Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:24 PM GMT

PDB ID	:	1TIS
Title	:	CRYSTAL STRUCTURE OF THYMIDYLATE SYNTHASE FROM T4 PHAGE
Authors	:	Finer-Moore, J.; Stroud, R.
Deposited on	:	1994-01-24
Resolution	:	2.70 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
http://wwpdb.org/validation/2016/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:

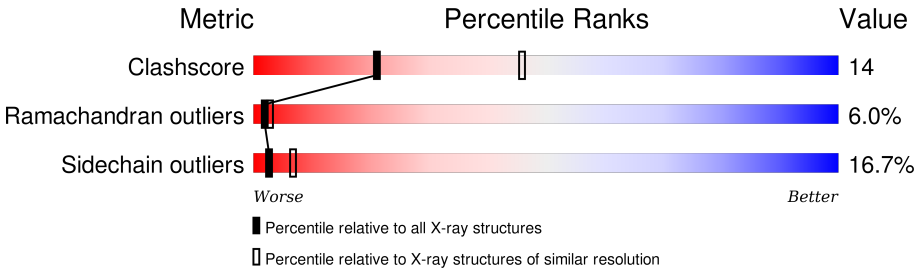
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

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 >=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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	286	46% 39% 12% •

2 Entry composition

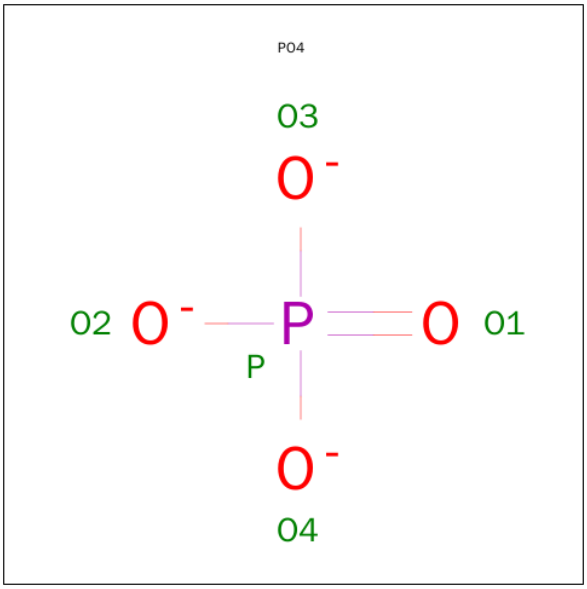
There are 3 unique types of molecules in this entry. The entry contains 2362 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 THYMIDYLATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	1	0
			2337	1512	398	416	11			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	20	Total	O	0	0
			20	20		

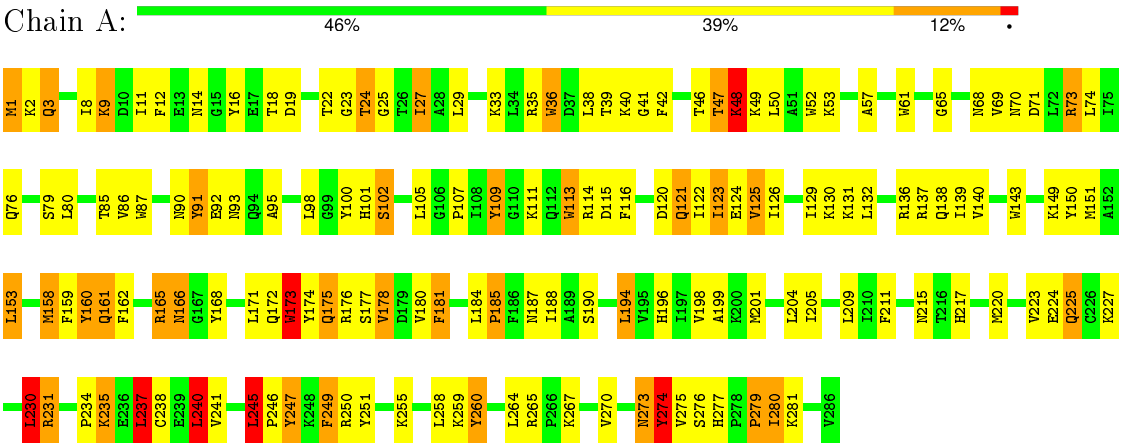
3 Residue-property plots (i)

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 (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.

Note EDS was not executed.

- Molecule 1: THYMIDYLATE SYNTHASE

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	68.02Å 68.02Å 140.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.199 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2362	wwPDB-VP
Average B, all atoms (Å^2)	28.0	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	0.89	1/2402 (0.0%)	1.91	80/3252 (2.5%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	173	TRP	CG-CD2	-5.21	1.34	1.43

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	36	TRP	CD1-CG-CD2	10.03	114.33	106.30
1	A	87	TRP	CG-CD2-CE3	8.99	141.99	133.90
1	A	61	TRP	CD1-CG-CD2	8.67	113.23	106.30
1	A	143	TRP	CD1-CG-CD2	8.61	113.19	106.30
1	A	52	TRP	CD1-CG-CD2	8.42	113.04	106.30
1	A	91	TYR	CB-CG-CD2	-8.29	116.03	121.00
1	A	231	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	A	36	TRP	CE2-CD2-CG	-7.86	101.02	107.30
1	A	87	TRP	CE2-CD2-CG	-7.84	101.03	107.30
1	A	87	TRP	CD1-CG-CD2	7.84	112.57	106.30
1	A	23	GLY	CA-C-N	-7.65	100.37	117.20
1	A	143	TRP	CE2-CD2-CG	-7.56	101.25	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	260	TYR	CB-CG-CD1	-7.53	116.48	121.00
1	A	61	TRP	CE2-CD2-CG	-7.53	101.28	107.30
1	A	166	ASN	N-CA-C	-7.25	91.43	111.00
1	A	113	TRP	CE2-CD2-CG	-7.02	101.68	107.30
1	A	230	LEU	CA-CB-CG	6.99	131.38	115.30
1	A	87	TRP	CB-CG-CD1	-6.95	117.96	127.00
1	A	158	MET	CG-SD-CE	-6.95	89.08	100.20
1	A	137	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	A	240	LEU	CA-CB-CG	6.81	130.96	115.30
1	A	274	TYR	CA-CB-CG	6.80	126.33	113.40
1	A	247	TYR	CB-CG-CD2	-6.70	116.98	121.00
1	A	52	TRP	CE2-CD2-CG	-6.65	101.98	107.30
1	A	160	TYR	CA-CB-CG	6.56	125.86	113.40
1	A	273	ASN	CA-C-N	-6.55	102.80	117.20
1	A	151	MET	CA-CB-CG	6.47	124.31	113.30
1	A	102	SER	CA-C-N	-6.36	103.48	116.20
1	A	173	TRP	CE2-CD2-CG	-6.27	102.28	107.30
1	A	258	LEU	CA-CB-CG	6.26	129.71	115.30
1	A	113	TRP	CD1-CG-CD2	6.23	111.28	106.30
1	A	181	PHE	CB-CG-CD1	6.19	125.14	120.80
1	A	231	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	47	THR	CA-C-N	-6.12	103.73	117.20
1	A	36	TRP	CG-CD1-NE1	-6.08	104.02	110.10
1	A	24	THR	N-CA-C	-6.08	94.58	111.00
1	A	178	VAL	CA-CB-CG1	-6.03	101.86	110.90
1	A	29	LEU	CA-CB-CG	6.01	129.12	115.30
1	A	181	PHE	CB-CG-CD2	-5.99	116.61	120.80
1	A	250	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	A	173	TRP	CD1-CG-CD2	5.93	111.05	106.30
1	A	109	TYR	CB-CG-CD1	-5.93	117.44	121.00
1	A	143	TRP	CG-CD2-CE3	5.89	139.20	133.90
1	A	274	TYR	N-CA-CB	-5.89	100.00	110.60
1	A	52	TRP	CE2-CD2-CE3	5.86	125.73	118.70
1	A	48	LYS	N-CA-C	-5.84	95.23	111.00
1	A	74	LEU	CA-CB-CG	5.84	128.74	115.30
1	A	237	LEU	CA-CB-CG	5.83	128.71	115.30
1	A	22	THR	CA-C-N	-5.80	104.59	116.20
1	A	61	TRP	CG-CD2-CE3	5.79	139.11	133.90
1	A	143	TRP	CG-CD1-NE1	-5.77	104.33	110.10
1	A	237	LEU	CA-C-N	-5.71	104.63	117.20
1	A	18	THR	N-CA-CB	-5.67	99.53	110.30
1	A	87	TRP	CG-CD1-NE1	-5.65	104.45	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	274	TYR	CB-CG-CD2	-5.65	117.61	121.00
1	A	1	MET	CA-CB-CG	5.65	122.90	113.30
1	A	181	PHE	CA-CB-CG	5.59	127.32	113.90
1	A	125	VAL	CA-CB-CG2	-5.55	102.57	110.90
1	A	265	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	A	23	GLY	O-C-N	5.45	131.42	122.70
1	A	93	ASN	CA-C-N	5.43	129.14	117.20
1	A	136	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	137	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	A	174	TYR	CB-CG-CD2	-5.41	117.76	121.00
1	A	270	VAL	N-CA-CB	-5.38	99.66	111.50
1	A	139	ILE	CA-C-N	5.35	128.97	117.20
1	A	12	PHE	CB-CG-CD2	-5.34	117.06	120.80
1	A	61	TRP	CG-CD1-NE1	-5.27	104.83	110.10
1	A	131	LYS	N-CA-CB	-5.27	101.12	110.60
1	A	121	GLN	CA-CB-CG	5.21	124.86	113.40
1	A	251	TYR	CB-CG-CD2	-5.16	117.90	121.00
1	A	245	LEU	CA-CB-CG	5.16	127.16	115.30
1	A	241	VAL	N-CA-C	5.15	124.90	111.00
1	A	153	LEU	CA-CB-CG	5.15	127.14	115.30
1	A	123	ILE	CA-CB-CG1	-5.11	101.30	111.00
1	A	73	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	A	52	TRP	CG-CD1-NE1	-5.09	105.01	110.10
1	A	161	GLN	CA-CB-CG	5.07	124.55	113.40
1	A	18	THR	CA-CB-CG2	5.05	119.46	112.40
1	A	101	HIS	O-C-N	5.03	130.75	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	274	TYR	Sidechain

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	2337	0	2334	67	0
2	A	5	0	0	0	0
3	A	20	0	0	0	0
All	All	2362	0	2334	67	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 14.

All (67) 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:158:MET:HE1	1:A:176:ARG:HB2	1.55	0.86
1:A:238:CYS:HG	1:A:274:TYR:HD1	1.25	0.84
1:A:9:LYS:NZ	1:A:230:LEU:HB2	1.94	0.83
1:A:33:LYS:HA	1:A:211:PHE:O	1.87	0.74
1:A:57:ALA:CB	1:A:76:GLN:HG2	2.23	0.68
1:A:114:ARG:HH11	1:A:122:ILE:HB	1.57	0.68
1:A:196:HIS:CE1	1:A:240:LEU:HD12	2.31	0.64
1:A:91:TYR:HB2	1:A:105:LEU:HD21	1.80	0.63
1:A:126:ILE:O	1:A:130:LYS:HG2	2.00	0.61
1:A:49:LYS:H	1:A:279:PRO:HB3	1.69	0.57
1:A:168:TYR:HA	1:A:205:ILE:O	2.05	0.56
1:A:165:ARG:HB2	1:A:168:TYR:HB2	1.87	0.56
1:A:25:GLY:HA3	1:A:220:MET:SD	2.45	0.56
1:A:238:CYS:SG	1:A:274:TYR:HD1	2.28	0.56
1:A:42:PHE:HB2	1:A:240:LEU:HD13	1.88	0.55
1:A:38:LEU:HD11	1:A:209:LEU:HB2	1.87	0.55
1:A:98:LEU:HD12	1:A:100:TYR:CE2	2.44	0.53
1:A:246:PRO:O	1:A:249:PHE:HB2	2.10	0.52
1:A:111:LYS:HD2	1:A:115:ASP:HB3	1.92	0.52
1:A:173:TRP:CH2	1:A:187:ASN:HB3	2.45	0.51
1:A:9:LYS:HZ3	1:A:230:LEU:HB2	1.73	0.51
1:A:129:ILE:HD13	1:A:138:GLN:OE1	2.11	0.51
1:A:199:ALA:HB1	1:A:204:LEU:O	2.11	0.50
1:A:11:ILE:HG22	1:A:27:ILE:HG22	1.93	0.50
1:A:14:ASN:OD1	1:A:16:TYR:N	2.45	0.50
1:A:8:ILE:HA	1:A:11:ILE:HD12	1.92	0.49
1:A:9:LYS:HZ1	1:A:230:LEU:HB2	1.76	0.48
1:A:158:MET:CE	1:A:176:ARG:HB2	2.35	0.48
1:A:171:LEU:HD23	1:A:172:GLN:N	2.28	0.48
1:A:65:GLY:CA	1:A:114:ARG:HG3	2.43	0.47
1:A:107:PRO:HD2	1:A:150:TYR:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:TRP:O	1:A:121:GLN:HG2	2.15	0.47
1:A:91:TYR:HA	1:A:95:ALA:HB3	1.97	0.47
1:A:11:ILE:O	1:A:14:ASN:HB3	2.15	0.47
1:A:125:VAL:O	1:A:129:ILE:HG12	2.15	0.46
1:A:259:LYS:HB2	1:A:259:LYS:HE3	1.76	0.46
1:A:280:ILE:HG22	1:A:281:LYS:H	1.81	0.46
1:A:173:TRP:HZ3	1:A:175:GLN:NE2	2.13	0.45
1:A:184:LEU:HB3	1:A:185:PRO:HD3	1.99	0.45
1:A:276:SER:O	1:A:277:HIS:ND1	2.49	0.45
1:A:69:VAL:HG22	1:A:105:LEU:HD11	2.00	0.44
1:A:245:LEU:HD12	1:A:249:PHE:CE2	2.53	0.44
1:A:48:LYS:O	1:A:50:LEU:N	2.50	0.44
1:A:224:GLU:HG3	1:A:227:LYS:HD2	2.00	0.44
1:A:126:ILE:HD13	1:A:201:MET:SD	2.59	0.43
1:A:38:LEU:HD23	1:A:196:HIS:CE1	2.53	0.43
1:A:180:VAL:HG13	1:A:184:LEU:HD23	2.00	0.43
1:A:41:GLY:HA3	1:A:237:LEU:HD13	2.00	0.43
1:A:194:LEU:O	1:A:198:VAL:HG23	2.19	0.43
1:A:2:LYS:HG3	1:A:3:GLN:N	2.33	0.43
1:A:73:ARG:HB3	1:A:79:SER:O	2.18	0.43
1:A:42:PHE:HB2	1:A:240:LEU:HB3	2.01	0.43
1:A:235:LYS:H	1:A:235:LYS:HE2	1.84	0.42
1:A:126:ILE:HG21	1:A:201:MET:CE	2.50	0.42
1:A:114:ARG:O	1:A:120:ASP:HA	2.19	0.42
1:A:173:TRP:CD1	1:A:173:TRP:N	2.87	0.42
1:A:68:ASN:HB3	1:A:71:ASP:OD2	2.20	0.42
1:A:184:LEU:O	1:A:188:ILE:HG13	2.20	0.42
1:A:162:PHE:CE1	1:A:171:LEU:HD12	2.55	0.41
1:A:70:ASN:HB3	1:A:80:LEU:HG	2.02	0.41
1:A:176:ARG:HD3	1:A:176:ARG:HH11	1.62	0.41
1:A:160:TYR:HA	1:A:172:GLN:O	2.19	0.41
1:A:223:VAL:HG12	1:A:227:LYS:HG3	2.01	0.41
1:A:149:LYS:HA	1:A:149:LYS:HD3	1.61	0.41
1:A:38:LEU:HD23	1:A:196:HIS:HE1	1.85	0.41
1:A:114:ARG:NH1	1:A:120:ASP:OD1	2.55	0.40
1:A:36:TRP:HE3	1:A:209:LEU:O	2.05	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	285/286 (100%)	230 (81%)	38 (13%)	17 (6%)	2 3

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	165	ARG
1	A	225	GLN
1	A	90	ASN
1	A	92	GLU
1	A	102	SER
1	A	231	ARG
1	A	249	PHE
1	A	24	THR
1	A	109	TYR
1	A	273	ASN
1	A	279	PRO
1	A	48	LYS
1	A	46	THR
1	A	47	THR
1	A	247	TYR
1	A	275	VAL
1	A	280	ILE

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	253/253 (100%)	211 (83%)	42 (17%)	3 7

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	GLN
1	A	9	LYS
1	A	19	ASP
1	A	27	ILE
1	A	35	ARG
1	A	39	THR
1	A	40	LYS
1	A	53	LYS
1	A	85	THR
1	A	86	VAL
1	A	116	PHE
1	A	123	ILE
1	A	124	GLU
1	A	132	LEU
1	A	140	VAL
1	A	153	LEU
1	A	159	PHE
1	A	161	GLN
1	A	166	ASN
1	A	173	TRP
1	A	175	GLN
1	A	177	SER
1	A	178	VAL
1	A	181	PHE
1	A	185	PRO
1	A	190	SER
1	A	194	LEU
1	A	215	ASN
1	A	217	HIS
1	A	225	GLN
1	A	230	LEU
1	A	234	PRO
1	A	235	LYS
1	A	237	LEU
1	A	240	LEU
1	A	245	LEU
1	A	255	LYS

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Mol	Chain	Res	Type
1	A	260	TYR
1	A	264	LEU
1	A	267	LYS
1	A	274	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	215	ASN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	287	-	4,4,4	1.54	1 (25%)	6,6,6	0.46	0

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
2	PO4	A	287	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	287	PO4	P-O1	2.06	1.61	1.52

There are no bond angle outliers.

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 (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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.