	0.50
1:B:234:GLN:HB2	1:B:273:LEU:CD1	2.41	0.50
1:A:31:TRP:CZ2	1:A:226:ARG:HB3	2.46	0.50
1:B:189:ASN:HB3	1:B:190:PRO:HD3	1.92	0.50
1:A:41:LEU:HD12	1:A:228:ILE:HD11	1.94	0.50
1:A:185:MET:SD	1:A:221:CYS:SG	3.09	0.50
1:A:227:HIS:CD2	1:A:275:PHE:HB3	2.47	0.49
1:A:270:GLY:O	1:A:271:ASP:HB2	2.13	0.49
1:A:49:ARG:HH12	1:B:45:SER:HB3	1.78	0.48
1:B:96:GLN:HG3	1:B:97:TRP:CD1	2.48	0.48
1:B:135:LYS:HA	1:B:135:LYS:HE3	1.96	0.48
1:B:111:GLN:HE22	1:B:152:GLU:HG3	1.78	0.48
1:B:93:ILE:HG13	1:B:94:TRP:CD1	2.48	0.48
1:A:27:VAL:HG12	1:A:29:THR:OG1	2.14	0.48
1:A:140:SER:HB3	1:A:143:HIS:CE1	2.49	0.47
1:A:123:LYS:HG2	3:A:379:HOH:O	2.13	0.47
1:B:11:ILE:HG21	1:B:185:MET:HE2	1.97	0.47
1:A:237:ARG:NH1	1:A:273:LEU:HG	2.30	0.46
1:A:12:ILE:O	1:A:16:ILE:HG23	2.15	0.46
1:A:141:ARG:HH21	1:B:40:THR:HG21	1.81	0.45
1:A:277:VAL:HG22	3:A:356:HOH:O	2.15	0.45
1:A:228:ILE:O	1:A:232:LYS:HG3	2.16	0.45
1:B:93:ILE:HG13	1:B:94:TRP:HD1	1.81	0.45
1:A:183:ASN:HB3	1:A:185:MET:CE	2.46	0.45
1:B:115:LYS:HG2	3:B:316:HOH:O	2.17	0.45
1:A:45:SER:HB3	1:B:49:ARG:NH1	2.28	0.45
1:A:166:GLN:HE22	1:B:181:ARG:HB2	1.81	0.45
1:B:11:ILE:CG2	1:B:185:MET:HE2	2.47	0.44
1:B:4:PHE:CE1	1:B:58:LEU:HD13	2.52	0.44
1:A:124:VAL:HG13	1:A:128:ASP:HB2	2.00	0.44
1:A:55:VAL:HG23	3:A:312:HOH:O	2.18	0.44
1:A:206:VAL:HB	3:A:369:HOH:O	2.16	0.44
1:B:172:GLY:O	1:B:209:TYR:HD1	2.01	0.44
1:B:230:ASN:ND2	1:B:274:LEU:O	2.51	0.43
1:B:15:ILE:HD12	1:B:223:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:THR:HG1	1:A:165:THR:HG1	1.65	0.43
1:B:65:TRP:CD1	1:B:264:LEU:HD12	2.53	0.43
1:B:168:TYR:HB2	1:B:175:HIS:HB2	2.01	0.43
1:B:144:ILE:HD11	1:B:166:GLN:NE2	2.34	0.43
1:A:181:ARG:HB2	1:B:166:GLN:HE22	1.85	0.42
1:B:48:MET:HE1	1:B:193:VAL:HG21	2.02	0.42
1:B:4:PHE:HE1	1:B:58:LEU:HD13	1.84	0.42
1:B:108:TYR:HE2	1:B:158:LEU:HD22	1.83	0.42
1:A:274:LEU:HD12	1:A:275:PHE:H	1.84	0.42
1:A:141:ARG:NH2	1:B:40:THR:HG21	2.34	0.42
1:A:43:VAL:CG1	1:A:44:ILE:N	2.82	0.42
1:A:179:ARG:HB2	3:A:339:HOH:O	2.20	0.41
1:A:24:GLU:C	1:A:26:ASP:N	2.77	0.41
1:B:3:GLN:HG3	1:B:6:LYS:HG2	2.01	0.41
1:A:270:GLY:O	1:A:271:ASP:CB	2.68	0.41
1:A:43:VAL:HG11	1:A:46:LYS:CE	2.49	0.41
1:A:226:ARG:NH2	3:A:310:HOH:O	2.53	0.41
1:A:59:THR:O	1:A:270:GLY:N	2.54	0.41
1:A:66:LYS:O	1:A:70:LYS:HG3	2.21	0.41
1:A:86:LEU:HD21	1:A:94:TRP:CD1	2.55	0.41
1:B:65:TRP:CG	1:B:264:LEU:HD12	2.56	0.41
1:B:49:ARG:HG2	1:B:215:ILE:HG12	2.03	0.40
1:A:39:HIS:HE1	3:A:331:HOH:O	2.05	0.40

There are no symmetry-related clashes.

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	273/278 (98%)	251 (92%)	18 (7%)	4 (2%)	8 16
1	B	276/278 (99%)	265 (96%)	10 (4%)	1 (0%)	30 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	549/556 (99%)	516 (94%)	28 (5%)	5 (1%)	14	27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	271	ASP
1	A	33	SER
1	B	3	GLN
1	A	3	GLN
1	A	45	SER

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	252/253 (100%)	241 (96%)	11 (4%)	25	50
1	B	253/253 (100%)	244 (96%)	9 (4%)	31	58
All	All	505/506 (100%)	485 (96%)	20 (4%)	28	54

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	21	SER
1	A	29	THR
1	A	124	VAL
1	A	158	LEU
1	A	171	HIS
1	A	173	LYS
1	A	183	ASN
1	A	237	ARG
1	A	238	GLU
1	A	271	ASP
1	B	2	THR
1	B	116	ASN

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Mol	Chain	Res	Type
1	B	135	LYS
1	B	153	LEU
1	B	158	LEU
1	B	183	ASN
1	B	231	LEU
1	B	236	GLU
1	B	279	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	87	ASN
1	A	92	HIS
1	A	111	GLN
1	A	120	ASN
1	A	133	GLN
1	A	137	ASN
1	A	192	ASN
1	A	195	GLN
1	A	222	HIS
1	A	269	HIS
1	B	17	ASN
1	B	87	ASN
1	B	99	GLN
1	B	116	ASN
1	B	132	HIS
1	B	133	GLN
1	B	137	ASN
1	B	234	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are 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	301	-	4,4,4	3.04	4 (100%)	6,6,6	2.02	2 (33%)
2	PO4	A	300	-	4,4,4	2.89	4 (100%)	6,6,6	2.29	4 (66%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	PO4	P-O1	4.76	1.61	1.50
2	A	300	PO4	P-O1	4.36	1.60	1.50
2	A	301	PO4	P-O4	-2.33	1.47	1.54
2	A	300	PO4	P-O3	-2.25	1.48	1.54
2	A	300	PO4	P-O2	-2.22	1.48	1.54
2	A	301	PO4	P-O3	-2.18	1.48	1.54
2	A	300	PO4	P-O4	-2.10	1.48	1.54
2	A	301	PO4	P-O2	-2.04	1.48	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	PO4	O3-P-O1	-3.07	100.09	110.95
2	A	301	PO4	O3-P-O1	-2.75	101.24	110.95
2	A	300	PO4	O4-P-O3	2.67	116.22	107.91
2	A	301	PO4	O3-P-O2	2.47	115.59	107.91
2	A	300	PO4	O3-P-O2	2.40	115.37	107.91
2	A	300	PO4	O4-P-O1	-2.03	103.78	110.95

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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.