wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 04:03 pm BST

PDB ID	:	1SQ5
Title	:	Crystal Structure of E. coli Pantothenate kinase
Authors	:	Ivey, R.A.; Zhang, Y.-M.; Virga, K.G.; Hevener, K.; Lee, R.E.; Rock, C.O.; Jackowski, S.; Park, H.-W.
Deposited on	:	2004-03-17
Resolution	:	2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) symbol.

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

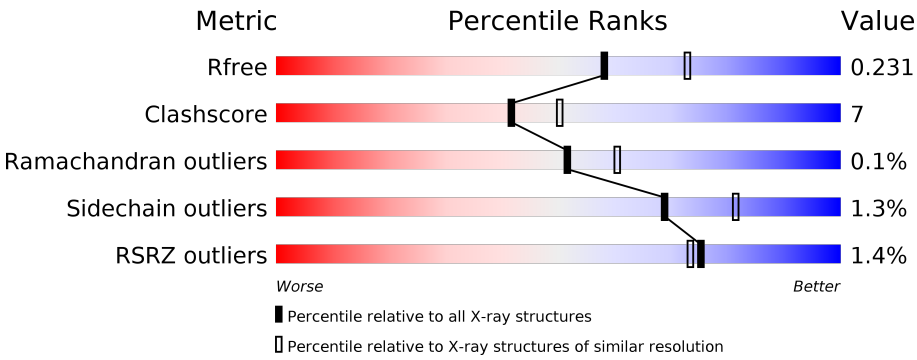
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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% 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	308	% 79% 19% • •
1	B	308	% 81% 16% •
1	C	308	% 81% 15% •
1	D	308	2% 81% 17% •

2 Entry composition (i)

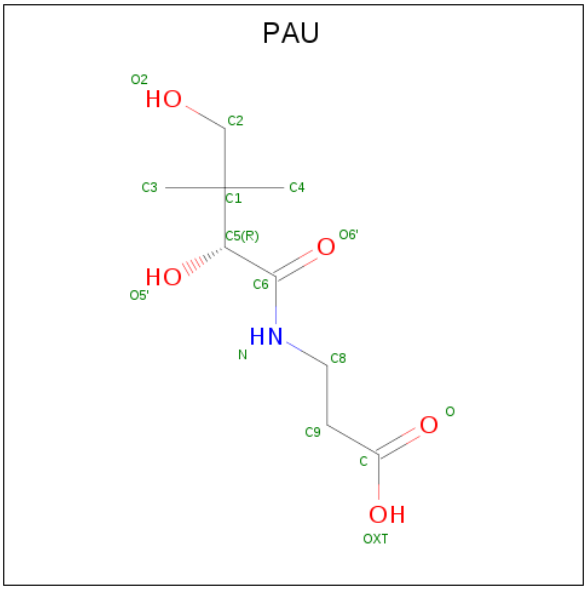
There are 4 unique types of molecules in this entry. The entry contains 10703 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Pantothenate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	302	2414	1555	411	442	6	0	0	0
1	B	302	2418	1558	411	444	5	0	0	0
1	C	298	2391	1541	404	440	6	0	0	0
1	D	304	2427	1564	412	445	6	0	0	0

- Molecule 2 is PANTOTHENOIC ACID (three-letter code: PAU) (formula: $C_9H_{17}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	15	9	1	5	0	0
2	B	1	15	9	1	5	0	0

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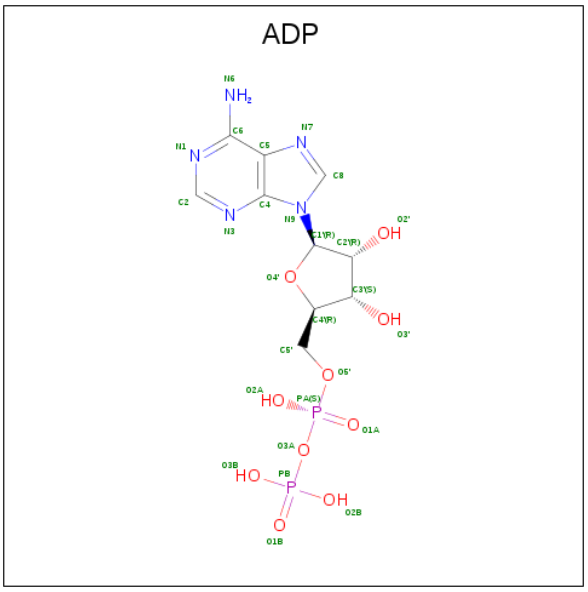
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	C	1	15	9	1	5	0	0
			Total	C	N	O		
2	D	1	15	9	1	5	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
3	B	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
3	C	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
3	D	1	27	10	5	10	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	235	235	235	0	0
			Total	O		
4	B	191	191	191	0	0
			Total	O		
4	C	230	230	230	0	0

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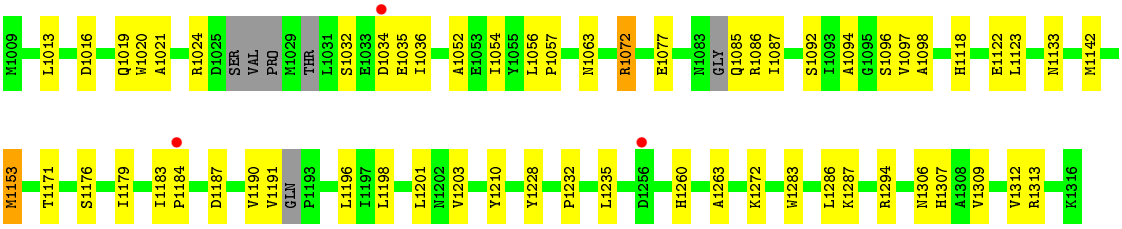
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	D	229	229	229	0	0

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 the various outlier classes 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.

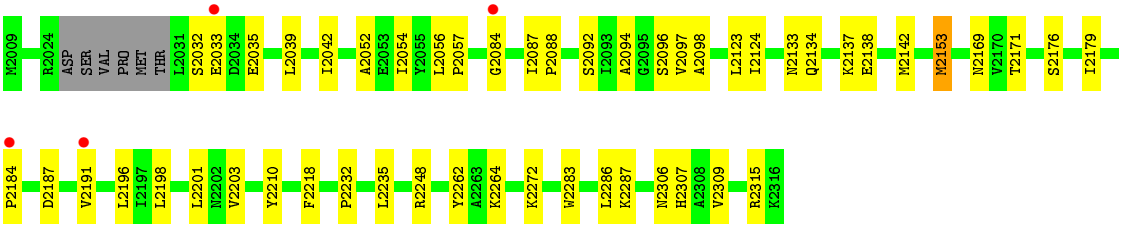
- Molecule 1: Pantothenate kinase

Chain A:



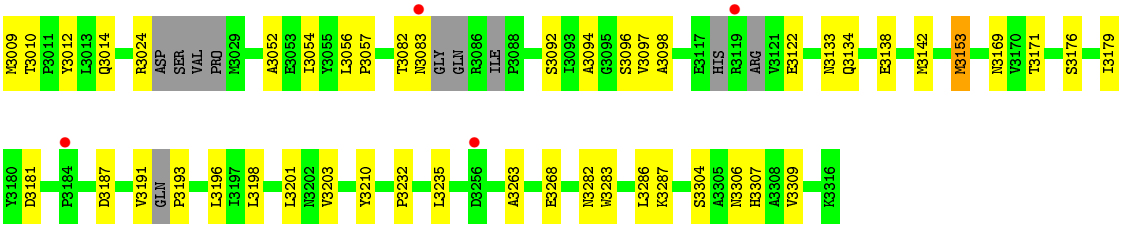
- Molecule 1: Pantothenate kinase

Chain B:



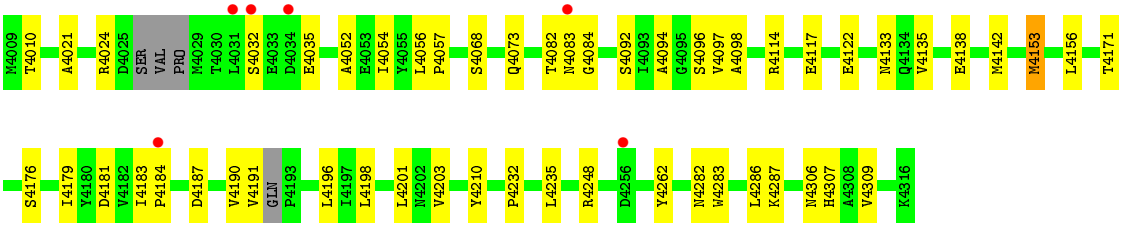
- Molecule 1: Pantothenate kinase

Chain C:



- Molecule 1: Pantothenate kinase

Chain D:


M4009
T4010
A4021
R4024
D4025
SER
VAL
PRO
M4029
T4030
L4031
S4032
E4033
D4034
E4035
A4052
E4053
I4054
Y4055
L4056
P4057
S4068
Q4073
T4082
M4083
G4084
S4092
I4093
A4094
G4095
S4096
V4097
A4098
R4114
E4117
E4122
M4133
Q4134
V4135
E4138
M4142
M4153
L4156
T4171
S4176
I4179
Y4180
D4181
V4182
I4183
P4184
D4187
V4190
V4191
GLN
P4193
L4196
I4197
L4198
L4201
M4202
V4203
Y4210
P4232
L4235
R4248
D4256
Y4262
M4282
W4283
L4286
K4287
M4306
H4307
A4308
V4309
K4316

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	181.20Å 181.66Å 47.42Å 90.00° 104.79° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 40.82 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (20.00-2.20) 88.7 (40.82-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.75 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.187 , 0.225 0.195 , 0.231	Depositor DCC
R_{free} test set	8528 reflections (8.87%)	wwPDB-VP
Wilson B-factor (Å^2)	22.3	Xtriage
Anisotropy	0.579	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 45.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for k+l,h+l,-l 0.000 for -k+l,-h-l,-l 0.024 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10703	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.64% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PAU, ADP

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	0.34	0/2468	0.58	0/3349
1	B	0.33	0/2475	0.57	0/3364
1	C	0.35	0/2442	0.57	0/3309
1	D	0.33	0/2483	0.57	0/3374
All	All	0.34	0/9868	0.57	0/13396

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 (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	2414	0	2381	39	0
1	B	2418	0	2392	32	0
1	C	2391	0	2370	35	1
1	D	2427	0	2400	33	0
2	A	15	0	16	0	0
2	B	15	0	16	0	0
2	C	15	0	16	1	0
2	D	15	0	16	1	0
3	A	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	27	0	12	0	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
4	A	235	0	0	6	0
4	B	191	0	0	5	0
4	C	230	0	0	8	0
4	D	229	0	0	5	0
All	All	10703	0	9655	136	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 7.

The worst 5 of 136 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:C:3263:ALA:HB2	4:C:7336:HOH:O	1.89	0.72
1:C:3010:THR:HG22	1:C:3012:TYR:H	1.55	0.72
1:A:1263:ALA:HB2	4:A:7647:HOH:O	1.89	0.71
1:C:3009:MET:HB3	4:C:7474:HOH:O	1.93	0.68
1:D:4021:ALA:O	1:D:4024:ARG:HG2	1.95	0.66

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)
1:C:3014:GLN:NE2	1:C:3014:GLN:NE2[2_555]	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	293/308 (95%)	287 (98%)	6 (2%)	0	100	100
1	B	298/308 (97%)	288 (97%)	9 (3%)	1 (0%)	41	46
1	C	286/308 (93%)	282 (99%)	4 (1%)	0	100	100
1	D	298/308 (97%)	292 (98%)	6 (2%)	0	100	100
All	All	1175/1232 (95%)	1149 (98%)	25 (2%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2084	GLY

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	260/277 (94%)	255 (98%)	5 (2%)	57	71
1	B	261/277 (94%)	258 (99%)	3 (1%)	73	85
1	C	260/277 (94%)	258 (99%)	2 (1%)	81	90
1	D	262/277 (95%)	258 (98%)	4 (2%)	65	78
All	All	1043/1108 (94%)	1029 (99%)	14 (1%)	69	81

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2196	LEU
1	B	2218	PHE
1	D	4083	ASN
1	B	2153	MET
1	D	4010	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1085	GLN
1	D	4177	HIS
1	D	4018	ASN
1	A	1063	ASN
1	A	1260	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

8 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	$\#\|Z\| > 2$
3	ADP	A	5001	-	24,29,29	0.93	1 (4%)	29,45,45	1.55	4 (13%)
2	PAU	C	6002	-	9,14,14	3.92	4 (44%)	14,19,19	1.28	2 (14%)
3	ADP	D	5004	-	24,29,29	0.99	1 (4%)	29,45,45	1.55	5 (17%)
2	PAU	A	6001	-	9,14,14	3.71	4 (44%)	14,19,19	1.11	2 (14%)
2	PAU	B	6003	-	9,14,14	3.85	4 (44%)	14,19,19	1.19	2 (14%)
3	ADP	C	5003	-	24,29,29	1.15	1 (4%)	29,45,45	1.82	9 (31%)
2	PAU	D	6004	-	9,14,14	4.20	4 (44%)	14,19,19	1.23	3 (21%)
3	ADP	B	5002	-	24,29,29	0.88	1 (4%)	29,45,45	1.59	4 (13%)

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
3	ADP	A	5001	-	-	3/12/32/32	0/3/3/3
2	PAU	C	6002	-	-	3/17/19/19	-
3	ADP	D	5004	-	-	3/12/32/32	0/3/3/3
2	PAU	A	6001	-	-	0/17/19/19	-
2	PAU	B	6003	-	-	3/17/19/19	-
3	ADP	C	5003	-	-	5/12/32/32	0/3/3/3
2	PAU	D	6004	-	-	5/17/19/19	-
3	ADP	B	5002	-	-	3/12/32/32	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	6004	PAU	C2-C1	10.78	1.60	1.53
2	C	6002	PAU	C2-C1	9.89	1.59	1.53
2	B	6003	PAU	C2-C1	9.34	1.59	1.53
2	A	6001	PAU	C2-C1	8.79	1.59	1.53
2	A	6001	PAU	O6'-C6	5.35	1.34	1.23

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	5002	ADP	C5-C6-N6	4.05	126.51	120.35
3	C	5003	ADP	C5-C6-N6	3.95	126.36	120.35
3	A	5001	ADP	C5-C6-N6	3.65	125.90	120.35
3	D	5004	ADP	C5-C6-N6	3.59	125.81	120.35
3	D	5004	ADP	N3-C2-N1	-3.57	123.09	128.68

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	5001	ADP	PA-O3A-PB-O3B
2	C	6002	PAU	C5-C6-N-C8
2	C	6002	PAU	O6'-C6-N-C8
3	D	5004	ADP	PA-O3A-PB-O3B
2	B	6003	PAU	C5-C6-N-C8

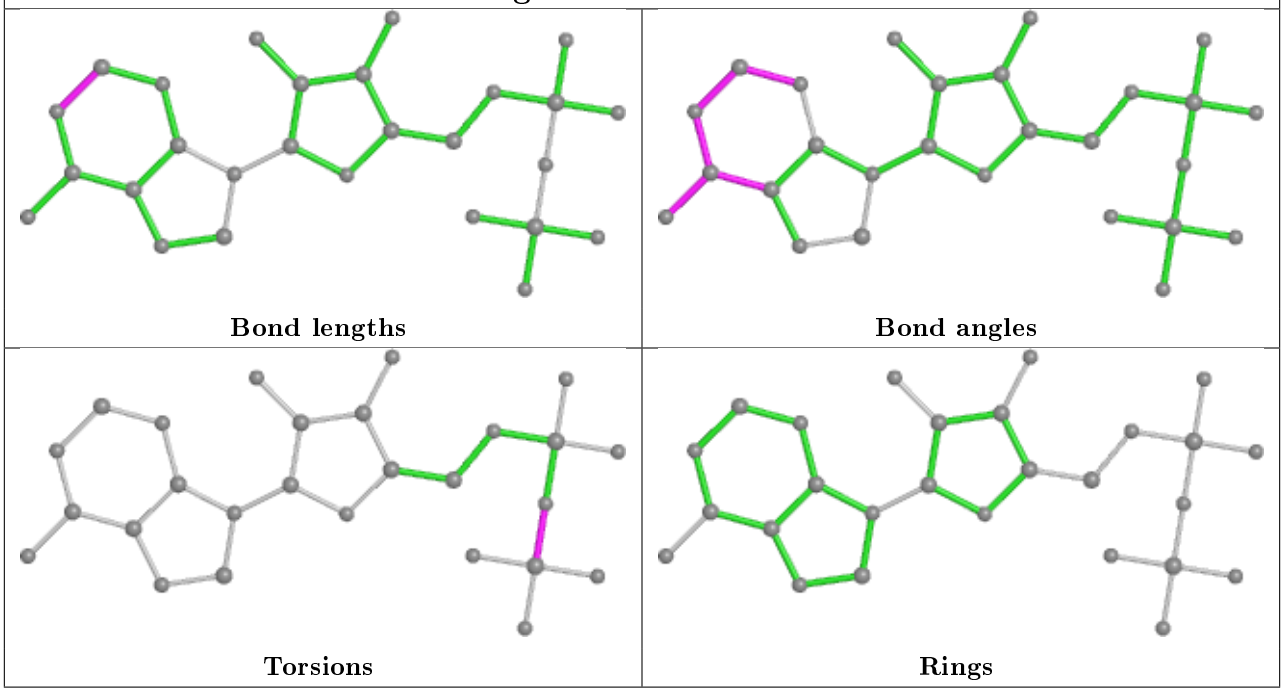
There are no ring outliers.

2 monomers are involved in 2 short contacts:

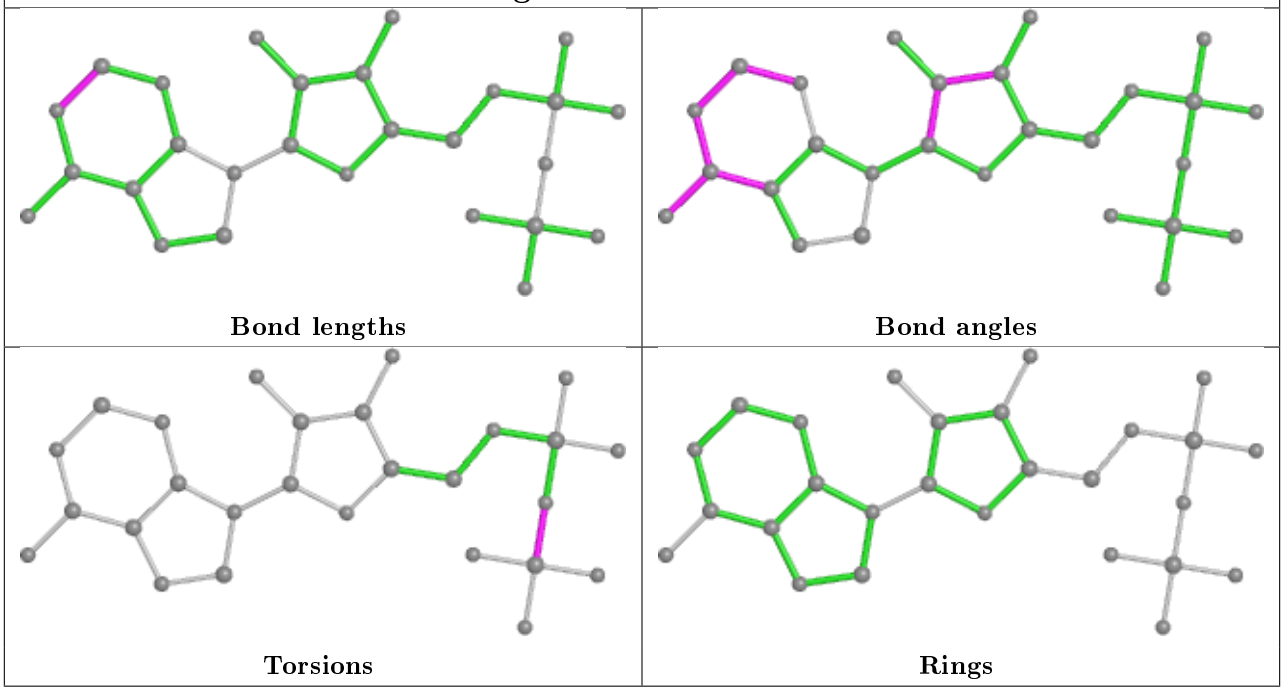
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	6002	PAU	1	0
2	D	6004	PAU	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

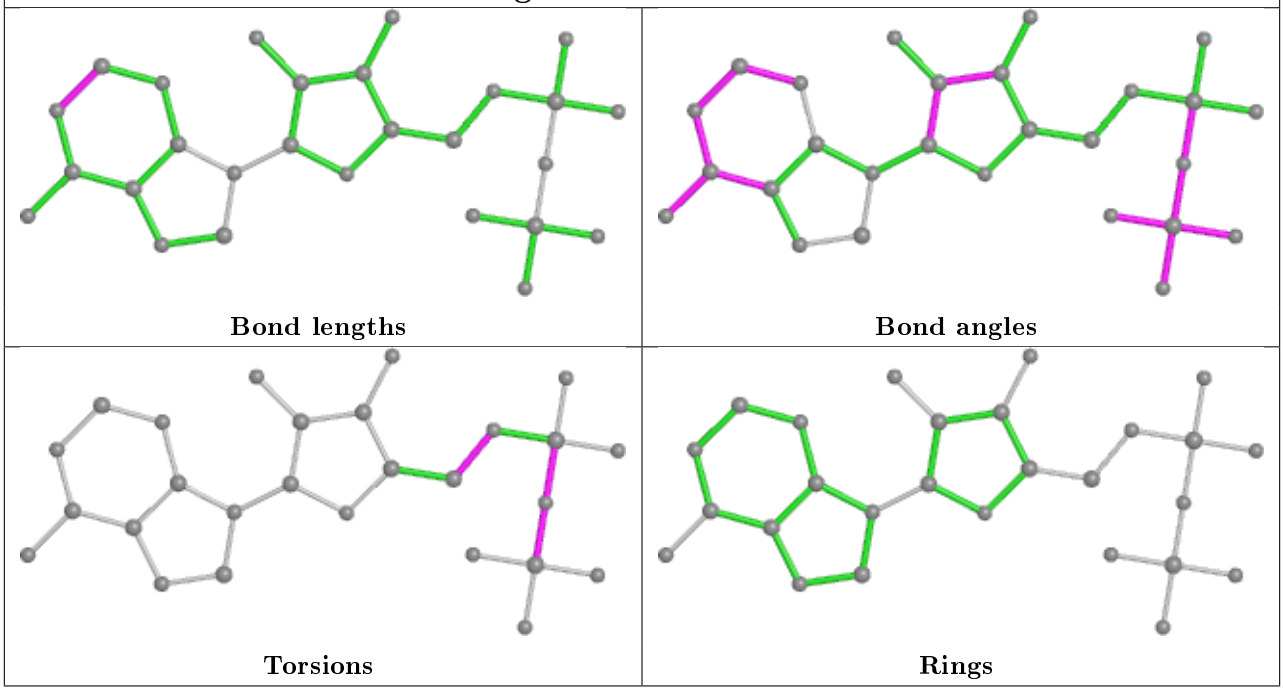
Ligand ADP A 5001



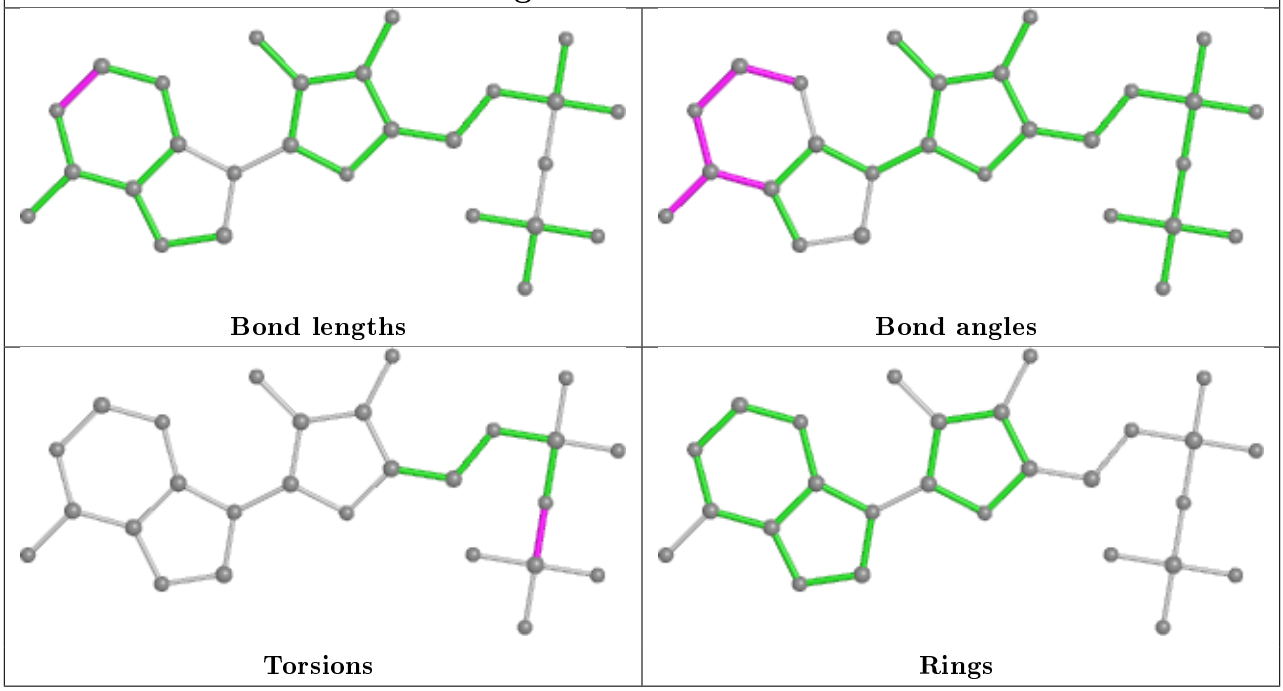
Ligand ADP D 5004



Ligand ADP C 5003



Ligand ADP B 5002



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, 95th 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^2)	Q<0.9
1	A	302/308 (98%)	-0.30	3 (0%)	82	81	15, 26, 47, 63	0
1	B	302/308 (98%)	-0.30	4 (1%)	77	75	16, 27, 47, 54	0
1	C	298/308 (96%)	-0.32	4 (1%)	77	75	14, 25, 45, 57	0
1	D	304/308 (98%)	-0.34	6 (1%)	65	63	17, 27, 49, 67	0
All	All	1206/1232 (97%)	-0.31	17 (1%)	75	73	14, 26, 48, 67	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	4184	PRO	4.0
1	C	3083	ASN	3.6
1	D	4256	ASP	2.9
1	B	2184	PRO	2.8
1	D	4083	ASN	2.7

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)

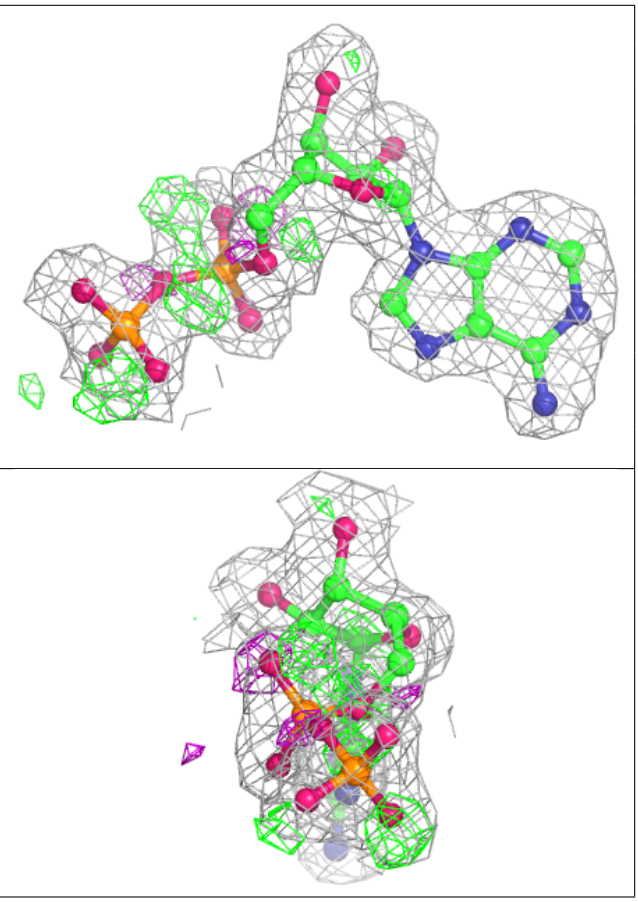
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PAU	B	6003	15/15	0.85	0.18	30,32,34,35	0
2	PAU	D	6004	15/15	0.88	0.15	30,32,34,35	0
2	PAU	C	6002	15/15	0.92	0.15	23,24,26,29	0
2	PAU	A	6001	15/15	0.93	0.14	22,24,29,29	0
3	ADP	C	5003	27/27	0.95	0.13	21,25,27,31	0
3	ADP	D	5004	27/27	0.96	0.10	21,28,33,35	0
3	ADP	A	5001	27/27	0.97	0.10	15,23,29,31	0
3	ADP	B	5002	27/27	0.97	0.09	16,21,26,26	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

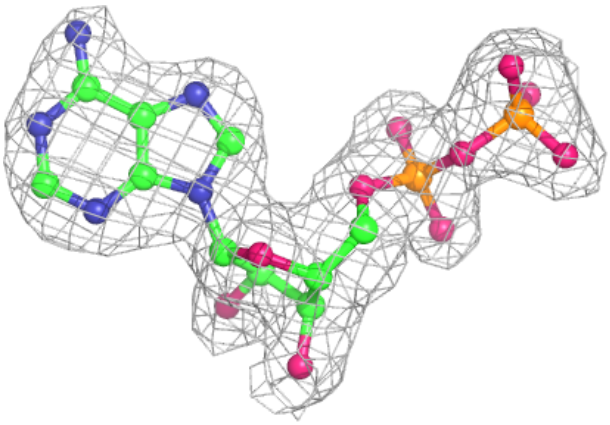
Electron density around ADP C 5003:

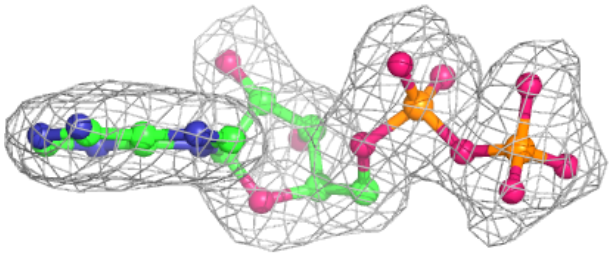
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

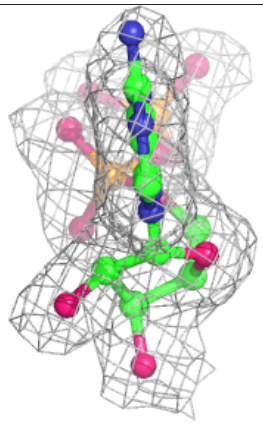


Electron density around ADP D 5004:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

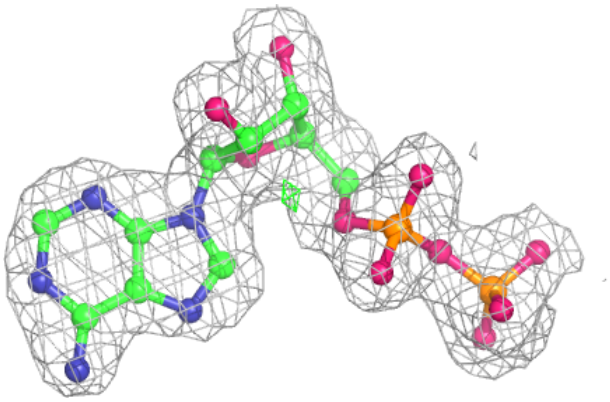


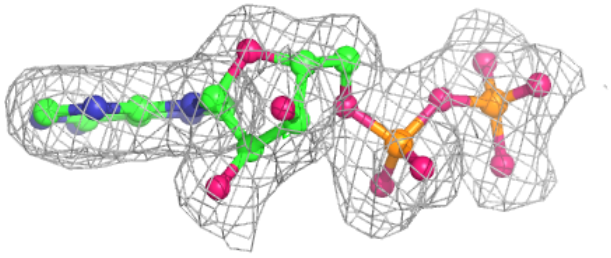


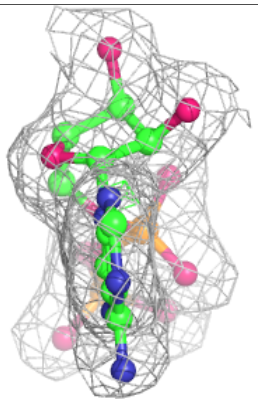


Electron density around ADP A 5001:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

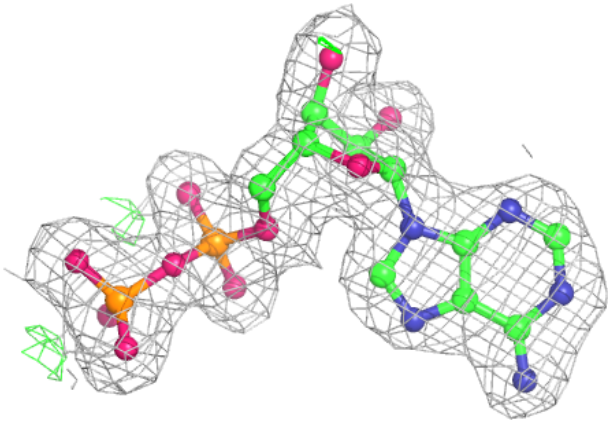


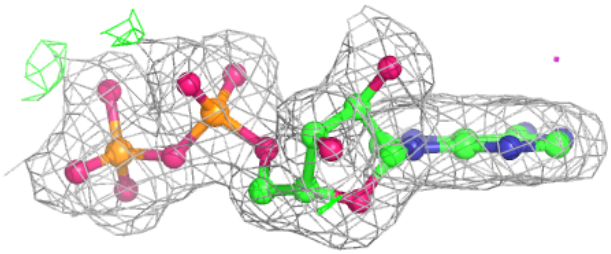


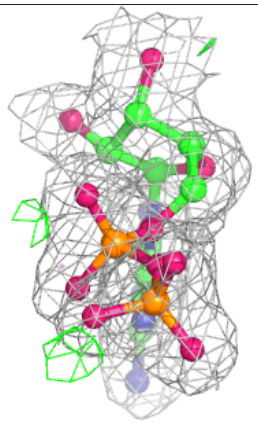


Electron density around ADP B 5002:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.