Full wwPDB X-ray Structure Validation Report (i)

Dec 3, 2023 – 09:12 pm GMT

PDB ID	:	1WC4
Title	:	Soluble adenylyl cyclase CyaC from S. platensis in complex with alpha, beta-methylene-ATP and Europium
Authors	:	Steegborn, C.; Litvin, T.N.; Levin, L.R.; Buck, J.; Wu, H.
Deposited on	:	2004-11-08
Resolution	:	3.00 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 (i)) were used in the production of this report:

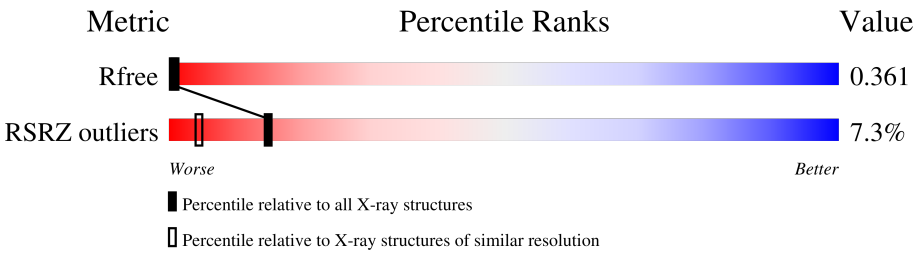
MolProbity	:	FAILED
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 3.00 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	2092 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

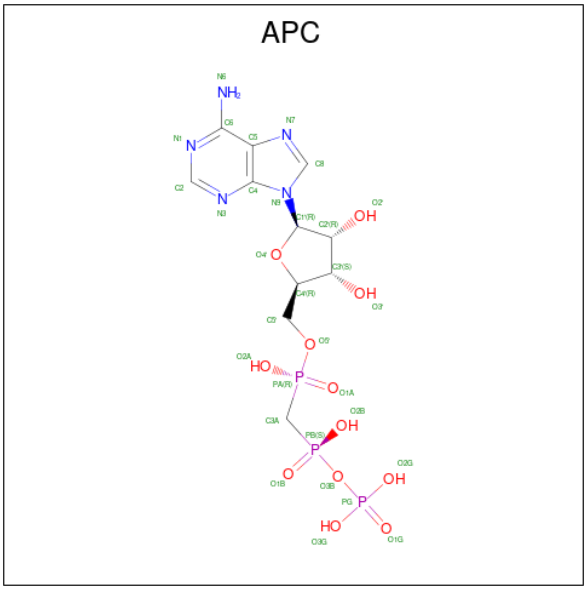
There are 4 unique types of molecules in this entry. The entry contains 3107 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ADENYLATE CYCLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	200	1537	964	271	289	13	0	0	1
1	B	196	1504	946	264	281	13	0	0	1

- Molecule 2 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	31	11	5	12	3	0	0
2	B	1	31	11	5	12	3	0	0

- Molecule 3 is EUROPIUM (III) ION (three-letter code: EU3) (formula: Eu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Eu		
3	A	1	1	1	0	0
3	B	1	1	1	0	0

- Molecule 4 is water.

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

MolProbity failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	53.60Å 70.20Å 99.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.91 – 3.00 19.70 – 2.97	Depositor EDS
% Data completeness (in resolution range)	71.1 (14.91-3.00) 90.3 (19.70-2.97)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.21 (at 2.98Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.274 , 0.315 0.311 , 0.361	Depositor DCC
R_{free} test set	598 reflections (7.46%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	1.013	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 6.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.84	EDS
Total number of atoms	3107	wwPDB-VP
Average B, all atoms (Å^2)	10.0	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 50.29 % 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 6.6105e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	APC	A	1500	-	27,33,33	1.61	6 (22%)	31,52,52	1.08	3 (9%)
2	APC	B	1500	-	27,33,33	1.22	4 (14%)	31,52,52	1.27	3 (9%)

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	APC	A	1500	-	-	2/15/38/38	0/3/3/3
2	APC	B	1500	-	-	3/15/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1500	APC	PB-O3B	4.53	1.63	1.58
2	A	1500	APC	O4'-C1'	2.99	1.45	1.41
2	A	1500	APC	C2-N1	2.99	1.39	1.33
2	A	1500	APC	C8-N7	-2.68	1.29	1.34
2	B	1500	APC	C8-N7	-2.57	1.30	1.34
2	B	1500	APC	O4'-C1'	2.41	1.44	1.41
2	B	1500	APC	C2-N1	2.29	1.38	1.33
2	A	1500	APC	C2-N3	2.08	1.35	1.32
2	B	1500	APC	PA-O1A	2.01	1.56	1.51
2	A	1500	APC	PA-O5'	2.01	1.60	1.57

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1500	APC	PB-O3B-PG	-4.34	117.32	132.62
2	A	1500	APC	PB-O3B-PG	-3.22	121.28	132.62
2	B	1500	APC	C4-C5-N7	2.70	112.22	109.40
2	A	1500	APC	C4-C5-N7	2.64	112.16	109.40
2	B	1500	APC	C3'-C2'-C1'	2.41	104.60	100.98
2	A	1500	APC	C3'-C2'-C1'	2.17	104.25	100.98

There are no chirality outliers.

All (5) torsion outliers are listed below:

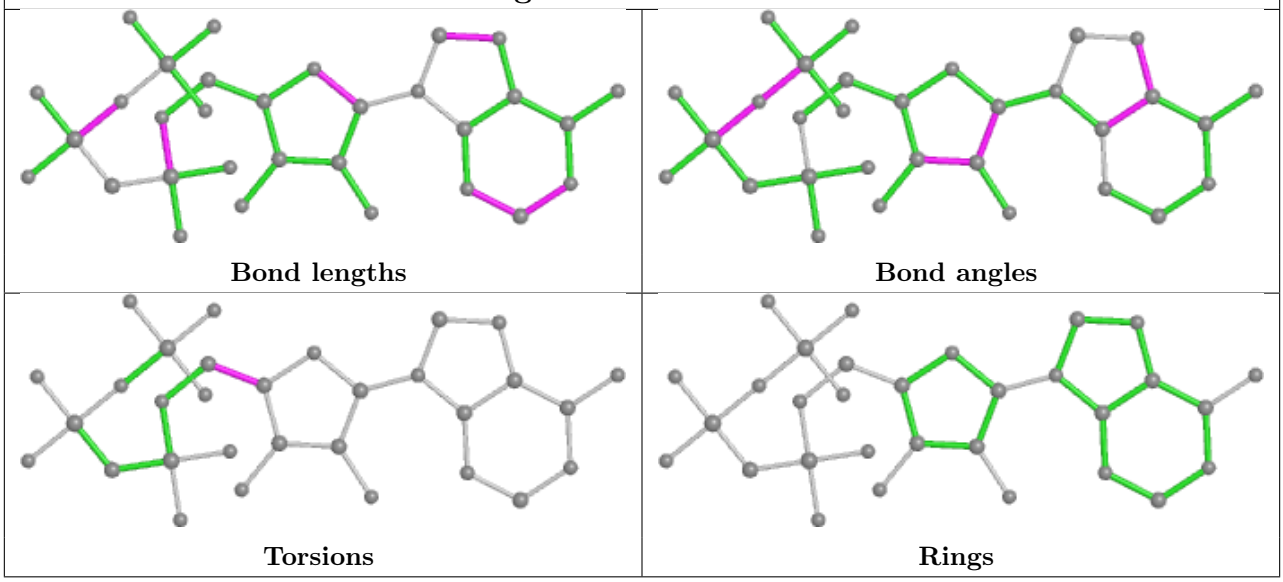
Mol	Chain	Res	Type	Atoms
2	A	1500	APC	O4'-C4'-C5'-O5'
2	B	1500	APC	O4'-C4'-C5'-O5'
2	B	1500	APC	C3'-C4'-C5'-O5'
2	A	1500	APC	C3'-C4'-C5'-O5'
2	B	1500	APC	C4'-C5'-O5'-PA

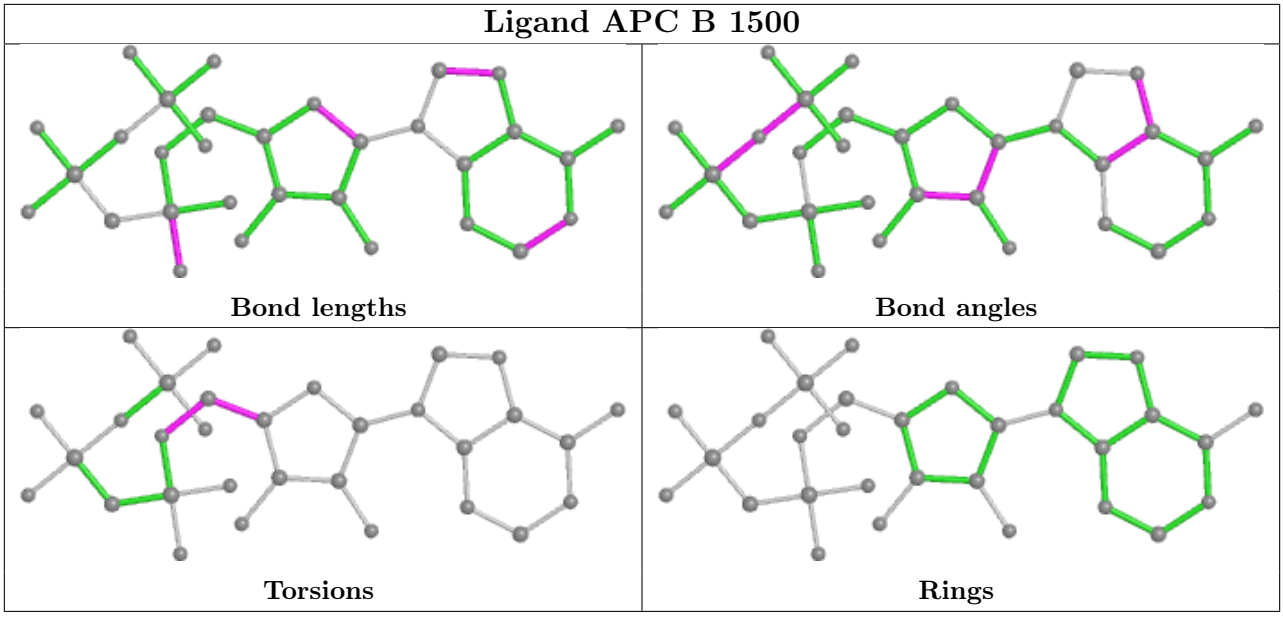
There are no ring outliers.

No monomer is involved in short contacts.

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 APC A 1500





4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data (i)

5.1 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	200/219 (91%)	0.48	15 (7%)	14	4	11, 11, 11, 11	0
1	B	196/219 (89%)	0.45	14 (7%)	16	5	11, 11, 11, 11	0
All	All	396/438 (90%)	0.47	29 (7%)	15	4	11, 11, 11, 11	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1020	GLY	5.1
1	A	1021	PHE	4.0
1	B	1024	MET	3.9
1	A	1187	ASP	3.6
1	A	1031	GLN	3.4
1	B	1023	ARG	3.3
1	B	1021	PHE	2.9
1	A	1109	ASN	2.9
1	B	1098	GLN	2.8
1	A	1020	GLY	2.8
1	B	1027	ALA	2.7
1	B	1026	ASN	2.6
1	B	1025	SER	2.6
1	A	1023	ARG	2.5
1	A	1027	ALA	2.5
1	B	1031	GLN	2.5
1	A	1030	SER	2.4
1	A	1184	LYS	2.4
1	A	1188	GLU	2.4
1	B	1005	ARG	2.4
1	B	1186	ILE	2.3
1	B	1007	GLU	2.3
1	B	1134	GLU	2.2
1	A	1025	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1024	MET	2.1
1	A	1185	GLY	2.1
1	B	1030	SER	2.1
1	A	1101	GLN	2.1
1	A	1004	MET	2.0

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

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

5.3 Carbohydrates (i)

There are no monosaccharides in this entry.

5.4 Ligands (i)

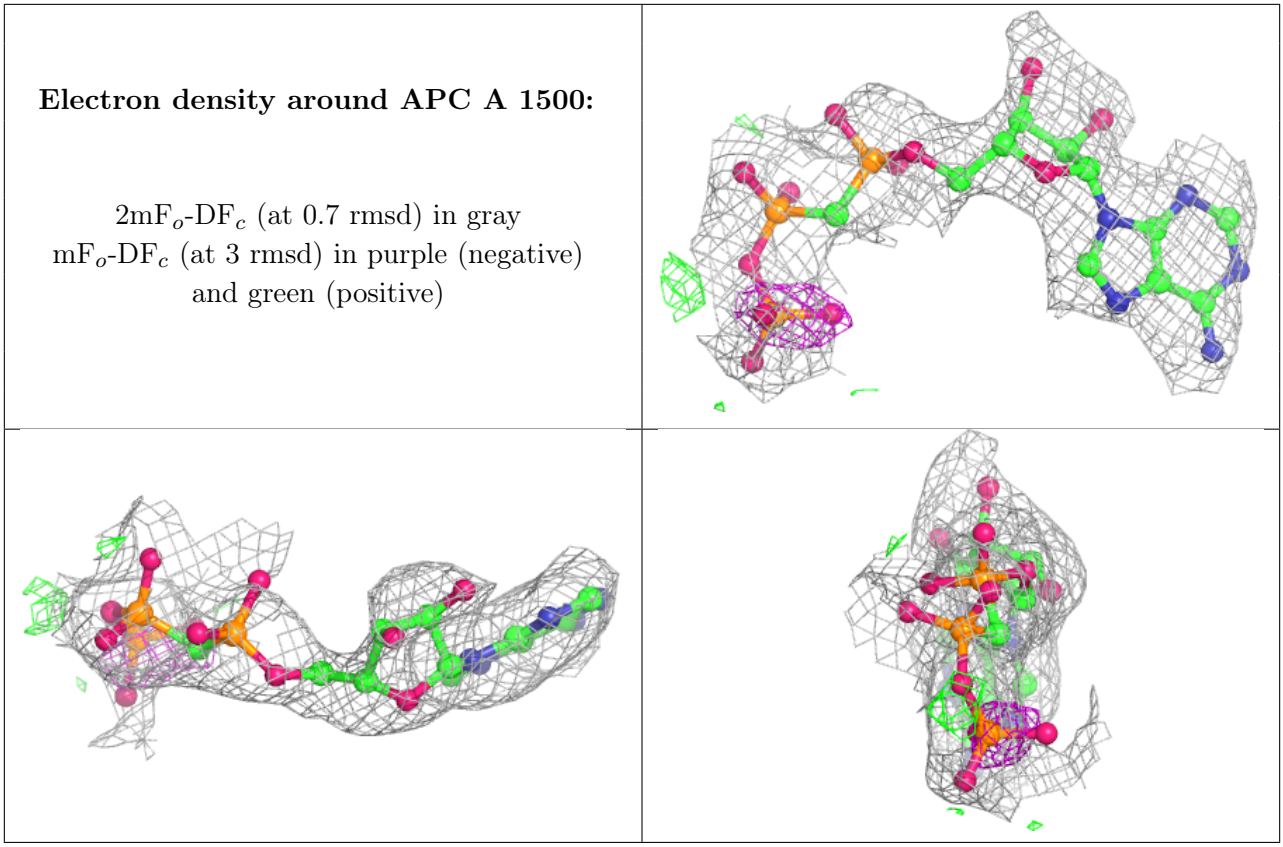
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	APC	A	1500	31/31	0.86	0.22	10,10,10,10	0
2	APC	B	1500	31/31	0.88	0.22	10,10,10,10	0
3	EU3	A	2100	1/1	0.99	0.02	10,10,10,10	0
3	EU3	B	2100	1/1	0.99	0.03	10,10,10,10	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.

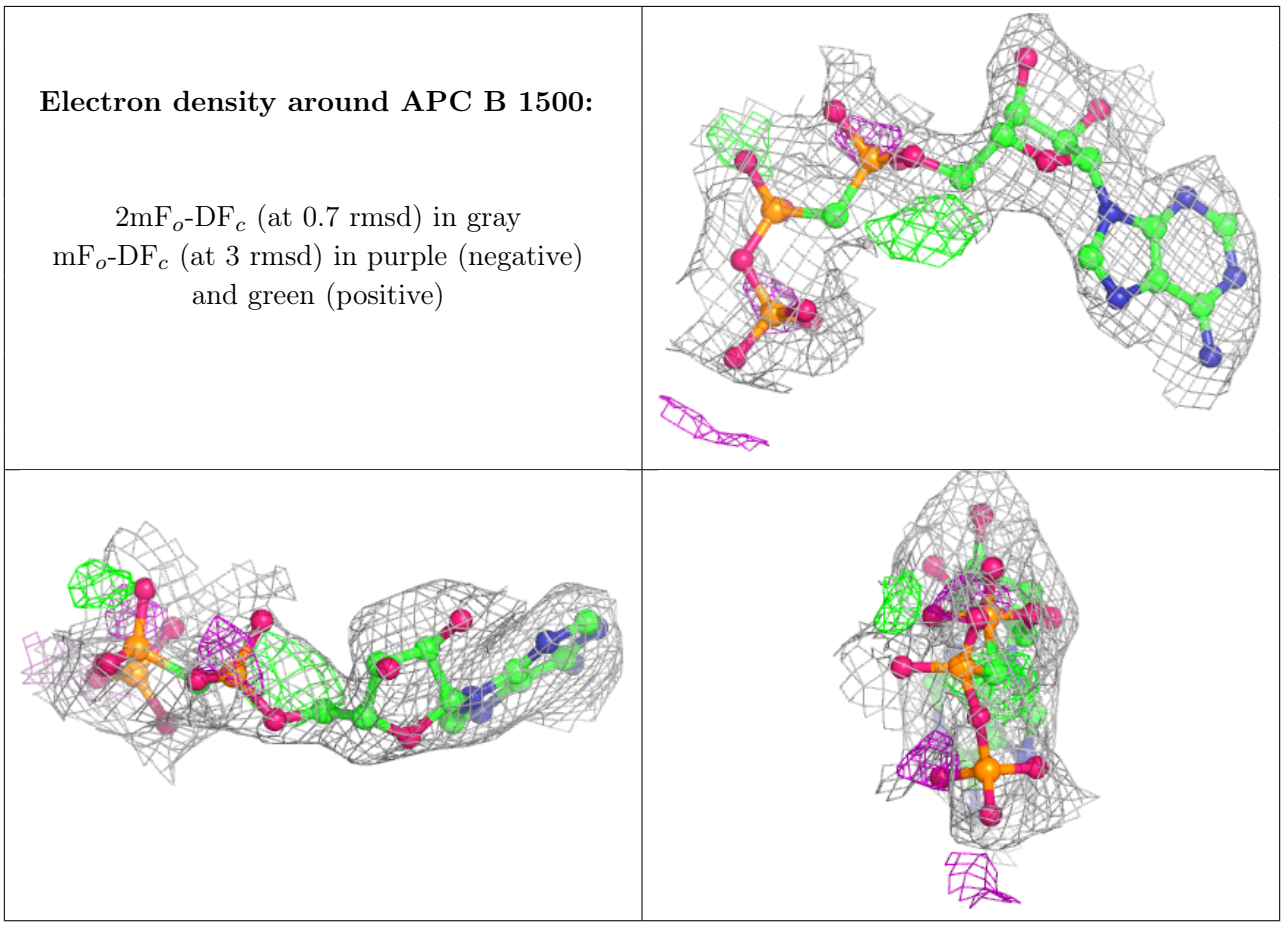
Electron density around APC A 1500:

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



Electron density around APC B 1500:

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



5.5 Other polymers (i)

There are no such residues in this entry.