



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:22 AM GMT

PDB ID : 3I7V  
Title : Crystal structure of AP4A hydrolase complexed with AP4A (ATP) (aq\_158) from Aquifex aeolicus Vf5  
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Deposited on : 2009-07-09  
Resolution : 1.95 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

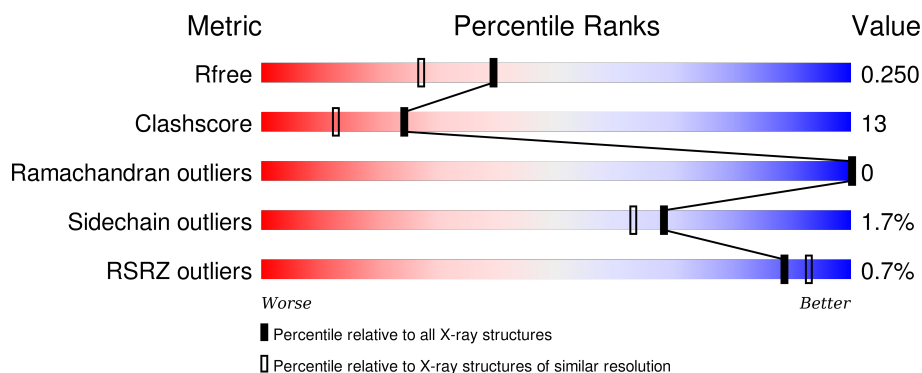
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	134	<div> <div></div> <div>70%</div> <div>29%</div> <div>.</div> </div>
1	B	134	<div> <div>75%</div> <div>25%</div> </div>

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
3	B4P	A	136	-	-	-	X
4	EDO	A	138	-	-	-	X
4	EDO	B	138	-	-	-	X
4	EDO	B	141	-	-	-	X
5	GOL	B	137	-	-	-	X

## 2 Entry composition [i](#)

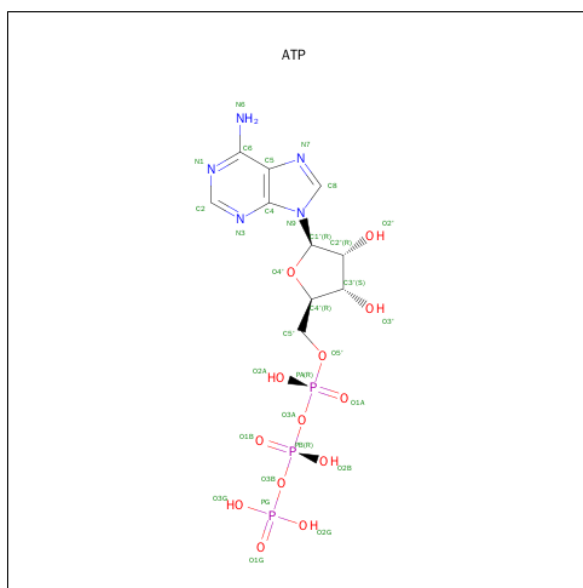
There are 6 unique types of molecules in this entry. The entry contains 2732 atoms, of which 0 are hydrogens and 0 are deuteriums.

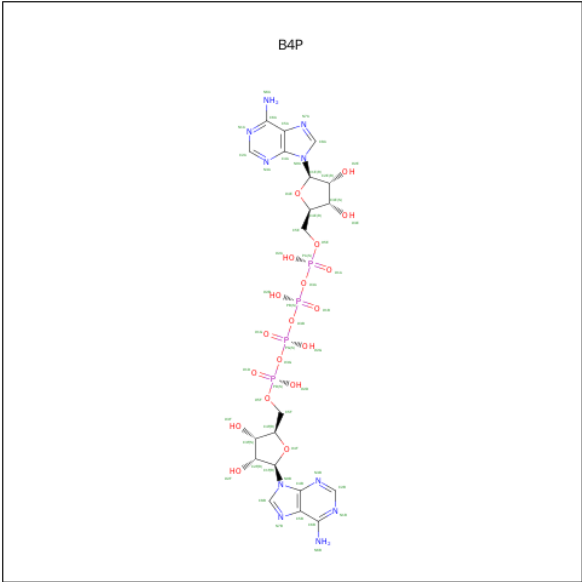
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called AP4A hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	134	Total	C	N	O	S	0	0	0
			1116	740	176	198	2			
1	B	134	Total	C	N	O	S	0	0	0
			1116	740	176	198	2			

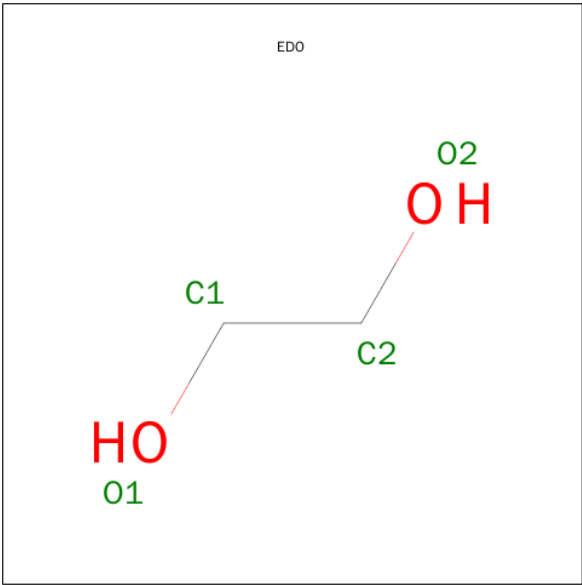
- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	20	10	19	4		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

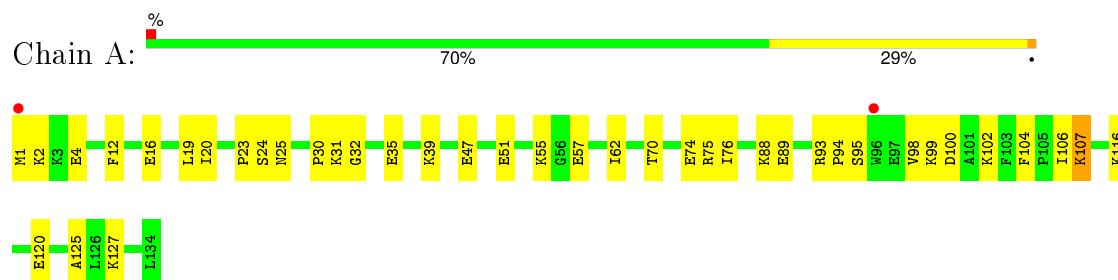
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	168	Total	O	0	0
			168	168		
6	B	177	Total	O	0	0
			177	177		

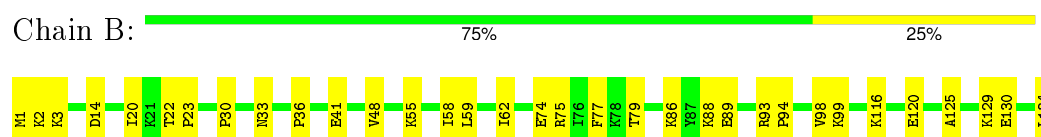
### 3 Residue-property plots

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.

- Molecule 1: AP4A hydrolase



- Molecule 1: AP4A hydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	35.30Å 59.23Å 67.42Å 90.00° 92.61° 90.00°	Depositor
Resolution (Å)	35.27 – 1.95 35.26 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.6 (35.27-1.95) 96.7 (35.26-1.95)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.93 (at 1.95Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.194 , 0.251 0.194 , 0.250	Depositor DCC
$R_{free}$ test set	1943 reflections (9.86%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.6	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 58.1	EDS
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 19708 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2732	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.16 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.7737e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: GOL, B4P, ATP, EDO

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	0.33	0/1146	0.59	0/1534
1	B	0.34	0/1146	0.61	0/1534
All	All	0.34	0/2292	0.60	0/3068

There are no bond length outliers.

There are no bond angle outliers.

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	1116	0	1151	33	0
1	B	1116	0	1151	28	0
2	A	31	0	12	1	0
2	B	31	0	12	1	0
3	A	53	0	23	4	0
4	A	12	0	15	2	0
4	B	16	0	20	2	0
5	B	12	0	12	2	0
6	A	168	0	0	5	0
6	B	177	0	0	4	0
All	All	2732	0	2396	62	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 13.

All (62) 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:127:LYS:HE2	6:A:528:HOH:O	1.64	0.96
1:B:1:MET:HE3	1:B:75:ARG:HG2	1.63	0.80
1:A:107:LYS:HA	1:A:107:LYS:HE3	1.65	0.78
3:A:136:B4P:H52B	6:A:509:HOH:O	1.84	0.76
2:A:135:ATP:HN61	4:A:138:EDO:H11	1.53	0.72
1:B:33:ASN:HB2	6:B:538:HOH:O	1.89	0.69
2:B:135:ATP:HN61	4:B:141:EDO:H12	1.58	0.68
1:B:41:GLU:HG2	5:B:137:GOL:H32	1.78	0.65
1:A:102:LYS:HE3	1:A:104:PHE:CZ	2.33	0.63
1:B:23:PRO:HA	1:B:99:LYS:HD2	1.82	0.61
1:A:35:GLU:O	1:B:2:LYS:NZ	2.34	0.60
1:A:107:LYS:HA	1:A:107:LYS:CE	2.35	0.57
3:A:136:B4P:C2A	1:B:2:LYS:HG2	2.35	0.56
1:A:107:LYS:HE3	1:A:107:LYS:CA	2.34	0.56
1:A:51:GLU:HA	1:A:95:SER:HB3	1.89	0.55
3:A:136:B4P:O1B	1:B:3:LYS:HE3	2.07	0.54
1:B:22:THR:HG21	4:B:138:EDO:H12	1.91	0.53
1:B:86:LYS:NZ	1:B:88:LYS:HD3	2.24	0.51
1:A:31:LYS:NZ	4:A:138:EDO:H21	2.26	0.51
1:B:79:THR:HG23	6:B:219:HOH:O	2.10	0.51
3:A:136:B4P:O3G	3:A:136:B4P:O2B	2.29	0.50
1:A:39:LYS:HE2	1:B:74:GLU:OE1	2.10	0.50
1:A:20:ILE:O	1:A:20:ILE:HD12	2.11	0.50
1:A:106:ILE:HG12	6:A:311:HOH:O	2.12	0.50
1:B:93:ARG:HH11	1:B:93:ARG:HG2	1.77	0.50
1:A:62:ILE:HD13	1:A:125:ALA:HB2	1.95	0.49
1:A:23:PRO:HA	1:A:99:LYS:HE3	1.95	0.48
1:B:1:MET:HE1	1:B:77:PHE:HB2	1.94	0.48
1:A:70:THR:HA	1:A:74:GLU:O	2.13	0.48
1:A:102:LYS:HE3	1:A:104:PHE:CE1	2.48	0.48
1:B:86:LYS:HZ2	1:B:88:LYS:HD3	1.79	0.48
1:A:24:SER:O	1:A:25:ASN:HB2	2.14	0.47
1:A:116:LYS:O	1:A:120:GLU:HG3	2.13	0.47
1:B:58:ILE:HG21	5:B:137:GOL:H31	1.97	0.47
1:A:30:PRO:HA	6:A:319:HOH:O	2.14	0.46
1:A:4:GLU:HG3	1:A:76:ILE:CG2	2.45	0.46
1:B:30:PRO:HG2	1:B:48:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:O	1:A:1:MET:HG3	2.15	0.46
1:A:55:LYS:HD2	1:A:89:GLU:CG	2.45	0.46
1:A:94:PRO:HB3	1:A:100:ASP:HA	1.98	0.46
1:B:129:LYS:HG3	1:B:134:LEU:HB3	1.97	0.45
1:B:94:PRO:HB2	1:B:98:VAL:HG23	1.98	0.45
1:B:20:ILE:HD12	1:B:20:ILE:O	2.15	0.45
1:B:59:LEU:HD12	1:B:134:LEU:HD22	1.98	0.45
1:B:14:ASP:HB2	6:B:230:HOH:O	2.16	0.45
1:B:88:LYS:NZ	1:B:88:LYS:HB3	2.32	0.45
1:A:4:GLU:OE2	1:B:36:PRO:HG3	2.18	0.44
1:A:57:GLU:OE1	1:A:88:LYS:HE3	2.18	0.44
1:A:55:LYS:HD2	1:A:89:GLU:CD	2.38	0.43
1:B:62:ILE:HD13	1:B:125:ALA:HB2	2.00	0.43
1:B:20:ILE:HD12	1:B:20:ILE:C	2.38	0.43
1:A:2:LYS:HD3	6:B:282:HOH:O	2.17	0.43
1:B:55:LYS:HD2	1:B:89:GLU:CG	2.48	0.43
1:A:32:GLY:HA3	1:A:47:GLU:HG3	2.01	0.43
1:A:20:ILE:C	1:A:20:ILE:HD12	2.40	0.43
1:A:55:LYS:NZ	6:A:503:HOH:O	2.52	0.42
1:A:4:GLU:HG3	1:A:76:ILE:HG21	2.02	0.42
1:B:94:PRO:CB	1:B:98:VAL:HG23	2.50	0.42
1:A:95:SER:H	1:A:98:VAL:HG22	1.85	0.41
1:A:19:LEU:HD12	1:A:104:PHE:CD2	2.55	0.41
1:B:116:LYS:O	1:B:120:GLU:HG3	2.21	0.40
1:A:12:PHE:HA	1:A:16:GLU:O	2.21	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	132/134 (98%)	130 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
All	All	264/268 (98%)	260 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	118/118 (100%)	115 (98%)	3 (2%)	55	45
1	B	118/118 (100%)	117 (99%)	1 (1%)	86	85
All	All	236/236 (100%)	232 (98%)	4 (2%)	68	63

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ARG
1	A	93	ARG
1	A	107	LYS
1	B	130	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	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 ⓘ

12 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	ATP	A	135	-	24,33,33	3.97	15 (62%)	31,52,52	3.12	11 (35%)
3	B4P	A	136	-	42,58,58	2.76	24 (57%)	51,91,91	2.93	25 (49%)
4	EDO	A	137	-	3,3,3	1.54	1 (33%)	2,2,2	0.62	0
4	EDO	A	138	-	3,3,3	1.63	1 (33%)	2,2,2	0.61	0
4	EDO	A	139	-	3,3,3	1.58	1 (33%)	2,2,2	0.62	0
2	ATP	B	135	-	24,33,33	3.93	15 (62%)	31,52,52	3.11	11 (35%)
5	GOL	B	136	-	5,5,5	2.34	2 (40%)	5,5,5	3.15	2 (40%)
5	GOL	B	137	-	5,5,5	2.33	2 (40%)	5,5,5	3.12	2 (40%)
4	EDO	B	138	-	3,3,3	1.56	1 (33%)	2,2,2	0.62	0
4	EDO	B	139	-	3,3,3	1.53	1 (33%)	2,2,2	0.59	0
4	EDO	B	140	-	3,3,3	1.55	1 (33%)	2,2,2	0.62	0
4	EDO	B	141	-	3,3,3	1.65	1 (33%)	2,2,2	0.63	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	ATP	A	135	-	-	0/18/38/38	0/3/3/3
3	B4P	A	136	-	-	0/30/70/70	0/6/6/6
4	EDO	A	137	-	-	0/1/1/1	0/0/0/0
4	EDO	A	138	-	-	0/1/1/1	0/0/0/0
4	EDO	A	139	-	-	0/1/1/1	0/0/0/0
2	ATP	B	135	-	-	0/18/38/38	0/3/3/3
5	GOL	B	136	-	-	0/4/4/4	0/0/0/0
5	GOL	B	137	-	-	0/4/4/4	0/0/0/0
4	EDO	B	138	-	-	0/1/1/1	0/0/0/0
4	EDO	B	139	-	-	0/1/1/1	0/0/0/0
4	EDO	B	140	-	-	0/1/1/1	0/0/0/0
4	EDO	B	141	-	-	0/1/1/1	0/0/0/0

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	135	ATP	O4'-C1'	-9.09	1.29	1.41
2	B	135	ATP	PA-O1A	-9.06	1.18	1.51
2	A	135	ATP	PA-O1A	-8.96	1.18	1.51
2	B	135	ATP	O4'-C1'	-8.43	1.30	1.41
2	A	135	ATP	PB-O1B	-7.57	1.23	1.51
2	B	135	ATP	PB-O1B	-7.38	1.24	1.51
3	A	136	B4P	O4F-C1F	-7.01	1.32	1.41
2	B	135	ATP	PA-O2A	-5.74	1.30	1.54
2	A	135	ATP	PA-O2A	-5.57	1.31	1.54
3	A	136	B4P	O4E-C1E	-5.12	1.34	1.41
2	B	135	ATP	C5-N7	-5.08	1.22	1.39
3	A	136	B4P	PG-O1G	-4.96	1.33	1.51
3	A	136	B4P	C4A-N3A	-4.91	1.28	1.35
2	A	135	ATP	C5-N7	-4.76	1.23	1.39
3	A	136	B4P	PB-O1B	-4.37	1.35	1.51
2	B	135	ATP	C8-N7	-4.33	1.26	1.34
2	A	135	ATP	C8-N7	-4.00	1.26	1.34
2	A	135	ATP	C4-N3	-3.78	1.29	1.35
2	A	135	ATP	PG-O3G	-3.74	1.41	1.54
2	B	135	ATP	C4-N3	-3.60	1.30	1.35
2	B	135	ATP	PG-O3G	-3.57	1.41	1.54
3	A	136	B4P	PD-O1D	-3.54	1.38	1.51
2	A	135	ATP	PG-O2G	-3.52	1.42	1.54
5	B	136	GOL	C1-C2	-3.50	1.38	1.52
3	A	136	B4P	PG-O2G	-3.50	1.40	1.54
5	B	137	GOL	C1-C2	-3.49	1.39	1.52
5	B	136	GOL	O3-C3	-3.43	1.27	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	137	GOL	O3-C3	-3.39	1.27	1.42
3	A	136	B4P	C5A-N7A	-3.36	1.28	1.39
2	B	135	ATP	PG-O2G	-3.31	1.42	1.54
3	A	136	B4P	C2B-N3B	-3.31	1.26	1.32
2	B	135	ATP	C3'-C4'	-3.08	1.44	1.53
3	A	136	B4P	PA-O2A	-3.05	1.41	1.54
3	A	136	B4P	C3F-C4F	-2.98	1.45	1.53
3	A	136	B4P	PD-O2D	-2.89	1.42	1.54
2	A	135	ATP	C3'-C4'	-2.88	1.45	1.53
4	B	141	EDO	O2-C2	-2.77	1.27	1.42
3	A	136	B4P	C8A-N7A	-2.72	1.29	1.34
4	A	138	EDO	O2-C2	-2.71	1.27	1.42
3	A	136	B4P	C5B-N7B	-2.69	1.30	1.39
4	A	139	EDO	O2-C2	-2.66	1.27	1.42
3	A	136	B4P	O3E-C3E	-2.63	1.36	1.43
4	B	138	EDO	O2-C2	-2.63	1.27	1.42
4	B	140	EDO	O2-C2	-2.61	1.27	1.42
4	A	137	EDO	O2-C2	-2.61	1.27	1.42
4	B	139	EDO	O2-C2	-2.60	1.28	1.42
2	B	135	ATP	O2'-C2'	-2.50	1.37	1.43
2	A	135	ATP	C6-N6	-2.32	1.27	1.34
2	A	135	ATP	PA-O5'	-2.27	1.48	1.59
2	A	135	ATP	C2'-C3'	-2.22	1.47	1.53
3	A	136	B4P	C2A-N1A	-2.20	1.29	1.33
2	B	135	ATP	C2'-C3'	-2.18	1.47	1.53
2	B	135	ATP	PA-O5'	-2.18	1.49	1.59
3	A	136	B4P	O5E-C5E	-2.18	1.35	1.44
3	A	136	B4P	O4F-C4F	-2.12	1.40	1.45
2	B	135	ATP	C6-N6	-2.12	1.28	1.34
3	A	136	B4P	C3E-C4E	-2.07	1.47	1.53
3	A	136	B4P	C5E-C4E	-2.04	1.45	1.51
3	A	136	B4P	O4E-C4E	-2.03	1.40	1.45
2	A	135	ATP	O2'-C2'	-2.02	1.38	1.43
3	A	136	B4P	C5A-C4A	2.08	1.45	1.40
3	A	136	B4P	C5B-C4B	3.23	1.47	1.40
2	B	135	ATP	C5-C4	3.25	1.47	1.40
2	A	135	ATP	C5-C4	3.27	1.47	1.40
3	A	136	B4P	C2A-N3A	3.49	1.38	1.32

All (51) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	135	ATP	N3-C2-N1	-7.31	123.30	128.89
2	B	135	ATP	N3-C2-N1	-7.25	123.34	128.89
2	B	135	ATP	C4-C5-N7	-6.93	103.10	109.48
2	A	135	ATP	C4-C5-N7	-6.85	103.18	109.48
2	A	135	ATP	O3G-PG-O1G	-6.80	88.68	110.58
2	B	135	ATP	O3G-PG-O1G	-6.79	88.73	110.58
3	A	136	B4P	N3B-C2B-N1B	-6.08	124.24	128.89
5	B	136	GOL	C3-C2-C1	-6.04	87.43	111.12
5	B	137	GOL	C3-C2-C1	-5.99	87.64	111.12
3	A	136	B4P	PG-O3B-PB	-4.78	119.31	132.73
3	A	136	B4P	O5F-PD-O1D	-4.34	92.78	109.62
3	A	136	B4P	O3F-C3F-C4F	-4.23	98.37	111.05
3	A	136	B4P	O3E-C3E-C4E	-4.04	98.93	111.05
3	A	136	B4P	N3A-C2A-N1A	-3.86	125.94	128.89
2	A	135	ATP	C1'-N9-C4	-3.78	121.25	126.94
2	B	135	ATP	C1'-N9-C4	-3.43	121.77	126.94
3	A	136	B4P	O2D-PD-O5F	-3.38	91.42	108.46
5	B	136	GOL	O1-C1-C2	-3.38	93.80	110.18
5	B	137	GOL	O1-C1-C2	-3.34	93.97	110.18
3	A	136	B4P	O2B-PB-O3B	-3.33	89.99	105.09
3	A	136	B4P	C4A-C5A-N7A	-3.05	106.67	109.48
3	A	136	B4P	O2B-PB-O3A	-2.85	92.15	105.09
3	A	136	B4P	O2G-PG-O3G	-2.83	92.24	105.09
3	A	136	B4P	C4B-C5B-N7B	-2.65	107.05	109.48
2	B	135	ATP	O3A-PA-O5'	-2.17	97.18	102.94
2	A	135	ATP	O3A-PA-O5'	-2.07	97.44	102.94
3	A	136	B4P	O4E-C4E-C5E	-2.04	102.04	109.32
3	A	136	B4P	O5E-C5E-C4E	-2.03	101.63	109.12
3	A	136	B4P	C2B-N1B-C6B	2.59	123.39	118.77
2	B	135	ATP	O4'-C4'-C5'	2.64	118.76	109.32
3	A	136	B4P	PD-O3G-PG	2.68	140.27	132.73
2	A	135	ATP	O4'-C4'-C5'	2.69	118.93	109.32
2	B	135	ATP	C2-N1-C6	2.69	123.57	118.77
2	A	135	ATP	C2-N1-C6	2.77	123.72	118.77
3	A	136	B4P	C1E-N9A-C4A	2.78	131.13	126.94
3	A	136	B4P	N6A-C6A-N1A	2.79	125.20	119.20
3	A	136	B4P	O4F-C4F-C5F	3.11	120.44	109.32
3	A	136	B4P	O2E-C2E-C3E	3.18	122.17	111.83
3	A	136	B4P	O2G-PG-O1G	3.43	131.12	112.53
2	A	135	ATP	PB-O3B-PG	3.66	144.94	132.67
2	B	135	ATP	PB-O3B-PG	3.69	145.03	132.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	136	B4P	O3A-PA-O5E	4.12	113.88	102.94
2	B	135	ATP	O2G-PG-O1G	4.51	125.10	110.58
2	A	135	ATP	O2G-PG-O1G	4.56	125.24	110.58
3	A	136	B4P	C4F-O4F-C1F	4.68	114.86	109.72
2	A	135	ATP	O3G-PG-O2G	4.82	125.75	107.38
3	A	136	B4P	O2D-PD-O1D	4.84	138.75	112.53
2	B	135	ATP	O3G-PG-O2G	4.84	125.81	107.38
2	A	135	ATP	C4'-O4'-C1'	6.46	116.81	109.72
2	B	135	ATP	C4'-O4'-C1'	6.46	116.81	109.72
3	A	136	B4P	C4E-O4E-C1E	9.81	120.49	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	135	ATP	1	0
3	A	136	B4P	4	0
4	A	138	EDO	2	0
2	B	135	ATP	1	0
5	B	137	GOL	2	0
4	B	138	EDO	1	0
4	B	141	EDO	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	134/134 (100%)	0.03	2 (1%) 76 84	13, 24, 39, 48	0
1	B	134/134 (100%)	-0.07	0 100 100	13, 21, 35, 47	0
All	All	268/268 (100%)	-0.02	2 (0%) 89 93	13, 22, 37, 48	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	96	TRP	4.6
1	A	1	MET	2.2

### 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
4	EDO	A	138	4/4	0.87	0.33	31.43	26,29,30,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	141	4/4	0.81	0.29	18.65	36,36,37,40	0
4	EDO	B	138	4/4	0.65	0.28	10.93	54,57,58,60	0
5	GOL	B	137	6/6	0.82	0.20	7.43	57,59,60,60	0
3	B4P	A	136	53/53	0.83	0.26	4.35	19,31,42,43	53
4	EDO	A	137	4/4	0.84	0.22	1.29	42,46,46,47	0
2	ATP	B	135	31/31	0.93	0.11	0.42	16,21,40,43	0
4	EDO	B	139	4/4	0.88	0.17	0.36	34,36,37,38	0
2	ATP	A	135	31/31	0.94	0.10	0.33	12,16,36,37	0
4	EDO	B	140	4/4	0.88	0.12	-0.40	51,52,52,52	0
5	GOL	B	136	6/6	0.87	0.17	-	33,42,43,44	0
4	EDO	A	139	4/4	0.83	0.14	-	65,65,65,66	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.