



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:15 PM UTC

PDB ID : 1II9 / pdb_00001ii9
Title : CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI ARSENITE-TRANSLOCATING ATPASE IN COMPLEX WITH AMP-PNP
Authors : Zhou, T.; Radaev, S.; Gatti, D.L.; Rosen, B.P.
Deposited on : 2001-04-21
Resolution : 2.60 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

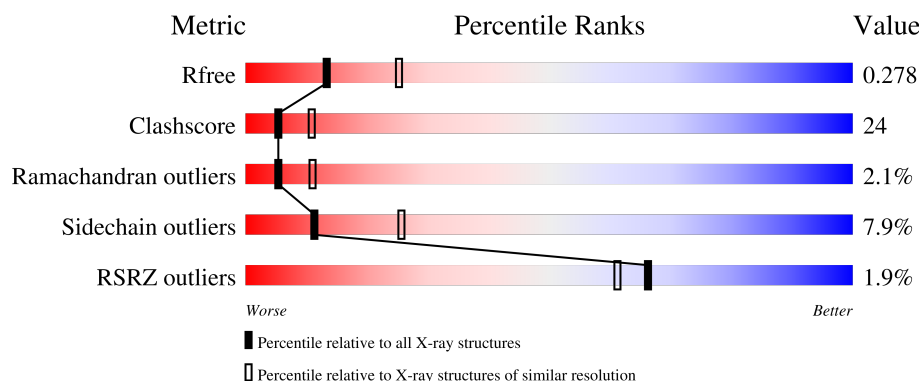
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 $\leq 5\%$. 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	589	
1	B	589	

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
7	TAS	A	701	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8786 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 ARSENICAL PUMP-DRIVING ATPASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	544	Total	C	N	O	S	0	0	0
			4163	2620	738	790	15			
1	B	550	Total	C	N	O	S	0	0	0
			4202	2641	744	802	15			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	ASN	ILE	SEE REMARK 999	UNP P08690
A	584	HIS	-	expression tag	UNP P08690
A	585	HIS	-	expression tag	UNP P08690
A	586	HIS	-	expression tag	UNP P08690
A	587	HIS	-	expression tag	UNP P08690
A	588	HIS	-	expression tag	UNP P08690
A	589	HIS	-	expression tag	UNP P08690
B	1060	ASN	ILE	SEE REMARK 999	UNP P08690
B	1584	HIS	-	expression tag	UNP P08690
B	1585	HIS	-	expression tag	UNP P08690
B	1586	HIS	-	expression tag	UNP P08690
B	1587	HIS	-	expression tag	UNP P08690
B	1588	HIS	-	expression tag	UNP P08690
B	1589	HIS	-	expression tag	UNP P08690

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		

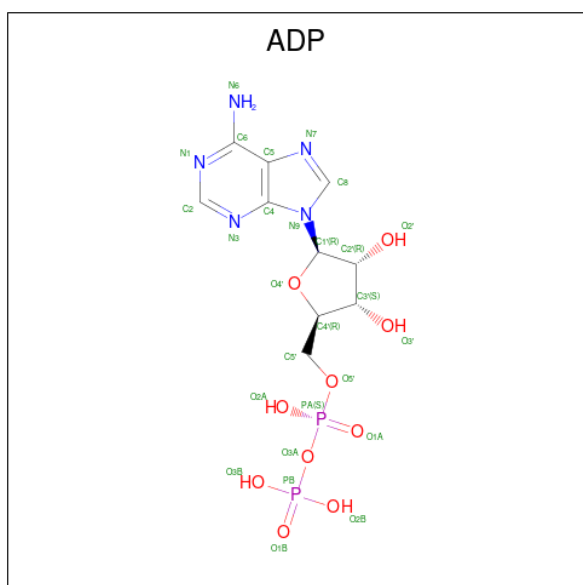
- Molecule 3 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	Cd	0	0
			9	9		
3	B	9	Total	Cd	0	0
			9	9		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

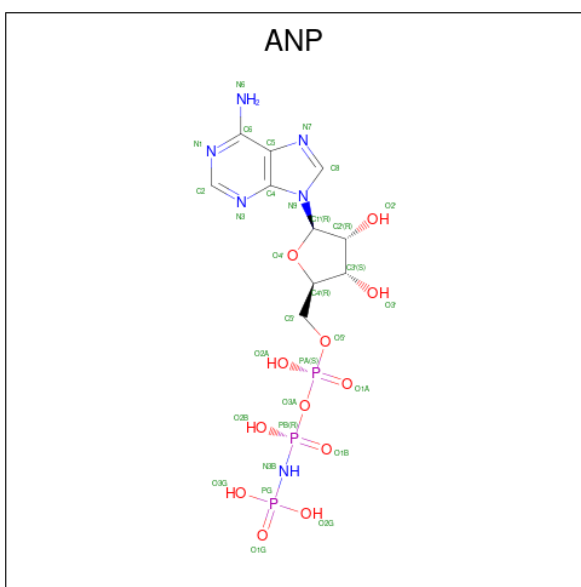
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Cl	0	0
			4	4		
4	B	3	Total	Cl	0	0
			3	3		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



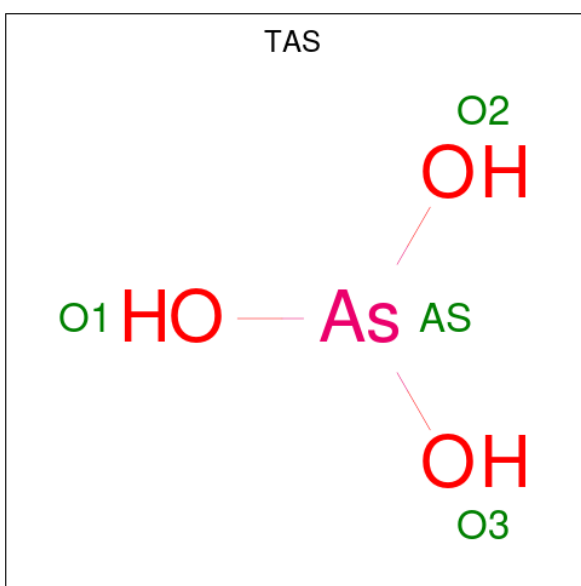
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
5	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 6 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
6	B	1	Total 31	C 10	N 6	O 12	P 3	0	0

- Molecule 7 is TRIHYDROXYARSENITE(III) (CCD ID: TAS) (formula: AsH_3O_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 4	As 1	O 3	0	0
7	B	1	Total 4	As 1	O 3	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	143	Total 143	O 143	0	0
8	B	125	Total 125	O 125	0	0

L1201	V1202	L1203	V1204	A1205	R1206	L1207	Q1208	K1209	S1210	T1211	L1212	Q1213	E1214	V1215	A1216	R1217	E1221	T1225	G1226	L1227	Q1230	Y1231	I1234	N1235	G1236	V1237	L1238	P1239	K1240	T1241	E1242	N1245	D1246	I1252	W1253	E1256	Q1257	L1260	A1261	N1262	L1263	P1264	L1267	L1270	P1271	T1272	D1273	T1274	L1275		
F1276	P1279	M1282	V1283	G1284	V1285	L1288	S1289	R1290	L1291	ASN	L1292	S1293	T1294	Q1295	PRO	VAL	ALA	SER	PRO	SER	SER	ASP	GLU	TYR	LEU	Q1307	Q1308	I1312	L1315	L1318	V1319	I1322	A1323	R1324	I1330	M1331	L1332	M1333	M1343	A1344	V1349	R1350	L1351	M1354	D1357	V1358	H1359	L1360			
T1361	D1364	P1365	A1366	A1367	HIS	LEU	SER	MET	THR	LEU	ASN	GLY	SER	L1377	N1378	N1379	L1380	Q1381	R1384	I1385	Y1394	R1395	Q1396	H1397	V1398	L1399	E1400	T1401	K1402	G1403	K1404	E1405	L1406	K1411	L1414	E1415	E1416	D1417	L1418	R1419	S1420	I1426	Q1430	A1431	F1432	S1433	R1434	V1435	I1436	R1437	K1441
R1442	F1443	M1446	A1449	L1455	L1456	L1457	A1460	T1461	GLY	ALA	TYR	HIS	ARG	GLU	ILE	ALA	LYS	LYS	MET	GLY	GLU	LYS	GLY	HIS	PHE	T1479	T1480	P1481	M1482	A1489	Q1486	D1487	P1488	E1489	L1495	V1496	T1497	L1498	T1502	P1503	V1504	L1505	L1510	L1514	E1515	R1516	A1517	W1522	T1526		
L1530	S1531	I1532	T1535	R1536	S1537	M1542	Q1545	Q1546	E1547	L1548	P1549	Q1550	I1551	E1552	S1553	V1554	K1555	R1556	Q1557	H1558	A1559	S1560	R1561	L1564	V1565	P1566	V1567	L1568	A1569	S1570	E1571	P1572	T1573	G1574	I1575	D1576	K1577	L1578	K1579	Q1580	L1581	A1582	G1583	H1584	H1585	H1588	H1589				

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	76.62Å 222.53Å 74.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.52 – 2.60 36.52 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.5 (36.52-2.60) 93.5 (36.52-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.191 , 0.265 (Not available) , 0.278	Depositor DCC
R_{free} test set	3730 reflections (9.71%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8786	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CL, MG, ANP, CD, ADP, TAS

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	0.55	0/4233	1.03	19/5752 (0.3%)
1	B	0.55	0/4271	1.01	15/5803 (0.3%)
All	All	0.55	0/8504	1.02	34/11555 (0.3%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1054	PHE	N-CA-C	-7.60	102.55	108.78
1	A	419	ARG	N-CA-C	-7.55	103.18	113.30
1	B	1406	LEU	N-CA-C	-7.47	95.98	108.75
1	A	39	VAL	N-CA-C	7.06	118.29	108.12
1	B	1419	ARG	N-CA-C	-7.03	103.81	112.88

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	4163	0	4226	217	0
1	B	4202	0	4259	194	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	9	0	0	0	0
3	B	9	0	0	0	0
4	A	4	0	0	1	0
4	B	3	0	0	0	0
5	A	27	0	12	5	0
5	B	27	0	12	2	0
6	A	31	0	13	2	0
6	B	31	0	13	0	0
7	A	4	0	0	2	0
7	B	4	0	0	0	0
8	A	143	0	0	3	0
8	B	125	0	0	6	0
All	All	8786	0	8535	409	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 24.

The worst 5 of 409 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:27:ALA:HB1	1:A:292:LEU:HD21	1.27	1.10
1:A:248:LEU:HD23	1:A:535:THR:HB	1.38	1.02
1:B:1322:ILE:HD13	1:B:1330:ILE:HD11	1.42	1.01
1:B:1209:LYS:HG2	1:B:1213:GLN:HE21	1.26	0.99
1:A:235:ASN:HD21	5:A:590:ADP:HN61	1.02	0.95

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	534/589 (91%)	488 (91%)	35 (7%)	11 (2%)	5	11
1	B	540/589 (92%)	495 (92%)	33 (6%)	12 (2%)	5	10
All	All	1074/1178 (91%)	983 (92%)	68 (6%)	23 (2%)	5	11

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	VAL
1	A	570	SER
1	B	1262	ASN
1	B	1293	SER
1	A	404	LYS

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	451/487 (93%)	415 (92%)	36 (8%)	11	25
1	B	455/487 (93%)	419 (92%)	36 (8%)	11	26
All	All	906/974 (93%)	834 (92%)	72 (8%)	11	26

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1399	LEU
1	B	1568	LEU
1	B	1414	LEU
1	B	1503	PRO
1	A	455	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1325	ASN

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Mol	Chain	Res	Type
1	B	1557	GLN
1	B	1379	ASN
1	B	1486	GLN
1	A	486	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 35 ligands modelled in this entry, 29 are monoatomic - leaving 6 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	$\# Z > 2$
6	ANP	B	1591	2	33,33,33	1.14	5 (15%)	45,52,52	3.45	19 (42%)
5	ADP	B	1590	2	28,29,29	1.21	2 (7%)	43,45,45	3.48	23 (53%)
7	TAS	A	701	-	0,3,3	-	-	0,3,3	-	-
7	TAS	B	1701	-	0,3,3	-	-	0,3,3	-	-
6	ANP	A	591	2	33,33,33	1.25	5 (15%)	45,52,52	3.23	14 (31%)
5	ADP	A	590	2	28,29,29	1.20	3 (10%)	43,45,45	4.12	29 (67%)

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
6	ANP	B	1591	2	-	5/18/38/38	0/3/3/3
5	ADP	B	1590	2	-	2/16/32/32	0/3/3/3
6	ANP	A	591	2	-	8/18/38/38	0/3/3/3
5	ADP	A	590	2	-	6/16/32/32	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	591	ANP	PG-O1G	3.47	1.51	1.46
6	A	591	ANP	PB-O1B	3.07	1.50	1.46
5	A	590	ADP	C1'-N9	2.95	1.54	1.46
5	B	1590	ADP	C8-N9	-2.88	1.32	1.37
6	A	591	ANP	PB-O2B	-2.87	1.49	1.56

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	590	ADP	C4'-O4'-C1'	11.77	135.45	109.47
6	A	591	ANP	O2B-PB-O1B	11.69	134.95	109.87
6	B	1591	ANP	O2B-PB-O1B	11.40	134.33	109.87
6	B	1591	ANP	O1B-PB-N3B	-11.29	95.15	111.77
5	A	590	ADP	O4'-C4'-C3'	-8.19	88.89	105.15

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	590	ADP	O4'-C4'-C5'-O5'
6	A	591	ANP	PB-N3B-PG-O1G
6	A	591	ANP	PG-N3B-PB-O1B
6	A	591	ANP	PG-N3B-PB-O3A
6	A	591	ANP	PA-O3A-PB-O2B

There are no ring outliers.

4 monomers are involved in 11 short contacts:

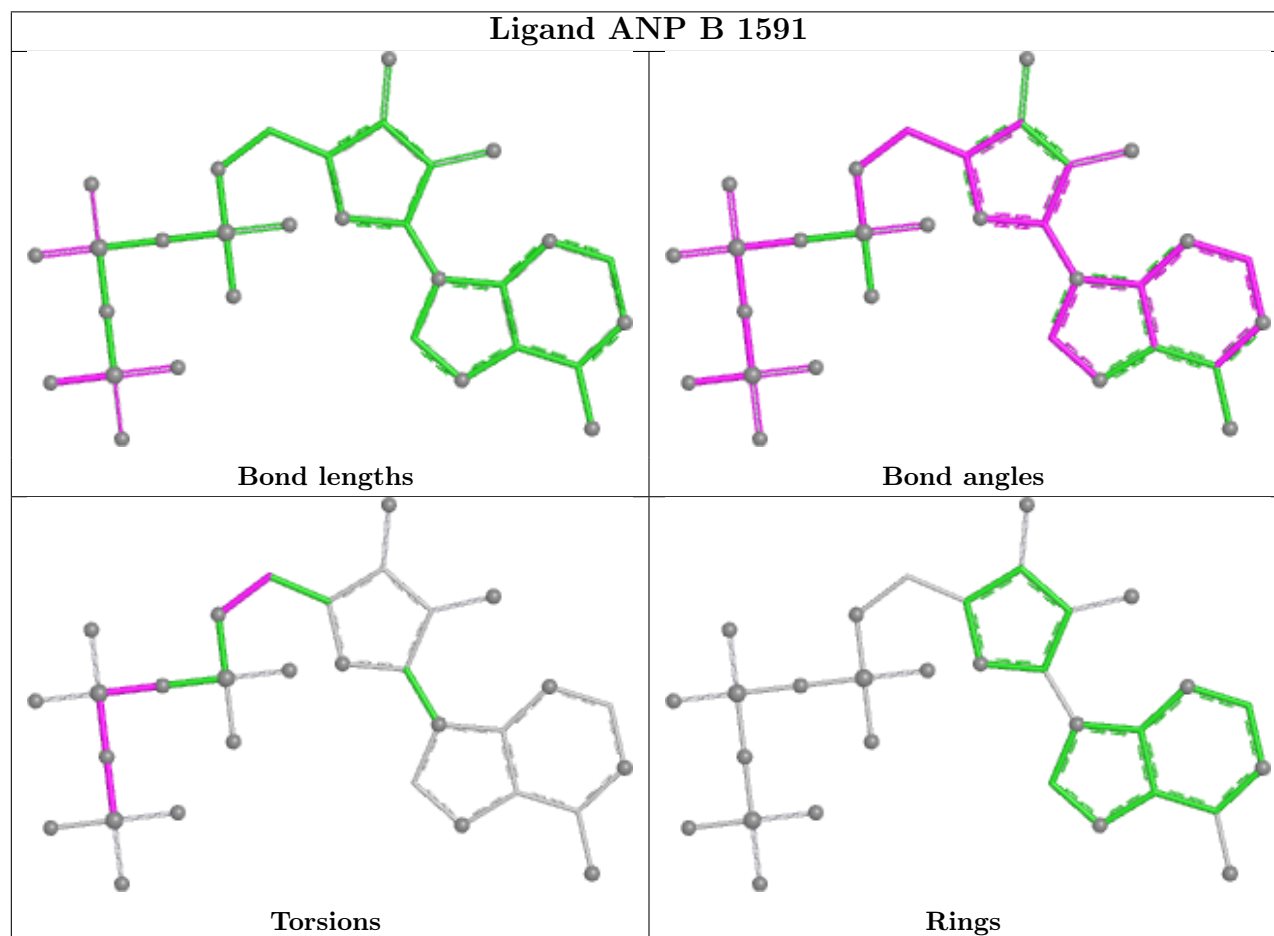
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1590	ADP	2	0

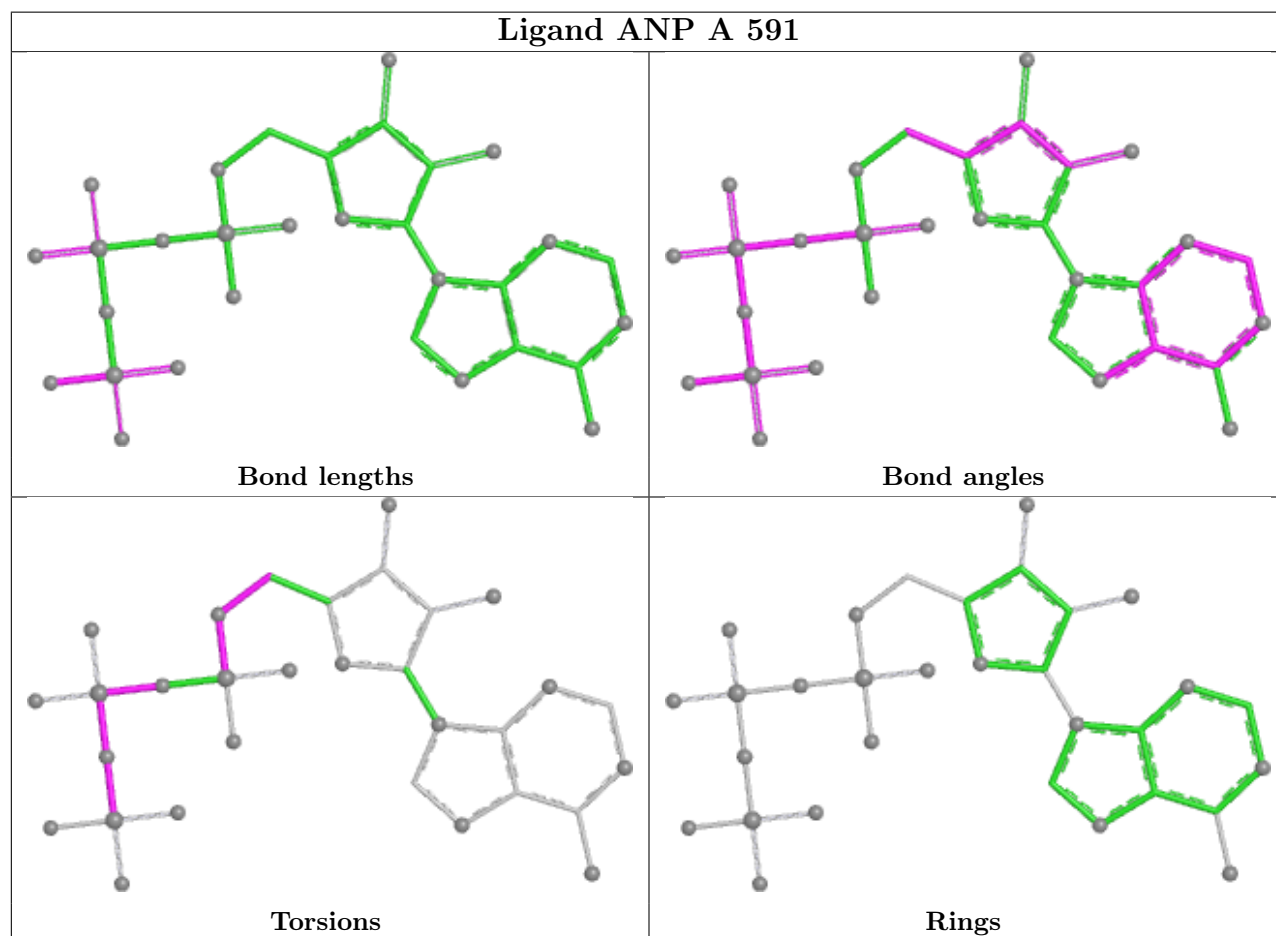
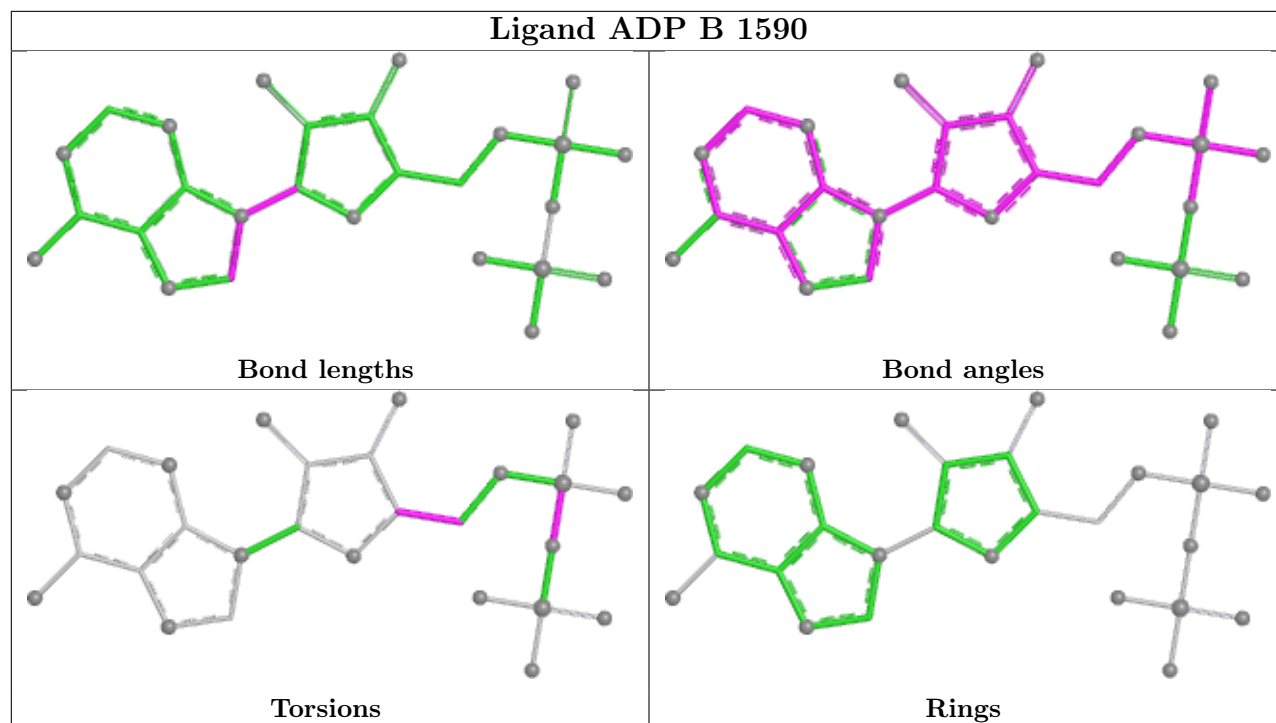
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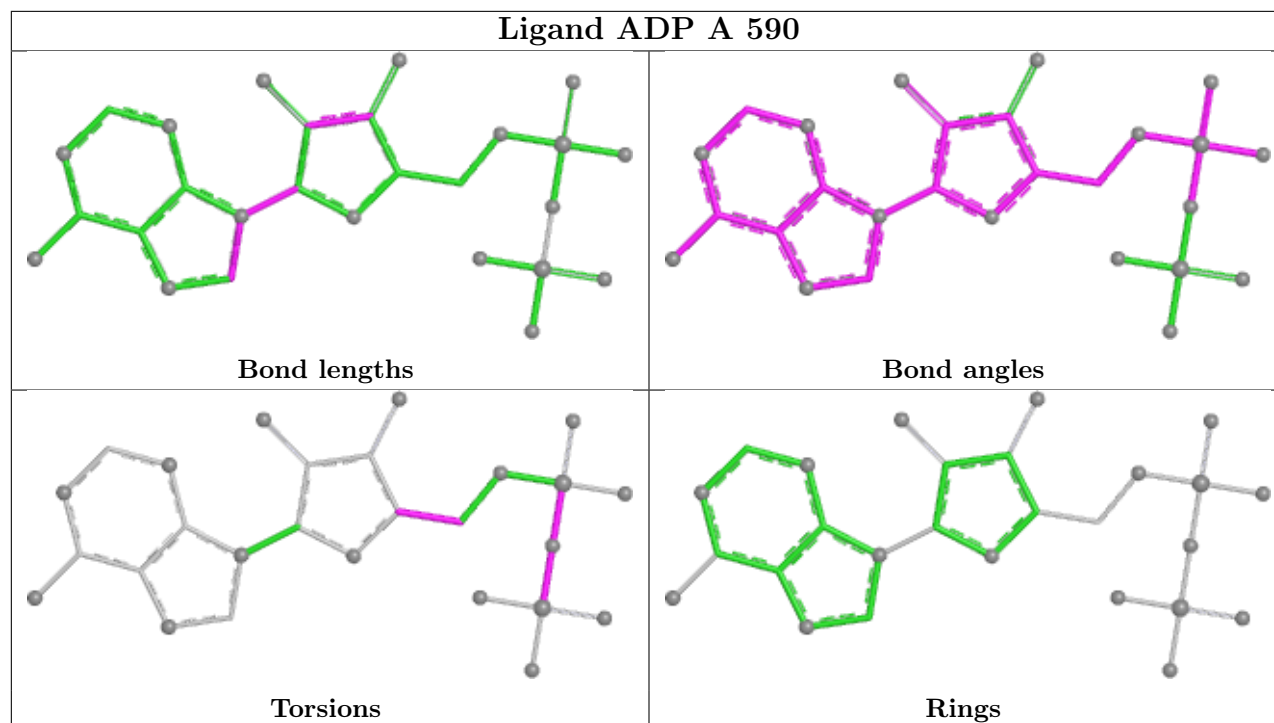
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	701	TAS	2	0
6	A	591	ANP	2	0
5	A	590	ADP	5	0

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 than 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](#)

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	544/589 (92%)	-0.13	10 (1%) 67 63	21, 42, 76, 94	0
1	B	550/589 (93%)	-0.12	11 (2%) 65 60	20, 42, 77, 100	0
All	All	1094/1178 (92%)	-0.13	21 (1%) 66 61	20, 42, 76, 100	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1162	PHE	3.9
1	A	365	PRO	3.6
1	B	1367	ALA	3.3
1	B	1377	LEU	3.0
1	B	1307	GLN	2.9

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

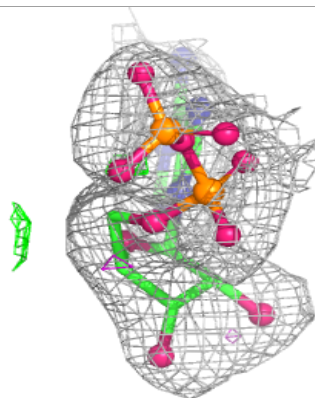
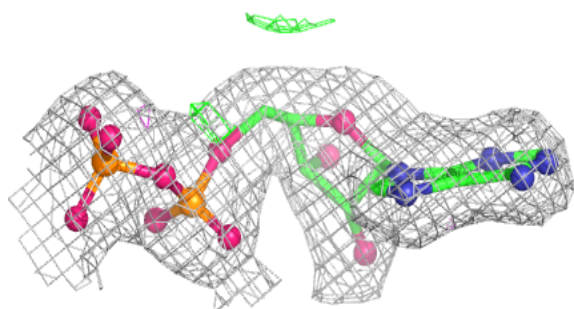
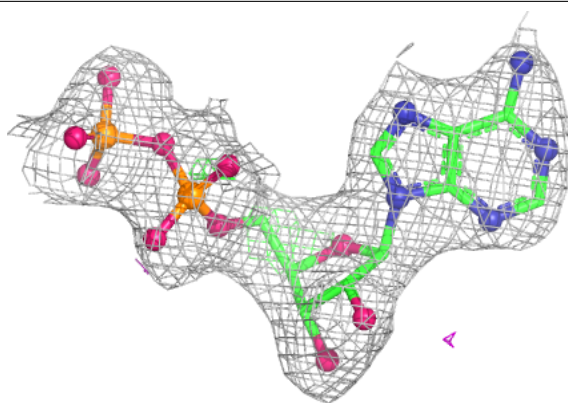
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	TAS	A	701	4/4	0.77	0.24	80,81,83,90	4
7	TAS	B	1701	4/4	0.77	0.25	72,74,74,85	4
3	CD	B	1606	1/1	0.82	0.16	118,118,118,118	1
3	CD	B	1605	1/1	0.93	0.15	89,89,89,89	1
3	CD	A	605	1/1	0.95	0.07	60,60,60,60	1
3	CD	A	603	1/1	0.96	0.05	98,98,98,98	0
5	ADP	B	1590	27/27	0.96	0.08	35,44,51,52	0
4	CL	A	599	1/1	0.97	0.10	69,69,69,69	0
6	ANP	A	591	31/31	0.97	0.06	27,41,52,54	0
4	CL	B	1599	1/1	0.97	0.12	75,75,75,75	0
5	ADP	A	590	27/27	0.97	0.08	37,45,56,59	0
3	CD	B	1603	1/1	0.98	0.04	78,78,78,78	0
6	ANP	B	1591	31/31	0.98	0.05	23,35,48,50	0
2	MG	A	593	1/1	0.99	0.02	21,21,21,21	0
4	CL	A	2000	1/1	0.99	0.03	27,27,27,27	0
4	CL	B	1597	1/1	0.99	0.04	28,28,28,28	0
4	CL	B	1598	1/1	0.99	0.05	32,32,32,32	0
3	CD	B	1602	1/1	0.99	0.02	38,38,38,38	0
2	MG	B	1593	1/1	0.99	0.02	14,14,14,14	0
2	MG	A	592	1/1	0.99	0.05	17,17,17,17	0
3	CD	A	604	1/1	0.99	0.02	46,46,46,46	0
3	CD	B	1607	1/1	0.99	0.05	84,84,84,84	0
4	CL	A	597	1/1	0.99	0.04	28,28,28,28	0
4	CL	A	598	1/1	0.99	0.04	35,35,35,35	0
3	CD	B	1594	1/1	1.00	0.01	35,35,35,35	0
3	CD	B	1595	1/1	1.00	0.01	30,30,30,30	0
3	CD	B	1596	1/1	1.00	0.01	36,36,36,36	0
3	CD	B	1601	1/1	1.00	0.01	32,32,32,32	0
3	CD	A	596	1/1	1.00	0.01	34,34,34,34	0
3	CD	A	600	1/1	1.00	0.01	29,29,29,29	0
3	CD	A	601	1/1	1.00	0.02	31,31,31,31	0
3	CD	A	602	1/1	1.00	0.01	39,39,39,39	0
2	MG	B	1592	1/1	1.00	0.02	24,24,24,24	0
3	CD	A	594	1/1	1.00	0.02	40,40,40,40	0
3	CD	A	595	1/1	1.00	0.02	34,34,34,34	0

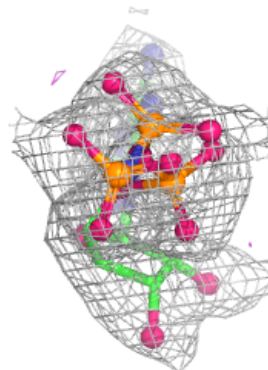
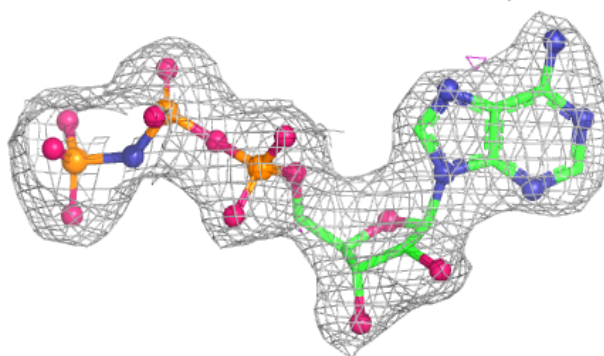
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP B 1590:

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

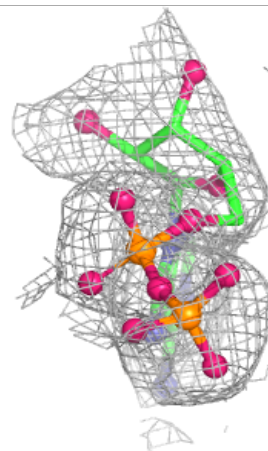
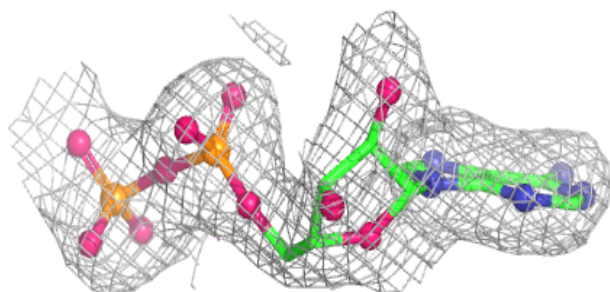
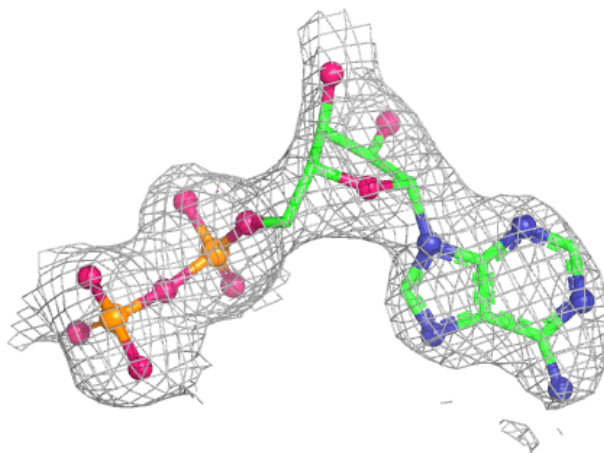
**Electron density around ANP A 591:**

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



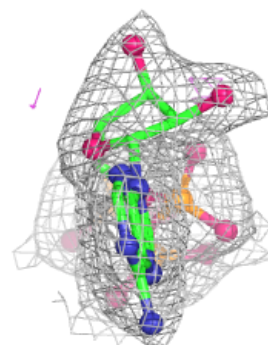
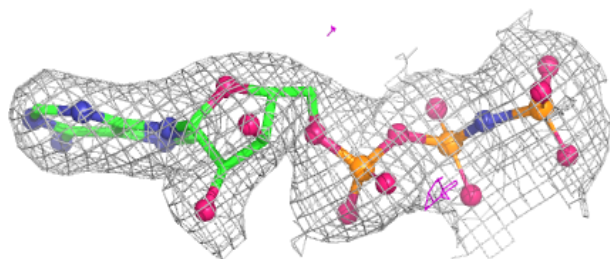
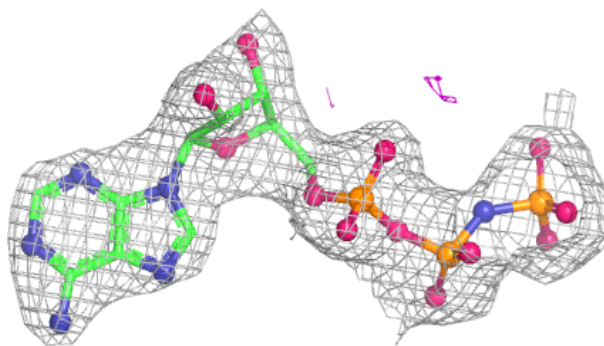
Electron density around ADP A 590:

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



Electron density around ANP B 1591:

$2mF_o - DF_c$ (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.