



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:41 AM UTC

PDB ID : 8CP9 / pdb_00008cp9
Title : 1,6-anhydro-n-actetylmuramic acid kinase (AnmK)in complex with non-hydrolyzable AMPPNP.
Authors : Jimenez-Faraco, E.; Hermoso, J.A.
Deposited on : 2023-03-02
Resolution : 2.20 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 ⓘ 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

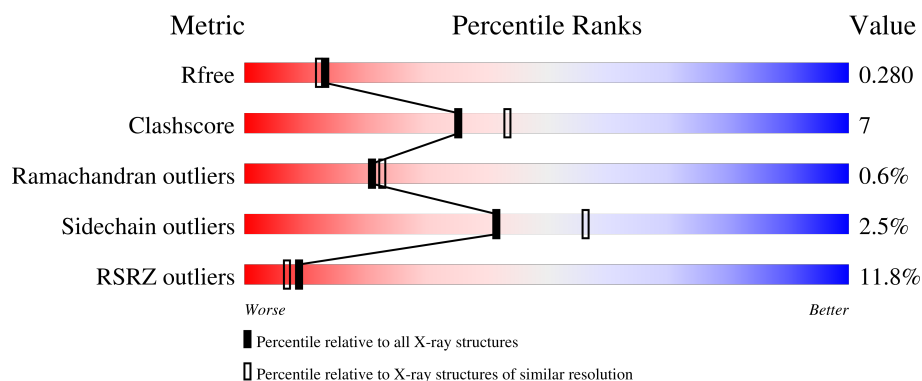
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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	368	12% 81% 16% ..
1	B	368	11% 80% 14% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5588 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.

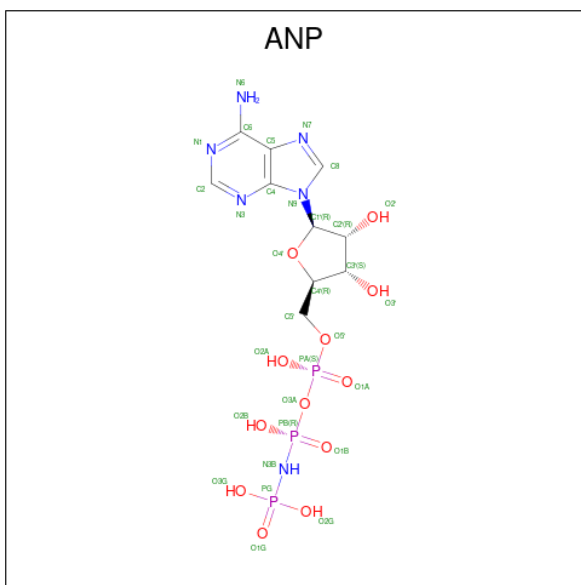
- Molecule 1 is a protein called Anhydro-N-acetylmuramic acid kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2735	1723	495	501	16			
1	B	352	Total	C	N	O	S	0	0	0
			2666	1683	476	491	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q9I5Q5
A	-3	ALA	-	expression tag	UNP Q9I5Q5
A	-2	GLY	-	expression tag	UNP Q9I5Q5
A	-1	ALA	-	expression tag	UNP Q9I5Q5
A	0	GLY	-	expression tag	UNP Q9I5Q5
B	-4	GLY	-	expression tag	UNP Q9I5Q5
B	-3	ALA	-	expression tag	UNP Q9I5Q5
B	-2	GLY	-	expression tag	UNP Q9I5Q5
B	-1	ALA	-	expression tag	UNP Q9I5Q5
B	0	GLY	-	expression tag	UNP Q9I5Q5

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

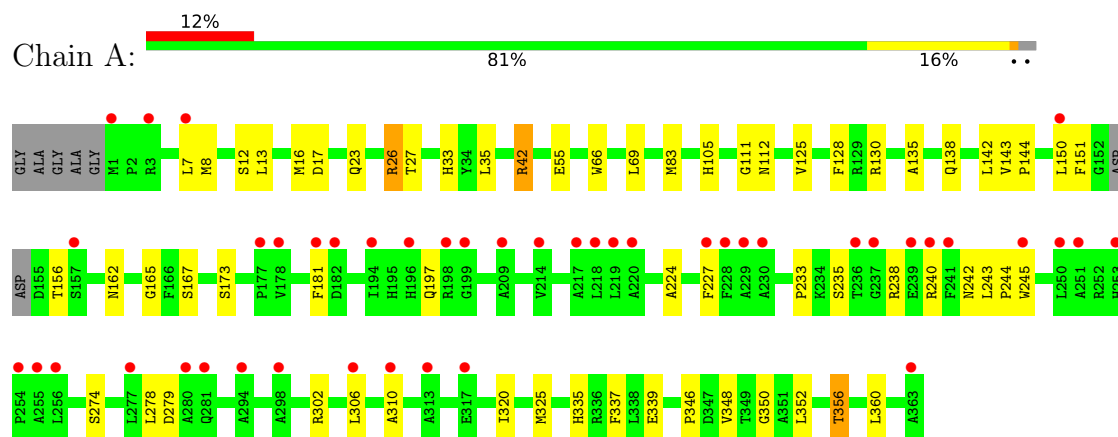
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total	O	0	0
			62	62		
4	B	61	Total	O	0	0
			61	61		

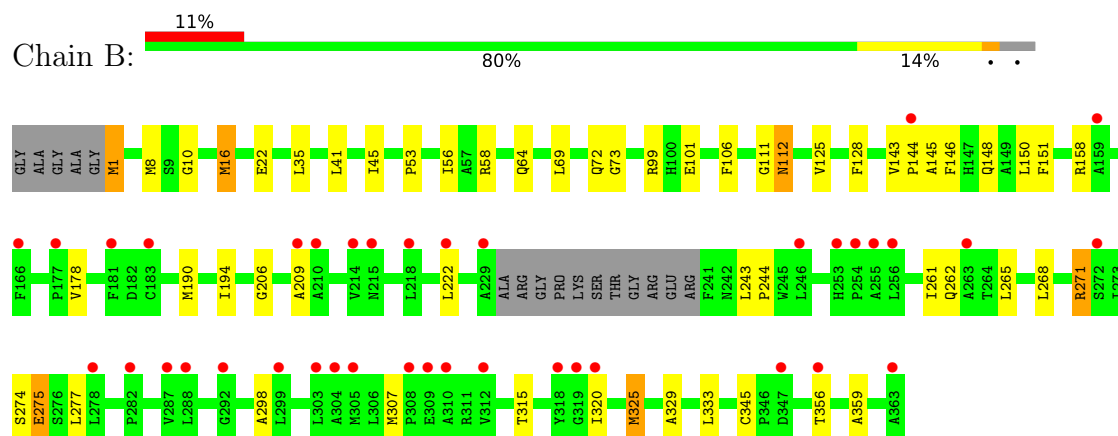
3 Residue-property plots [i](#)

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 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: Anhydro-N-acetylmuramic acid kinase



- Molecule 1: Anhydro-N-acetylmuramic acid kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	89.94Å 89.94Å 176.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.02 – 2.20 47.02 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.02-2.20) 99.9 (47.02-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.183 , 0.231 0.221 , 0.280	Depositor DCC
R_{free} test set	2042 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.179 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.536 for H, K, L 0.464 for -K, -H, -L	Depositor
Outliers	1 of 41048 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5588	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: ANP, MG

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	0.53	0/2799	0.93	1/3805 (0.0%)
1	B	0.52	0/2729	0.93	0/3713
All	All	0.52	0/5528	0.93	1/7518 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	356	THR	CB-CA-C	5.74	119.07	109.89

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	2735	0	2698	39	0
1	B	2666	0	2618	43	0
2	A	31	0	13	1	0
2	B	31	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	62	0	0	8	0
4	B	61	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5588	0	5342	80	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 7.

All (80) 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:16:MET:HE3	1:A:69:LEU:HD23	1.59	0.83
1:A:105:HIS:HB2	1:B:64:GLN:HE22	1.45	0.80
1:B:274:SER:HA	1:B:307:MET:HE3	1.65	0.79
1:B:16:MET:HE1	1:B:69:LEU:HD23	1.71	0.73
1:B:22:GLU:CD	4:B:504:HOH:O	2.37	0.67
1:A:233:PRO:HA	4:A:528:HOH:O	1.98	0.63
1:A:151:PHE:HE2	1:A:325:MET:HE1	1.66	0.61
1:B:261:ILE:O	1:B:265:LEU:HG	2.01	0.61
1:B:271:ARG:NH2	1:B:275:GLU:HB3	2.15	0.61
1:B:271:ARG:HH21	1:B:275:GLU:HB3	1.66	0.60
1:B:101:GLU:HG3	1:B:106:PHE:CZ	2.37	0.59
1:A:165:GLY:H	2:A:401:ANP:HNB1	1.50	0.58
1:B:99:ARG:NH1	4:B:503:HOH:O	2.32	0.58
1:B:111:GLY:O	1:B:112:ASN:C	2.47	0.57
1:A:135:ALA:O	1:A:352:LEU:HD13	2.04	0.57
1:A:130:ARG:CZ	4:A:505:HOH:O	2.53	0.57
1:B:277:LEU:HD13	1:B:307:MET:HE1	1.87	0.56
1:A:335:HIS:CE1	1:A:339:GLU:HG3	2.40	0.56
1:A:173:SER:HB3	4:A:547:HOH:O	2.04	0.56
1:A:26:ARG:HG3	1:A:27:THR:H	1.70	0.56
1:B:315:THR:HG21	1:B:325:MET:HE3	1.89	0.55
1:B:16:MET:CE	1:B:69:LEU:HD23	2.35	0.55
1:A:143:VAL:N	1:A:144:PRO:CD	2.71	0.54
1:B:150:LEU:HD21	1:B:320:ILE:HD13	1.89	0.54
1:B:143:VAL:N	1:B:144:PRO:CD	2.70	0.54
1:B:150:LEU:HD21	1:B:320:ILE:CD1	2.38	0.54
1:B:148:GLN:HB2	1:B:178:VAL:HG21	1.90	0.53
1:A:130:ARG:NH2	4:A:505:HOH:O	2.40	0.53
1:B:277:LEU:HD23	1:B:277:LEU:O	2.09	0.53
1:B:8:MET:HE3	1:B:10:GLY:N	2.24	0.52
1:A:130:ARG:NE	4:A:505:HOH:O	2.43	0.51
1:A:337:PHE:CD1	1:A:337:PHE:C	2.89	0.51
1:A:310:ALA:HB3	4:A:537:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:VAL:HA	1:B:359:ALA:O	2.10	0.51
1:B:143:VAL:N	1:B:144:PRO:HD3	2.26	0.51
1:B:209:ALA:HB2	1:B:262:GLN:HG3	1.94	0.50
1:A:144:PRO:HG2	1:A:348:VAL:HG11	1.93	0.50
1:B:145:ALA:HB2	1:B:345:CYS:SG	2.53	0.49
1:B:243:LEU:HB3	1:B:244:PRO:HD3	1.95	0.48
1:B:146:PHE:CZ	1:B:150:LEU:HD22	2.48	0.48
1:B:8:MET:HE3	1:B:10:GLY:CA	2.43	0.48
1:A:55:GLU:HB3	1:B:56:ILE:HG13	1.95	0.48
1:A:33:HIS:CD2	1:A:35:LEU:HD21	2.48	0.48
1:A:13:LEU:HB3	1:A:42:ARG:HG3	1.95	0.48
1:A:23:GLN:HE22	1:A:26:ARG:NH2	2.11	0.48
1:A:138:GLN:HE21	1:A:235:SER:HB2	1.77	0.47
1:A:150:LEU:HD13	1:A:320:ILE:CD1	2.44	0.47
1:A:302:ARG:O	1:A:306:LEU:HG	2.15	0.47
1:A:227:PHE:CD1	1:A:238:ARG:HB3	2.49	0.47
1:A:227:PHE:HD1	1:A:238:ARG:HB3	1.80	0.46
1:B:148:GLN:OE1	1:B:178:VAL:CG2	2.64	0.46
1:A:16:MET:HE3	1:A:69:LEU:CD2	2.40	0.45
1:B:101:GLU:HG3	1:B:106:PHE:CE1	2.51	0.45
1:A:150:LEU:HD13	1:A:320:ILE:HD12	1.99	0.45
1:A:181:PHE:HB3	4:A:528:HOH:O	2.16	0.45
1:B:190:MET:O	1:B:194:ILE:HG22	2.17	0.45
1:A:12:SER:O	1:A:13:LEU:HB2	2.17	0.44
1:A:243:LEU:HB3	1:A:244:PRO:HD3	2.00	0.44
1:A:142:LEU:C	1:A:144:PRO:HD2	2.42	0.44
1:A:197:GLN:NE2	4:A:511:HOH:O	2.47	0.44
1:B:277:LEU:HB3	1:B:307:MET:CE	2.48	0.44
1:B:53:PRO:O	1:B:58:ARG:NH1	2.48	0.43
1:B:146:PHE:CD2	1:B:329:ALA:HB2	2.54	0.43
1:A:242:ASN:O	1:A:245:TRP:HB3	2.17	0.43
1:B:128:PHE:CE1	1:B:333:LEU:HB3	2.53	0.43
1:A:8:MET:HB3	1:A:17:ASP:HB2	2.00	0.43
1:B:35:LEU:HD11	1:B:73:GLY:HA3	2.00	0.43
1:A:125:VAL:HG12	1:A:128:PHE:CZ	2.54	0.43
1:B:222:LEU:HB3	1:B:268:LEU:HD13	2.00	0.43
1:A:162:ASN:O	1:A:167:SER:HA	2.18	0.42
1:B:277:LEU:HD13	1:B:307:MET:CE	2.49	0.42
1:A:7:LEU:HD21	1:A:66:TRP:CH2	2.54	0.42
1:B:41:LEU:O	1:B:45:ILE:HG13	2.19	0.42
1:B:72:GLN:HG3	4:B:522:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:THR:HG21	1:B:325:MET:CE	2.50	0.42
1:B:1:MET:HB2	4:B:504:HOH:O	2.19	0.41
1:B:206:GLY:HA3	1:B:298:ALA:HB3	2.02	0.41
1:A:346:PRO:O	1:A:350:GLY:N	2.42	0.41
1:B:151:PHE:HB3	1:B:158:ARG:HH11	1.86	0.41
1:A:278:LEU:O	1:A:279:ASP:C	2.64	0.41

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	357/368 (97%)	345 (97%)	9 (2%)	3 (1%)	16	16
1	B	348/368 (95%)	335 (96%)	12 (3%)	1 (0%)	36	42
All	All	705/736 (96%)	680 (96%)	21 (3%)	4 (1%)	21	23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	ASN
1	A	224	ALA
1	B	112	ASN
1	A	111	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	278/280 (99%)	270 (97%)	8 (3%)	37	51
1	B	272/280 (97%)	266 (98%)	6 (2%)	45	61
All	All	550/560 (98%)	536 (98%)	14 (2%)	42	56

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

Mol	Chain	Res	Type
1	A	26	ARG
1	A	42	ARG
1	A	83	MET
1	A	156	THR
1	A	240	ARG
1	A	274	SER
1	A	356	THR
1	A	360	LEU
1	B	1	MET
1	B	16	MET
1	B	271	ARG
1	B	275	GLU
1	B	325	MET
1	B	356	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	138	GLN
1	A	197	GLN
1	A	335	HIS
1	B	64	GLN
1	B	105	HIS

5.3.3 RNA ⓘ

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 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	ANP	A	401	3	33,33,33	0.76	1 (3%)	45,52,52	0.69	0
2	ANP	B	401	3	33,33,33	0.79	1 (3%)	45,52,52	0.71	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	ANP	A	401	3	-	1/18/38/38	0/3/3/3
2	ANP	B	401	3	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	ANP	PA-O3A	3.19	1.62	1.59
2	A	401	ANP	PA-O3A	3.18	1.62	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

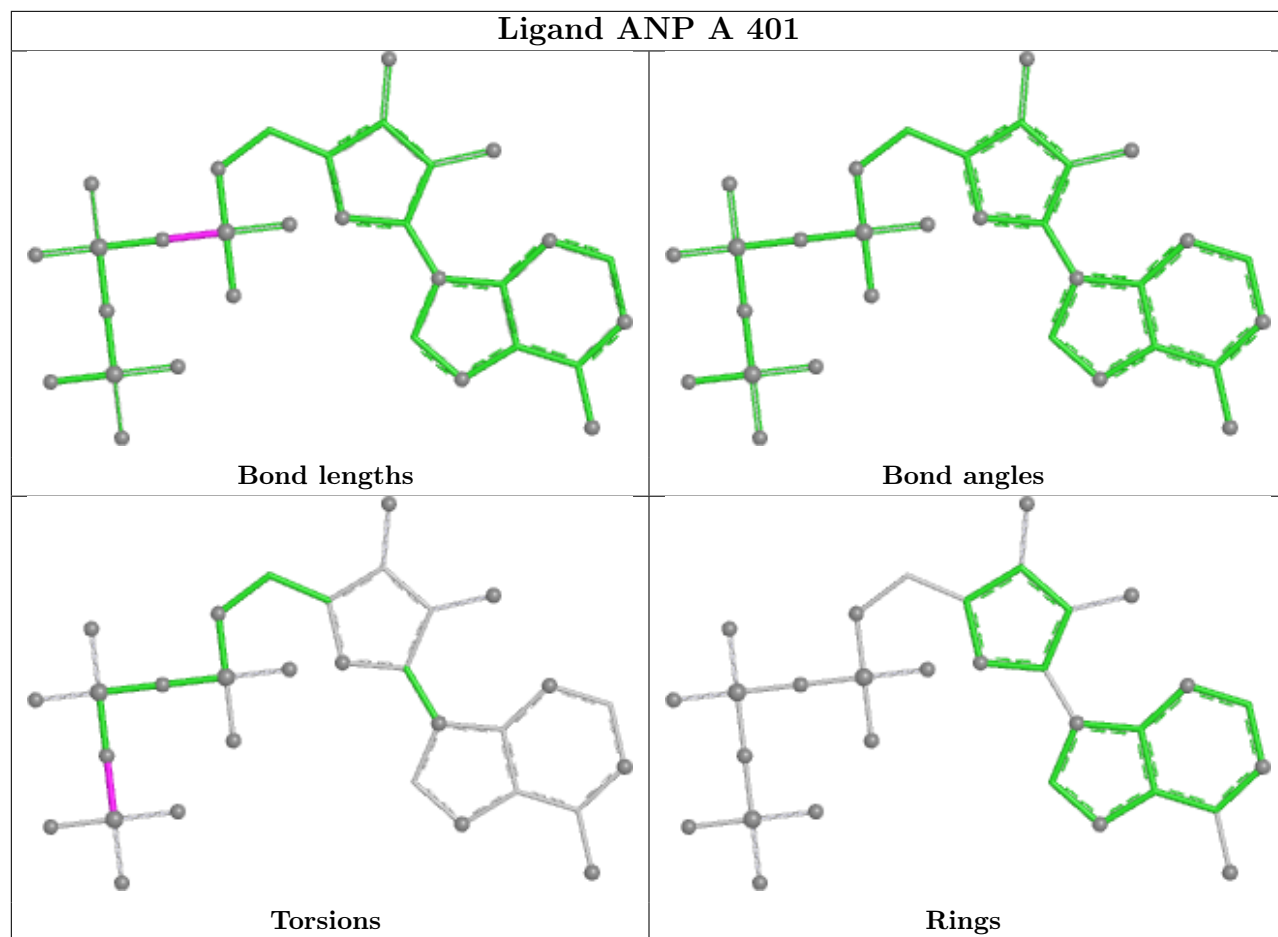
Mol	Chain	Res	Type	Atoms
2	A	401	ANP	PB-N3B-PG-O1G
2	B	401	ANP	PB-N3B-PG-O1G
2	B	401	ANP	PG-N3B-PB-O1B
2	B	401	ANP	PG-N3B-PB-O3A

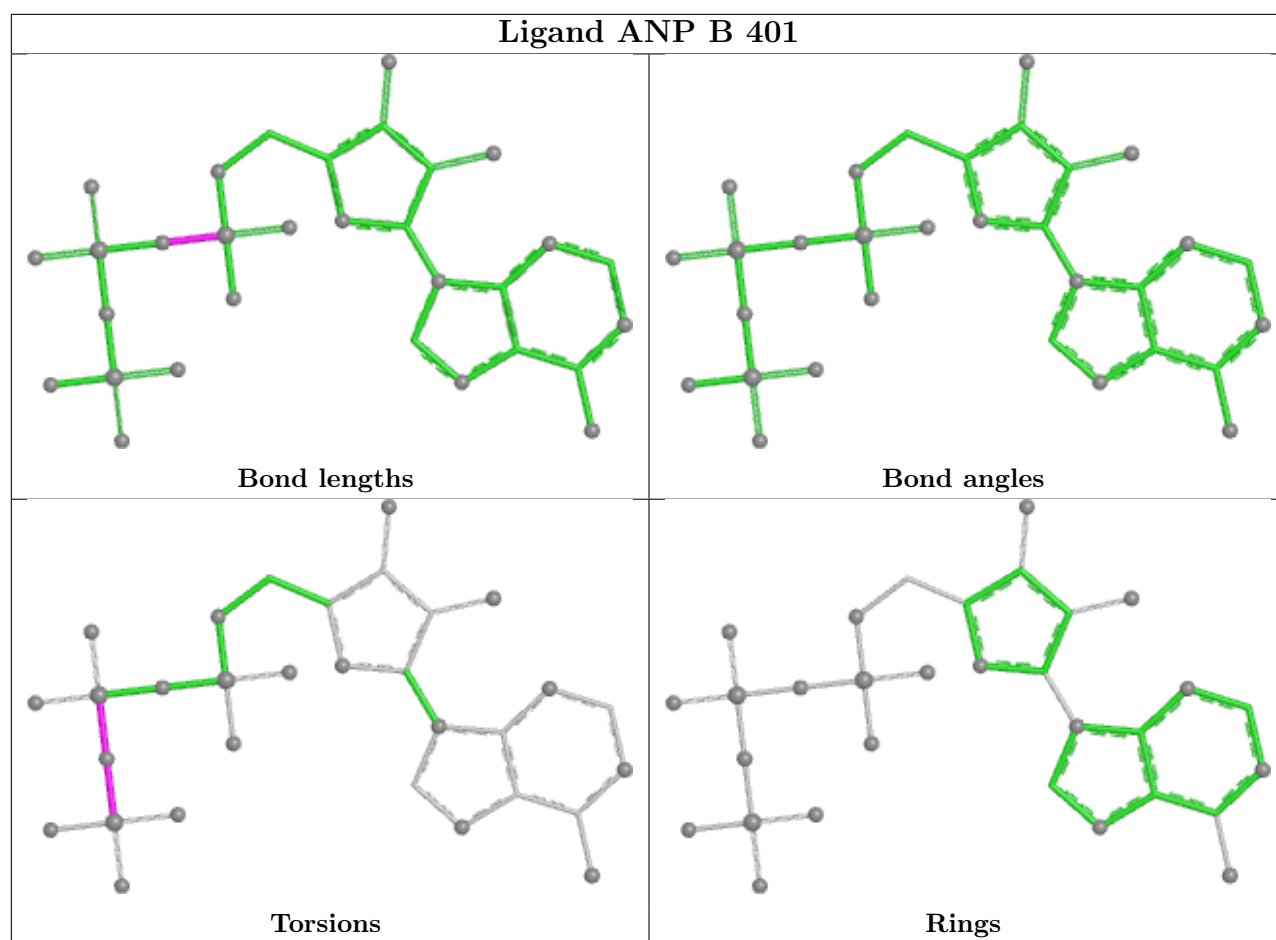
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	ANP	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 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

6.1 Protein, DNA and RNA chains

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	361/368 (98%)	1.03	45 (12%) 8 6	32, 50, 84, 108	0
1	B	352/368 (95%)	1.03	39 (11%) 10 8	32, 54, 87, 99	0
All	All	713/736 (96%)	1.03	84 (11%) 9 7	32, 52, 86, 108	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	ALA	7.3
1	A	280	ALA	4.9
1	A	236	THR	4.3
1	A	214	VAL	4.2
1	A	237	GLY	4.1
1	A	254	PRO	4.1
1	A	228	PHE	3.9
1	A	220	ALA	3.8
1	A	306	LEU	3.6
1	B	166	PHE	3.5
1	B	310	ALA	3.4
1	B	255	ALA	3.4
1	B	304	ALA	3.3
1	B	214	VAL	3.0
1	B	318	TYR	3.0
1	A	217	ALA	3.0
1	B	254	PRO	3.0
1	B	256	LEU	2.9
1	B	299	LEU	2.9
1	B	246	LEU	2.9
1	A	256	LEU	2.8
1	B	303	LEU	2.8
1	A	1	MET	2.8
1	B	181	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	194	ILE	2.8
1	A	198	ARG	2.8
1	B	305	MET	2.7
1	B	177	PRO	2.7
1	A	219	LEU	2.7
1	A	181	PHE	2.7
1	B	319	GLY	2.7
1	A	253	HIS	2.7
1	B	312	VAL	2.6
1	B	356	THR	2.6
1	A	209	ALA	2.6
1	A	199	GLY	2.6
1	B	159	ALA	2.5
1	A	182	ASP	2.5
1	A	241	PHE	2.5
1	B	320	ILE	2.5
1	B	278	LEU	2.5
1	A	227	PHE	2.5
1	B	287	VAL	2.5
1	B	222	LEU	2.5
1	A	313	ALA	2.5
1	A	317	GLU	2.5
1	A	230	ALA	2.5
1	A	245	TRP	2.4
1	A	239	GLU	2.4
1	A	277	LEU	2.4
1	A	363	ALA	2.4
1	B	282	PRO	2.4
1	B	210	ALA	2.4
1	B	253	HIS	2.3
1	A	157	SER	2.3
1	B	309	GLU	2.3
1	A	255	ALA	2.3
1	A	178	VAL	2.3
1	B	218	LEU	2.2
1	B	144	PRO	2.2
1	A	298	ALA	2.2
1	B	229	ALA	2.2
1	A	218	LEU	2.2
1	A	3	ARG	2.2
1	B	308	PRO	2.2
1	A	251	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	294	ALA	2.2
1	B	215	ASN	2.2
1	A	250	LEU	2.1
1	B	183	CYS	2.1
1	B	292	GLY	2.1
1	B	347	ASP	2.1
1	A	229	ALA	2.1
1	A	177	PRO	2.1
1	A	196	HIS	2.0
1	A	281	GLN	2.0
1	A	7	LEU	2.0
1	A	150	LEU	2.0
1	B	288	LEU	2.0
1	B	272	SER	2.0
1	A	310	ALA	2.0
1	B	209	ALA	2.0
1	B	263	ALA	2.0
1	A	240	ARG	2.0

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](#)

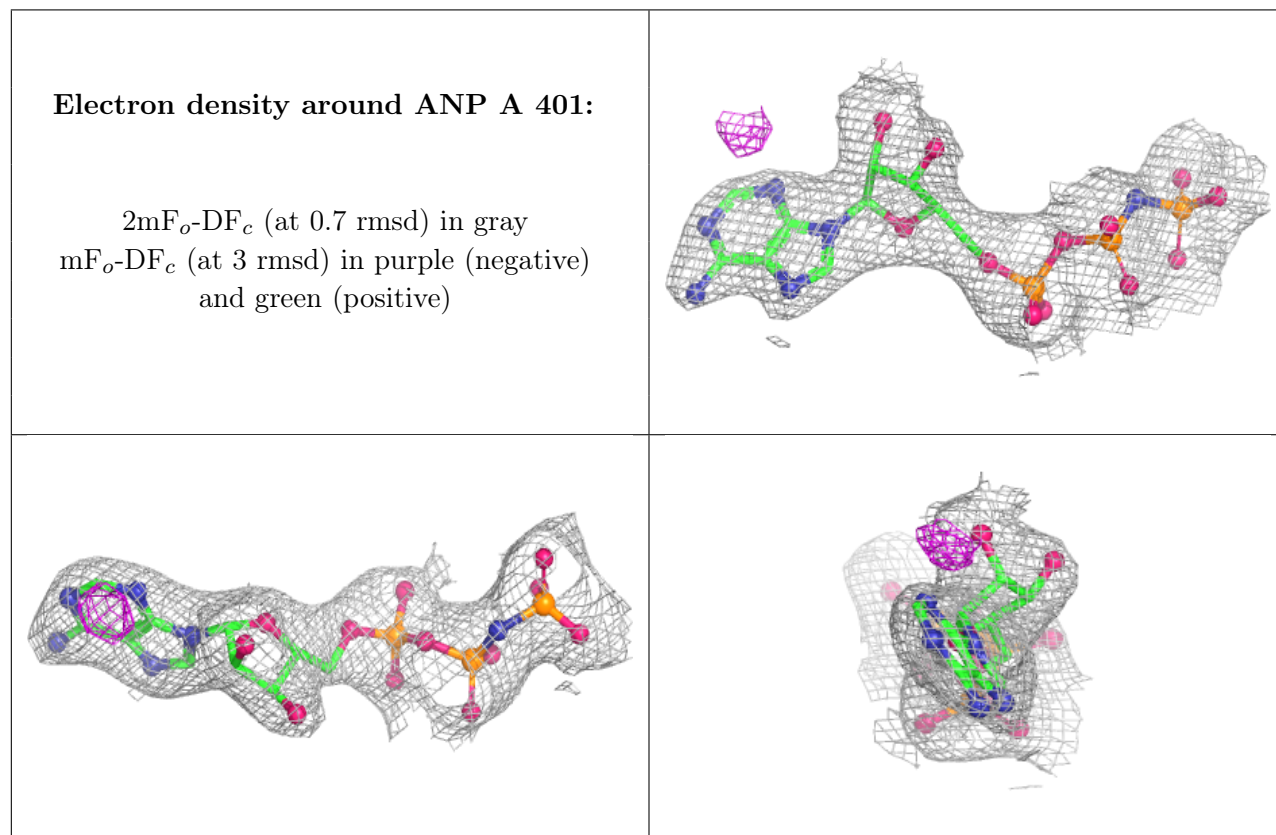
There are no oligosaccharides in this entry.

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.

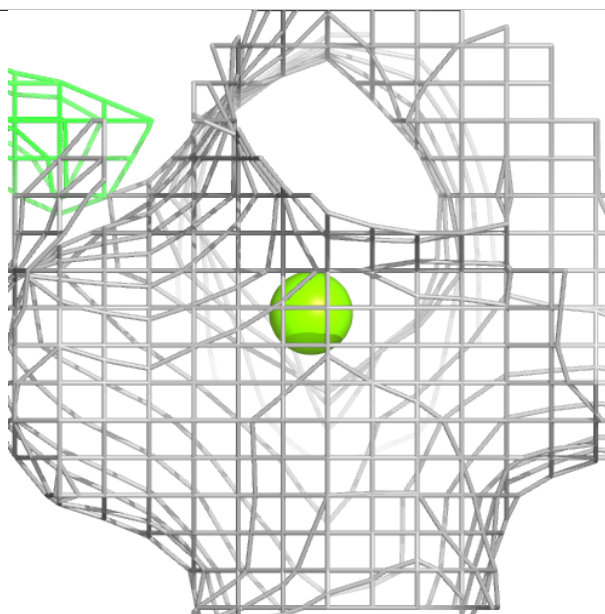
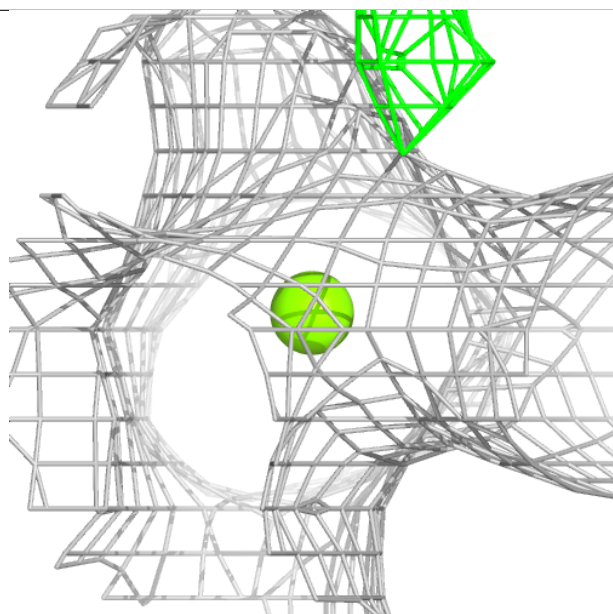
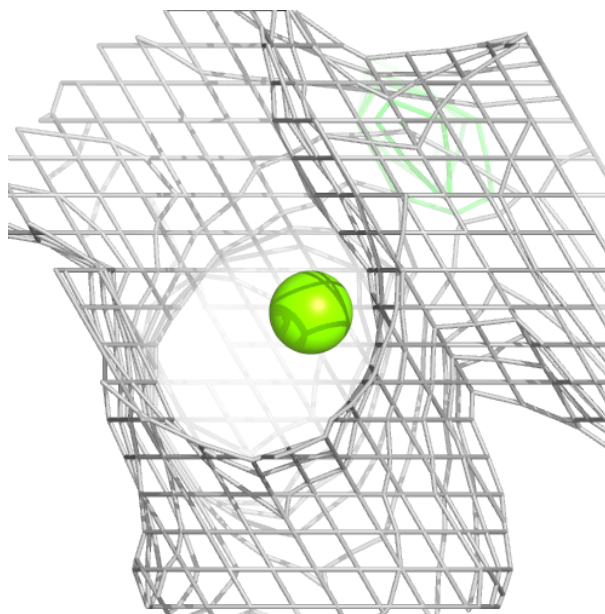
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ANP	A	401	31/31	0.93	0.10	48,56,65,70	0
3	MG	B	402	1/1	0.93	0.06	57,57,57,57	0
2	ANP	B	401	31/31	0.95	0.08	42,49,61,66	0
3	MG	A	402	1/1	0.98	0.04	60,60,60,60	0

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.



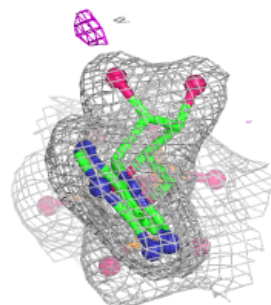
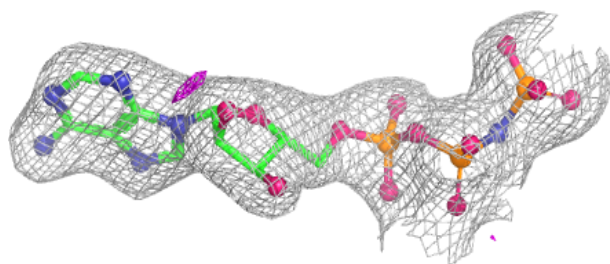
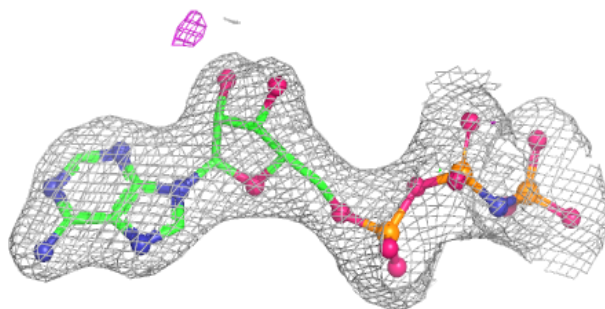
Electron density around MG B 402:

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



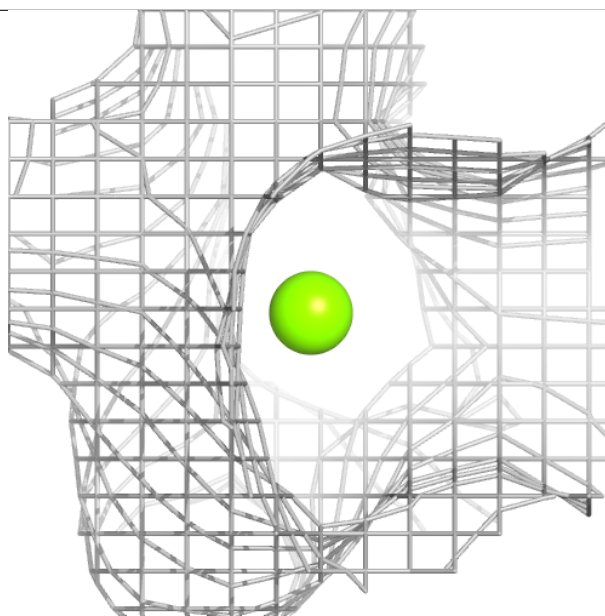
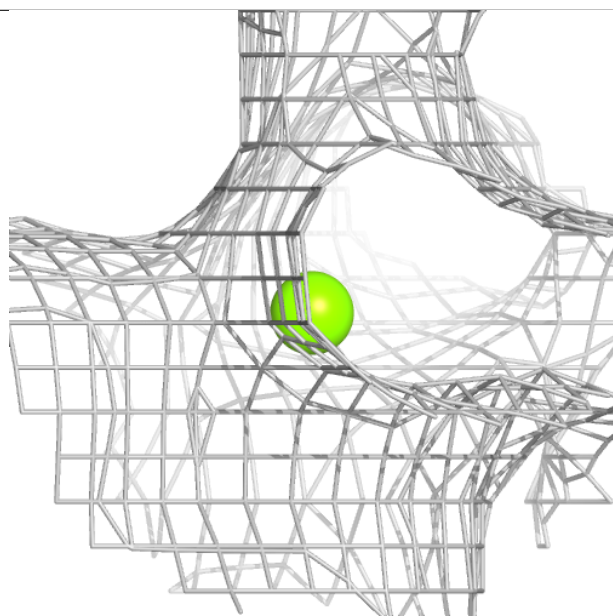
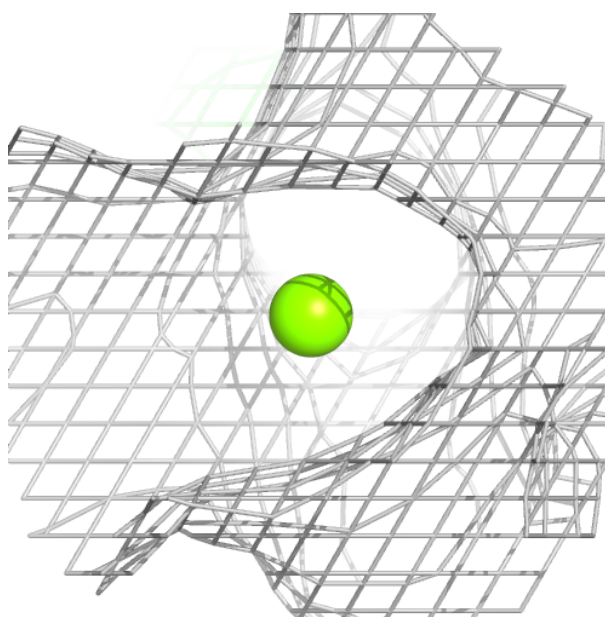
Electron density around ANP B 401:

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



Electron density around MG A 402:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.