

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 5, 2024 – 09:17 AM EST

PDB ID : 2ZE6

Title : Crystal Structure of adenosine phosphate-isopentenyltransferase complexed

with substrate analog, DMASPP

Authors : Sakakibara, H. Deposited on : 2007-12-06

Resolution : 2.10 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 (i) 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 (1)) 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: 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

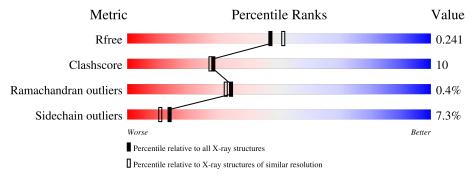
Validation Pipeline (wwPDB-VP) : 2.36

## 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 2.10 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	Similar resolution			
Wictiic	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$			
$R_{free}$	130704	5197 (2.10-2.10)			
Clashscore	141614	5710 (2.10-2.10)			
Ramachandran outliers	138981	5647 (2.10-2.10)			
Sidechain outliers	138945	5648 (2.10-2.10)			

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%

Mol	Chain	Length	Quality of chain			
1	A	253	67%	19%	·	10%



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1899 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 Isopentenyl transferase.

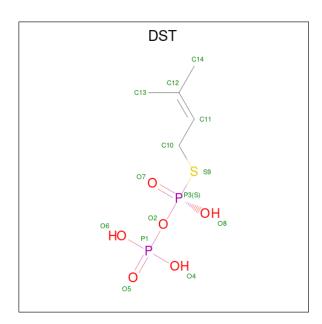
$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	227	Total 1824	C 1151	N 328	O 336	S 9	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	GLY	-	expression tag	UNP P58758
A	245	SER	-	expression tag	UNP P58758
A	246	ARG	-	expression tag	UNP P58758
A	247	SER	-	expression tag	UNP P58758
A	248	HIS	-	expression tag	UNP P58758
A	249	HIS	-	expression tag	UNP P58758
A	250	HIS	_	expression tag	UNP P58758
A	251	HIS	-	expression tag	UNP P58758
A	252	HIS	-	expression tag	UNP P58758
A	253	HIS	-	expression tag	UNP P58758

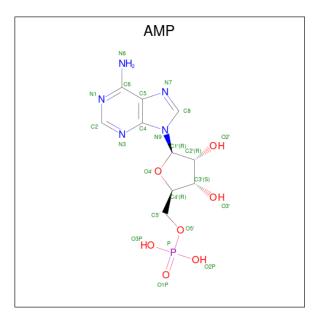
• Molecule 2 is DIMETHYLALLYL S-THIOLODIPHOSPHATE (three-letter code: DST) (formula:  $C_5H_{12}O_6P_2S$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	С	O	P	S	0	0
			14	5	6	2	1		

 $\bullet \ \ Molecule\ 3\ is\ ADENOSINE\ MONOPHOSPHATE\ (three-letter\ code:\ AMP)\ (formula:\ C_{10}H_{14}N_5O_7P).$ 



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
9	Λ	1	Total	С	N	О	Р	0	0
3	A	1	23	10	5	7	1	U	0

• Molecule 4 is water.



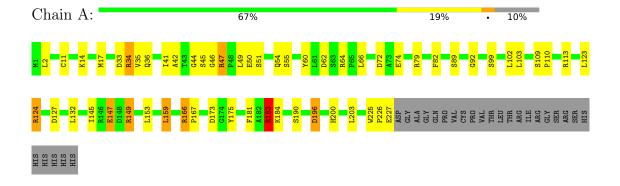
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	38	Total O 38 38	0	0



## 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.

• Molecule 1: Isopentenyl transferase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants	96.42Å 96.42Å 65.07Å	Donositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.20 - 2.10	Depositor
Resolution (A)	47.07 - 2.31	EDS
% Data completeness	98.3 (68.20-2.10)	Depositor
(in resolution range)	98.1 (47.07-2.31)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.15 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.196 , 0.264	Depositor
$R, R_{free}$	0.243 , $0.241$	DCC
$R_{free}$ test set	682 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage
Anisotropy	0.567	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.32, 49.7	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	1899	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



 $<sup>^1 {\</sup>rm Intensities}$  estimated from amplitudes.

## 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: AMP, DST

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	Boı	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	1.24	5/1865~(0.3%)	1.33	$13/2526 \ (0.5\%)$	

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
1	A	50	GLU	CG-CD	5.72	1.60	1.51
1	A	183	ARG	CB-CG	5.61	1.67	1.52
1	A	82	PHE	CE1-CZ	5.55	1.47	1.37
1	A	11	CYS	CB-SG	5.50	1.91	1.82
1	A	50	GLU	CD-OE2	5.29	1.31	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	47	ARG	NE-CZ-NH1	26.26	133.43	120.30
1	A	47	ARG	NE-CZ-NH2	-19.44	110.58	120.30
1	A	47	ARG	CD-NE-CZ	8.97	136.16	123.60
1	A	166	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	A	66	LEU	CA-CB-CG	6.37	129.95	115.30
1	A	159	LEU	CA-CB-CG	5.91	128.90	115.30
1	A	17	MET	CG-SD-CE	-5.77	90.96	100.20
1	A	183	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	173	ASP	CB-CG-OD1	5.35	123.11	118.30
1	A	34	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	145	ILE	CB-CA-C	-5.19	101.22	111.60
1	A	46	GLY	N-CA-C	5.08	125.80	113.10
1	A	79	ARG	NE-CZ-NH2	-5.08	117.76	120.30

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	1824	0	1805	34	0
2	A	14	0	10	1	0
3	A	23	0	11	4	0
4	A	38	0	0	1	0
All	All	1899	0	1826	36	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 10.

All (36) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + 1	A 4 a 2	Interatomic	Clash	
Atom-1	Atom-2	${\rm distance}\ (\mathring{\rm A})$	overlap (Å)	
3:A:401:AMP:H5'2	3:A:401:AMP:C8	2.02	0.95	
3:A:401:AMP:H5'2	3:A:401:AMP:H8	1.37	0.88	
1:A:124:ARG:HH11	1:A:124:ARG:CG	1.95	0.79	
1:A:34:ARG:HH21	3:A:401:AMP:H5'1	1.54	0.73	
1:A:42:ALA:HA	1:A:47:ARG:HD3	1.71	0.72	
1:A:99:SER:O	1:A:103:LEU:HD12	1.90	0.72	
1:A:124:ARG:HH11	1:A:124:ARG:HG2	1.57	0.70	
1:A:147:GLU:H	1:A:147:GLU:CD	1.99	0.65	
1:A:47:ARG:HG2	1:A:60:TYR:OH	1.99	0.62	
1:A:166:ARG:HB2	1:A:167:PRO:HD3	1.84	0.60	
1:A:49:LEU:CD2	1:A:149:ARG:HG2	2.33	0.58	
1:A:72:ASP:OD2	1:A:74:GLU:HG2	2.07	0.55	
1:A:124:ARG:HG2	1:A:124:ARG:NH1	2.23	0.54	
1:A:54:GLN:O	1:A:55:SER:HB2	2.13	0.49	
1:A:127:ASP:HB3	4:A:411:HOH:O	2.12	0.48	
1:A:110:PRO:HA	1:A:113:ARG:HG3	1.95	0.48	
1:A:181:PHE:CG	1:A:203:LEU:HD13	2.49	0.48	
1:A:34:ARG:NH2	3:A:401:AMP:H5'1	2.27	0.48	
1:A:33:ASP:CG	1:A:36:GLN:HG3	2.35	0.47	
1:A:124:ARG:HH11	1:A:124:ARG:HG3	1.75	0.46	
1:A:49:LEU:HD22	1:A:149:ARG:HG2	1.98	0.46	
1:A:62:ASP:OD1	1:A:64:ARG:HD2	2.17	0.45	
1:A:41:ILE:O	1:A:42:ALA:C	2.54	0.44	

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Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance}\left( \mathrm{\AA}\right)$	overlap (Å)
1:A:109:SER:HA	1:A:110:PRO:HD3	1.67	0.44
1:A:166:ARG:HB2	1:A:167:PRO:CD	2.47	0.44
1:A:44:GLY:HA3	1:A:175:TYR:OH	2.17	0.44
1:A:14:LYS:NZ	2:A:400:DST:O8	2.42	0.43
1:A:225:TRP:CD1	1:A:226:PRO:HD2	2.52	0.43
1:A:153:LEU:HD23	1:A:153:LEU:HA	1.79	0.42
1:A:64:ARG:HD2	1:A:64:ARG:HH11	1.78	0.41
1:A:2:LEU:O	1:A:92:GLY:HA2	2.20	0.41
1:A:183:ARG:CG	1:A:183:ARG:HH11	2.33	0.41
1:A:147:GLU:CD	1:A:147:GLU:N	2.68	0.41
1:A:35:VAL:HG12	1:A:45:SER:HB2	2.02	0.41
1:A:99:SER:HB3	1:A:102:LEU:HB3	2.03	0.40
1:A:183:ARG:HH11	1:A:183:ARG:HG2	1.86	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	225/253~(89%)	220 (98%)	4 (2%)	1 (0%)	34	32

#### All (1) Ramachandran outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type
1	A	196	ASP

#### 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	193/215 (90%)	179 (93%)	14 (7%)	14 11	

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	SER
1	A	89	SER
1	A	123	LEU
1	A	124	ARG
1	A	132	LEU
1	A	147	GLU
1	A	149	ARG
1	A	159	LEU
1	A	183	ARG
1	A	184	LYS
1	A	190	SER
1	A	196	ASP
1	A	200	HIS
1	A	227	GLU

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

Mol	Chain	Res	Type
1	A	4	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 monosaccharides 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).

Mal	Type Chain		in Res	s Link	Bond lengths			Bond angles		
Mol	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
3	AMP	A	401	-	22,25,25	1.73	6 (27%)	25,38,38	3.12	14 (56%)
2	DST	A	400	-	9,13,13	1.12	0	11,19,19	2.32	2 (18%)

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.

$\mathbf{Mol}$	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
3	AMP	A	401	-	-	4/6/26/26	0/3/3/3
2	DST	A	400	-	-	0/7/13/13	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$Ideal(\AA)$
3	A	401	AMP	C2-N3	3.25	1.37	1.32
3	A	401	AMP	O3'-C3'	-3.25	1.35	1.43
3	A	401	AMP	C5-C4	3.17	1.49	1.40
3	A	401	AMP	C2'-C1'	-2.67	1.49	1.53
3	A	401	AMP	P-O3P	-2.51	1.45	1.54
3	A	401	AMP	O4'-C1'	2.14	1.44	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	A	401	AMP	C5'-C4'-C3'	-6.62	90.36	115.18
3	A	401	AMP	O2P-P-O5'	-6.46	89.55	106.73
2	A	400	DST	O8-P3-O7	5.92	124.16	109.82
3	A	401	AMP	O3'-C3'-C4'	-5.00	96.59	111.05
3	A	401	AMP	C2'-C3'-C4'	4.48	111.35	102.64

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
3	A	401	AMP	O3P-P-O5'	4.08	117.59	106.73
3	A	401	AMP	C3'-C2'-C1'	-3.84	95.19	100.98
3	A	401	AMP	C2-N1-C6	3.71	125.10	118.75
2	A	400	DST	O4-P1-O5	3.61	124.80	110.68
3	A	401	AMP	O4'-C1'-C2'	3.16	111.55	106.93
3	A	401	AMP	C5-C6-N6	3.09	125.05	120.35
3	A	401	AMP	N3-C2-N1	-3.08	123.86	128.68
3	A	401	AMP	C1'-N9-C4	-2.82	121.68	126.64
3	A	401	AMP	C4-C5-N7	-2.67	106.62	109.40
3	A	401	AMP	P-O5'-C5'	-2.65	111.00	118.30
3	A	401	AMP	C5-C6-N1	-2.04	115.74	120.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	AMP	C5'-O5'-P-O1P
3	A	401	AMP	O4'-C4'-C5'-O5'
3	A	401	AMP	C3'-C4'-C5'-O5'
3	A	401	AMP	C5'-O5'-P-O2P

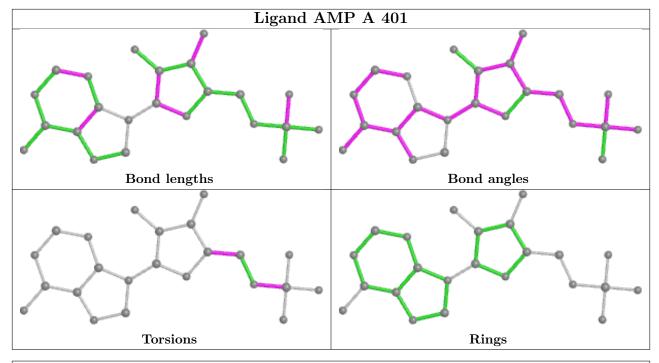
There are no ring outliers.

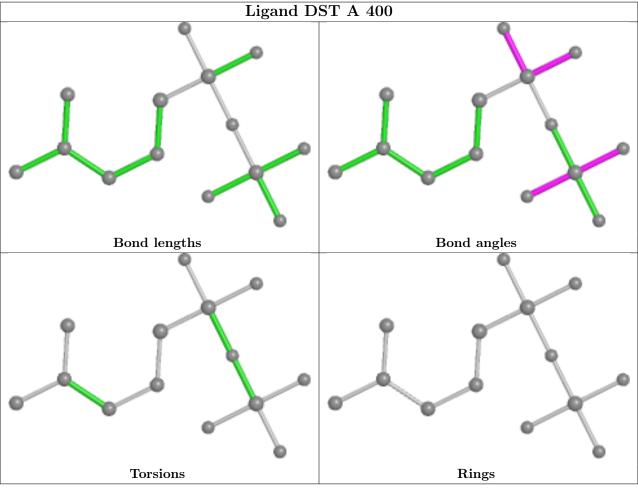
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	AMP	4	0
2	A	400	DST	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.









## 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)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

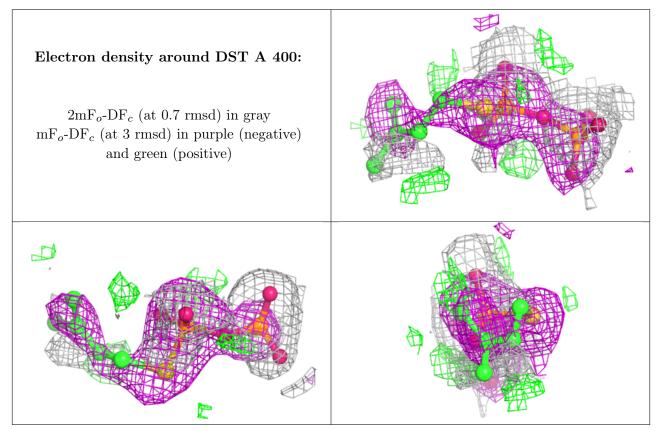
## 6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

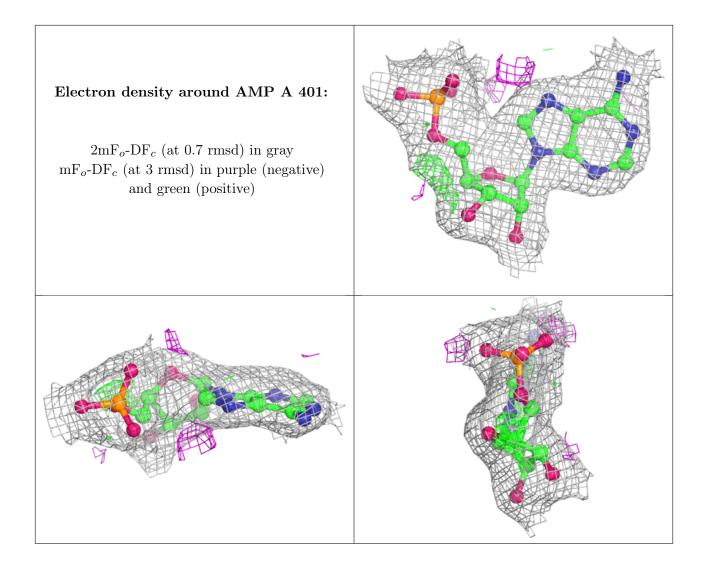
## 6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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.







## 6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

