



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 12, 2021 – 10:11 AM EDT

PDB ID : 6WK0  
Title : Crystal structure of human ribokinase in complex with AMPPCP and ribose  
Authors : Park, J.  
Deposited on : 2020-04-15  
Resolution : 2.00 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.18  
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) : 2.18

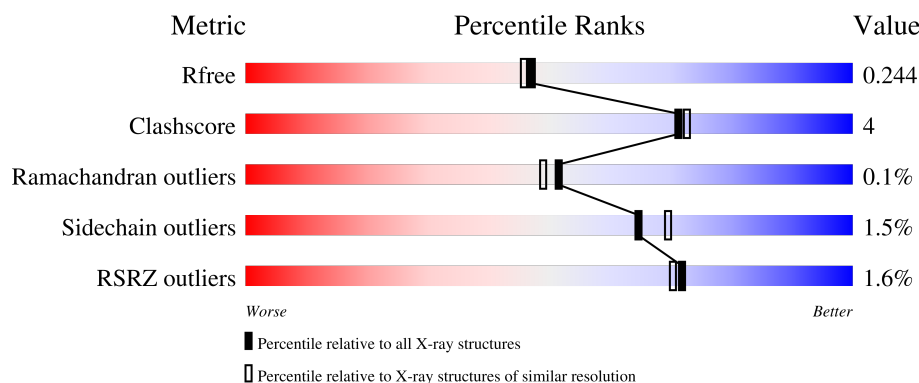
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*




The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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  $\geq 3$ , 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	317	 92% 7% .
1	B	317	 90% 7% ..
1	C	317	 93% 7%
1	D	317	 6% 91% 9%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10510 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 Ribokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	5	0
			2384	1502	403	462	17			
1	B	311	Total	C	N	O	S	0	3	0
			2307	1457	384	452	14			
1	C	317	Total	C	N	O	S	0	1	0
			2334	1472	391	456	15			
1	D	316	Total	C	N	O	S	0	2	0
			2324	1467	391	452	14			

There are 32 discrepancies between the modelled and reference sequences:

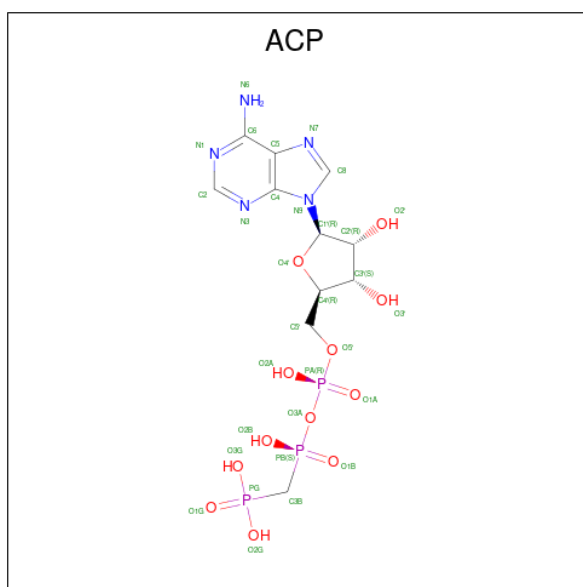
Chain	Residue	Modelled	Actual	Comment	Reference
A	323	LEU	-	expression tag	UNP Q9H477
A	324	GLU	-	expression tag	UNP Q9H477
A	325	HIS	-	expression tag	UNP Q9H477
A	326	HIS	-	expression tag	UNP Q9H477
A	327	HIS	-	expression tag	UNP Q9H477
A	328	HIS	-	expression tag	UNP Q9H477
A	329	HIS	-	expression tag	UNP Q9H477
A	330	HIS	-	expression tag	UNP Q9H477
B	323	LEU	-	expression tag	UNP Q9H477
B	324	GLU	-	expression tag	UNP Q9H477
B	325	HIS	-	expression tag	UNP Q9H477
B	326	HIS	-	expression tag	UNP Q9H477
B	327	HIS	-	expression tag	UNP Q9H477
B	328	HIS	-	expression tag	UNP Q9H477
B	329	HIS	-	expression tag	UNP Q9H477
B	330	HIS	-	expression tag	UNP Q9H477
C	323	LEU	-	expression tag	UNP Q9H477
C	324	GLU	-	expression tag	UNP Q9H477
C	325	HIS	-	expression tag	UNP Q9H477
C	326	HIS	-	expression tag	UNP Q9H477
C	327	HIS	-	expression tag	UNP Q9H477

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Chain	Residue	Modelled	Actual	Comment	Reference
C	328	HIS	-	expression tag	UNP Q9H477
C	329	HIS	-	expression tag	UNP Q9H477
C	330	HIS	-	expression tag	UNP Q9H477
D	323	LEU	-	expression tag	UNP Q9H477
D	324	GLU	-	expression tag	UNP Q9H477
D	325	HIS	-	expression tag	UNP Q9H477
D	326	HIS	-	expression tag	UNP Q9H477
D	327	HIS	-	expression tag	UNP Q9H477
D	328	HIS	-	expression tag	UNP Q9H477
D	329	HIS	-	expression tag	UNP Q9H477
D	330	HIS	-	expression tag	UNP Q9H477

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula:  $C_{11}H_{18}N_5O_{12}P_3$ ) (labeled as "Ligand of Interest" by depositor).

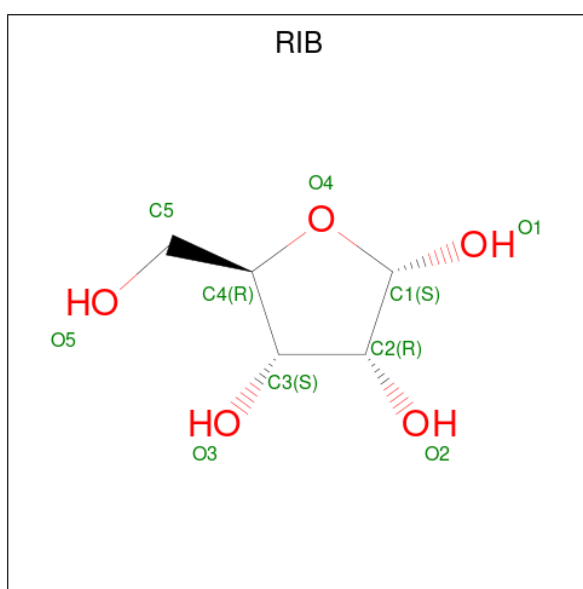


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
2	B	1	Total	C	N	O	P	0	1
			62	22	10	24	6		
2	C	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
2	D	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Na 2 2	0	0
3	B	2	Total Na 2 2	0	0
3	C	2	Total Na 2 2	0	0
3	D	2	Total Na 2 2	0	0

- Molecule 4 is alpha-D-ribofuranose (three-letter code: RIB) (formula: C<sub>5</sub>H<sub>10</sub>O<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 10 5 5	0	0
4	C	1	Total C O 10 5 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	368	Total O 368 368	0	0
5	B	248	Total O 248 248	0	0
5	C	253	Total O 253 253	0	0

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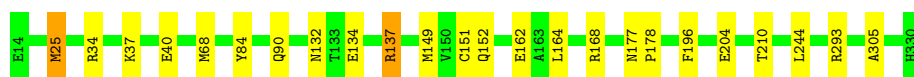
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	109	Total 109	O 109	0	0

### 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 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: Ribokinase

Chain A: 



- Molecule 1: Ribokinase

Chain B: 

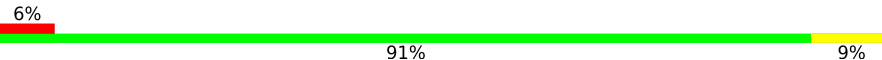


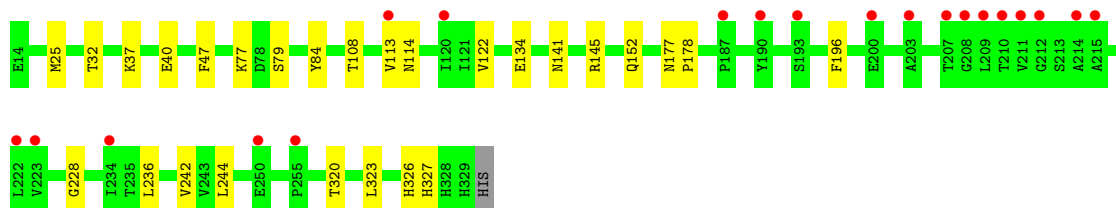
- Molecule 1: Ribokinase

Chain C: 



- Molecule 1: Ribokinase

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.02Å 89.35Å 144.70Å 90.00° 98.61° 90.00°	Depositor
Resolution (Å)	51.43 – 2.00 51.43 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (51.43-2.00) 98.6 (51.43-2.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.24 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.197 , 0.239 0.203 , 0.244	Depositor DCC
$R_{free}$ test set	4355 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.7	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10510	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ACP, RIB, NA

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	0.87	1/2423 (0.0%)	0.93	3/3294 (0.1%)
1	B	0.84	1/2340 (0.0%)	0.92	0/3184
1	C	0.83	3/2373 (0.1%)	0.90	0/3231
1	D	0.83	3/2361 (0.1%)	0.86	0/3216
All	All	0.84	8/9497 (0.1%)	0.90	3/12925 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	324	GLU	CD-OE2	7.15	1.33	1.25
1	D	326	HIS	CB-CG	6.94	1.62	1.50
1	A	204	GLU	CD-OE1	6.38	1.32	1.25
1	D	326	HIS	CG-CD2	6.22	1.46	1.35
1	C	257	GLU	CD-OE1	5.82	1.32	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	293	ARG	NE-CZ-NH2	-6.03	117.29	120.30
1	A	25	MET	CG-SD-CE	-5.67	91.12	100.20
1	A	168	ARG	CG-CD-NE	-5.37	100.53	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	305	ALA	Peptide

## 5.2 Too-close contacts ⓘ

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	2384	0	2369	20	0
1	B	2307	0	2321	14	0
1	C	2334	0	2297	15	0
1	D	2324	0	2291	15	0
2	A	31	0	14	2	0
2	B	62	0	28	6	0
2	C	31	0	14	1	0
2	D	31	0	14	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	B	10	0	0	1	0
4	C	10	0	0	0	0
5	A	368	0	0	12	2
5	B	248	0	0	8	0
5	C	253	0	0	4	1
5	D	109	0	0	4	0
All	All	10510	0	9348	67	2

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 4.

The worst 5 of 67 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)
2:B:402[B]:ACP:O1G	5:B:503:HOH:O	1.53	1.22
2:B:402[B]:ACP:H3B1	5:B:570:HOH:O	1.62	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:THR:O	2:B:402[B]:ACP:H3B2	1.83	0.77
1:D:236:LEU:HD11	1:D:242:VAL:HG23	1.68	0.76
1:A:151[B]:CYS:SG	1:A:164:LEU:HD21	2.26	0.76

All (2) 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)
5:A:699:HOH:O	5:C:688:HOH:O[1_455]	2.15	0.05
5:A:842:HOH:O	5:A:867:HOH:O[1_455]	2.16	0.04

## 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	320/317 (101%)	313 (98%)	7 (2%)	0	100	100
1	B	312/317 (98%)	308 (99%)	3 (1%)	1 (0%)	41	37
1	C	316/317 (100%)	311 (98%)	5 (2%)	0	100	100
1	D	316/317 (100%)	310 (98%)	6 (2%)	0	100	100
All	All	1264/1268 (100%)	1242 (98%)	21 (2%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	307	THR

### 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	256/256 (100%)	252 (98%)	4 (2%)	62	67
1	B	249/256 (97%)	244 (98%)	5 (2%)	55	58
1	C	247/256 (96%)	245 (99%)	2 (1%)	81	86
1	D	244/256 (95%)	239 (98%)	5 (2%)	55	58
All	All	996/1024 (97%)	980 (98%)	16 (2%)	65	67

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	84	TYR
1	D	79	SER
1	B	275	LEU
1	D	77	LYS
1	B	242[B]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	C	328	HIS
1	D	141	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 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	ACP	D	401	3	27,33,33	1.48	5 (18%)	32,52,52	1.34	5 (15%)
2	ACP	B	402[A]	3	27,33,33	1.40	5 (18%)	32,52,52	1.42	5 (15%)
2	ACP	C	402	3	27,33,33	1.70	6 (22%)	32,52,52	1.65	4 (12%)
2	ACP	A	401	3	27,33,33	2.06	6 (22%)	32,52,52	1.27	4 (12%)
4	RIB	C	401	-	10,10,10	0.64	0	13,14,14	1.46	2 (15%)
4	RIB	B	401	-	10,10,10	0.76	0	13,14,14	2.20	2 (15%)
2	ACP	B	402[B]	-	27,33,33	1.67	4 (14%)	32,52,52	1.23	4 (12%)

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	ACP	D	401	3	-	2/15/38/38	0/3/3/3
2	ACP	B	402[A]	3	-	1/15/38/38	0/3/3/3
2	ACP	C	402	3	-	3/15/38/38	0/3/3/3
2	ACP	A	401	3	-	5/15/38/38	0/3/3/3
4	RIB	C	401	-	-	0/2/18/18	0/1/1/1
4	RIB	B	401	-	-	0/2/18/18	0/1/1/1
2	ACP	B	402[B]	-	-	2/15/38/38	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	ACP	PB-O3A	6.57	1.65	1.58
2	B	402[B]	ACP	PB-O3A	6.00	1.65	1.58
2	C	402	ACP	PB-O3A	5.27	1.64	1.58
2	A	401	ACP	PG-O2G	4.55	1.65	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	ACP	PG-O3G	4.08	1.64	1.54

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	RIB	O1-C1-O4	-6.31	103.05	111.13
2	C	402	ACP	O2G-PG-C3B	4.32	116.88	106.40
2	C	402	ACP	N3-C2-N1	-4.02	122.40	128.68
4	B	401	RIB	O4-C1-C2	3.88	109.24	104.46
2	D	401	ACP	N3-C2-N1	-3.72	122.87	128.68

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402[B]	ACP	O4'-C4'-C5'-O5'
2	D	401	ACP	O4'-C4'-C5'-O5'
2	B	402[B]	ACP	C3'-C4'-C5'-O5'
2	A	401	ACP	C5'-O5'-PA-O3A
2	C	402	ACP	C5'-O5'-PA-O3A

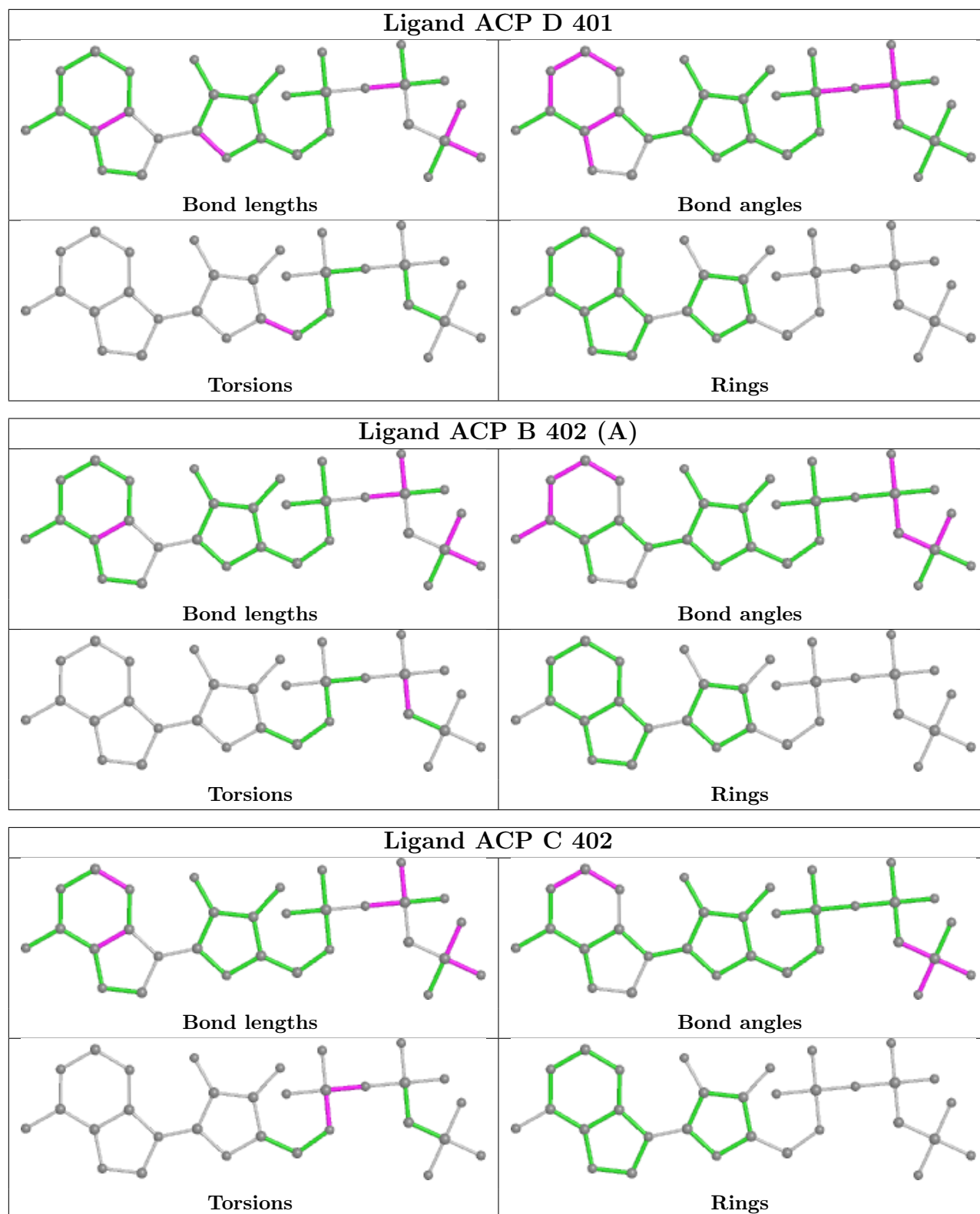
There are no ring outliers.

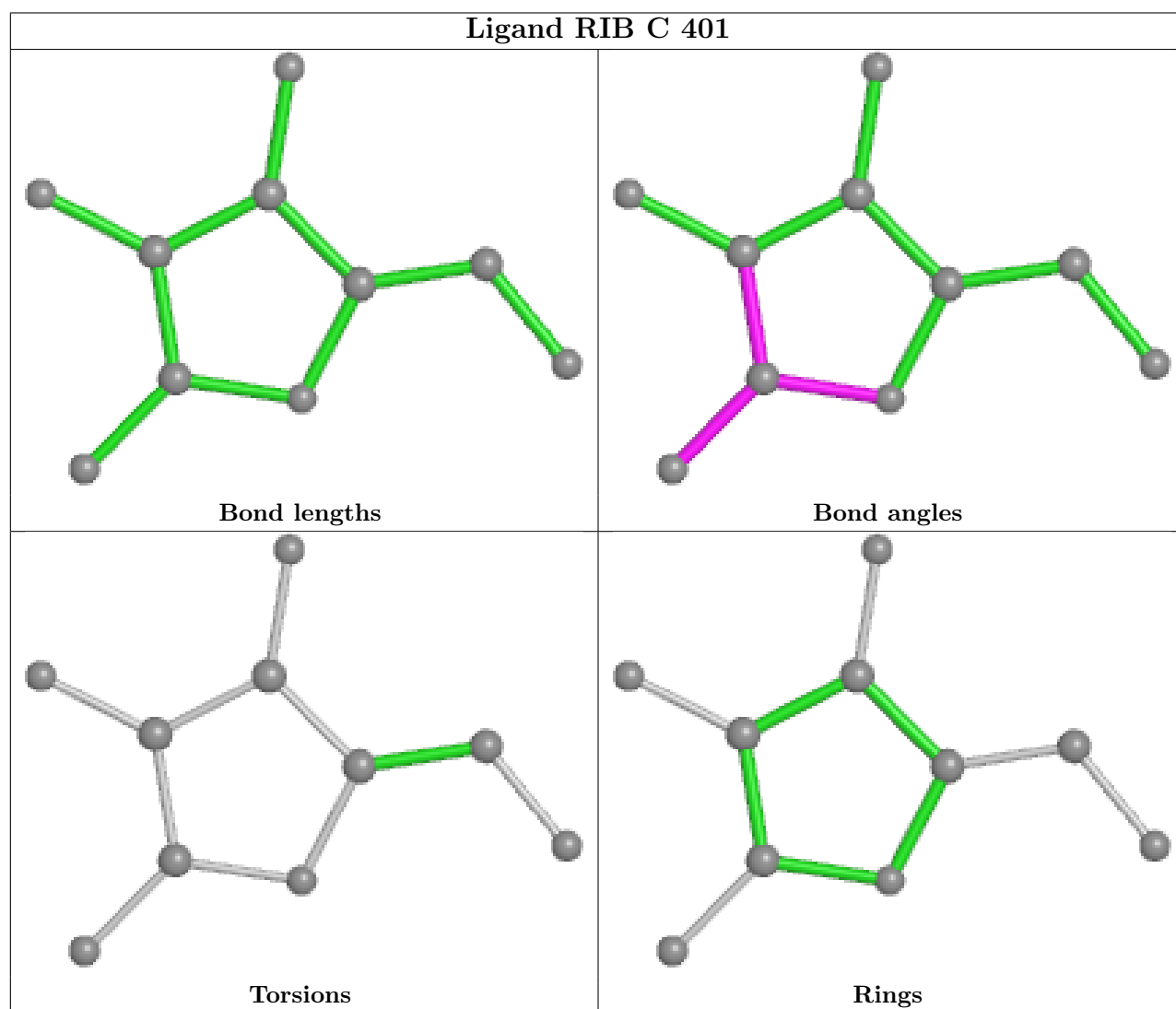
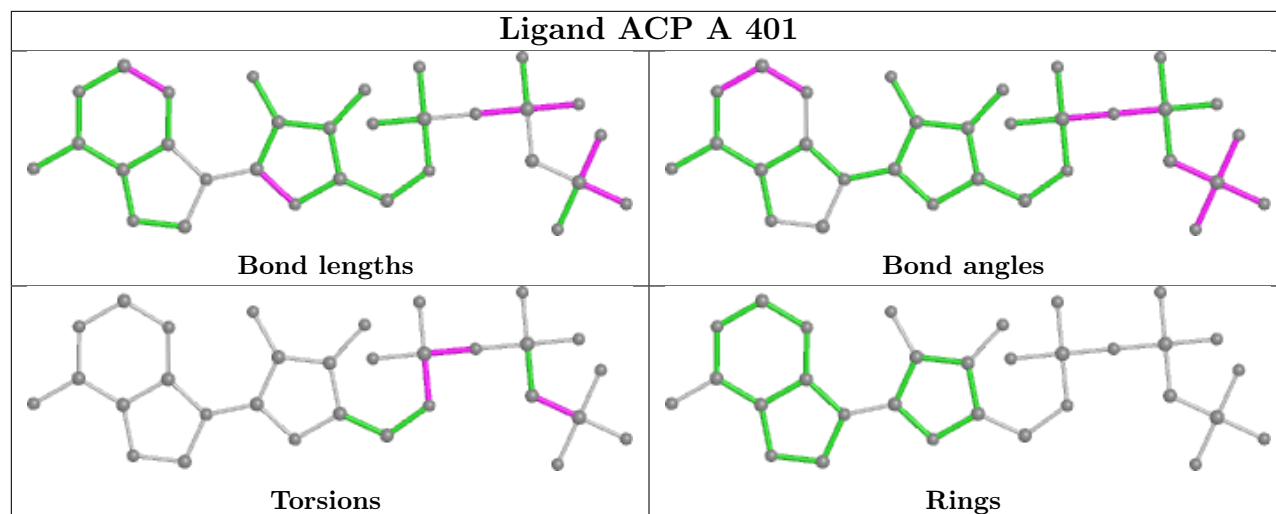
5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	402[A]	ACP	2	0
2	C	402	ACP	1	0
2	A	401	ACP	2	0
4	B	401	RIB	1	0
2	B	402[B]	ACP	4	0

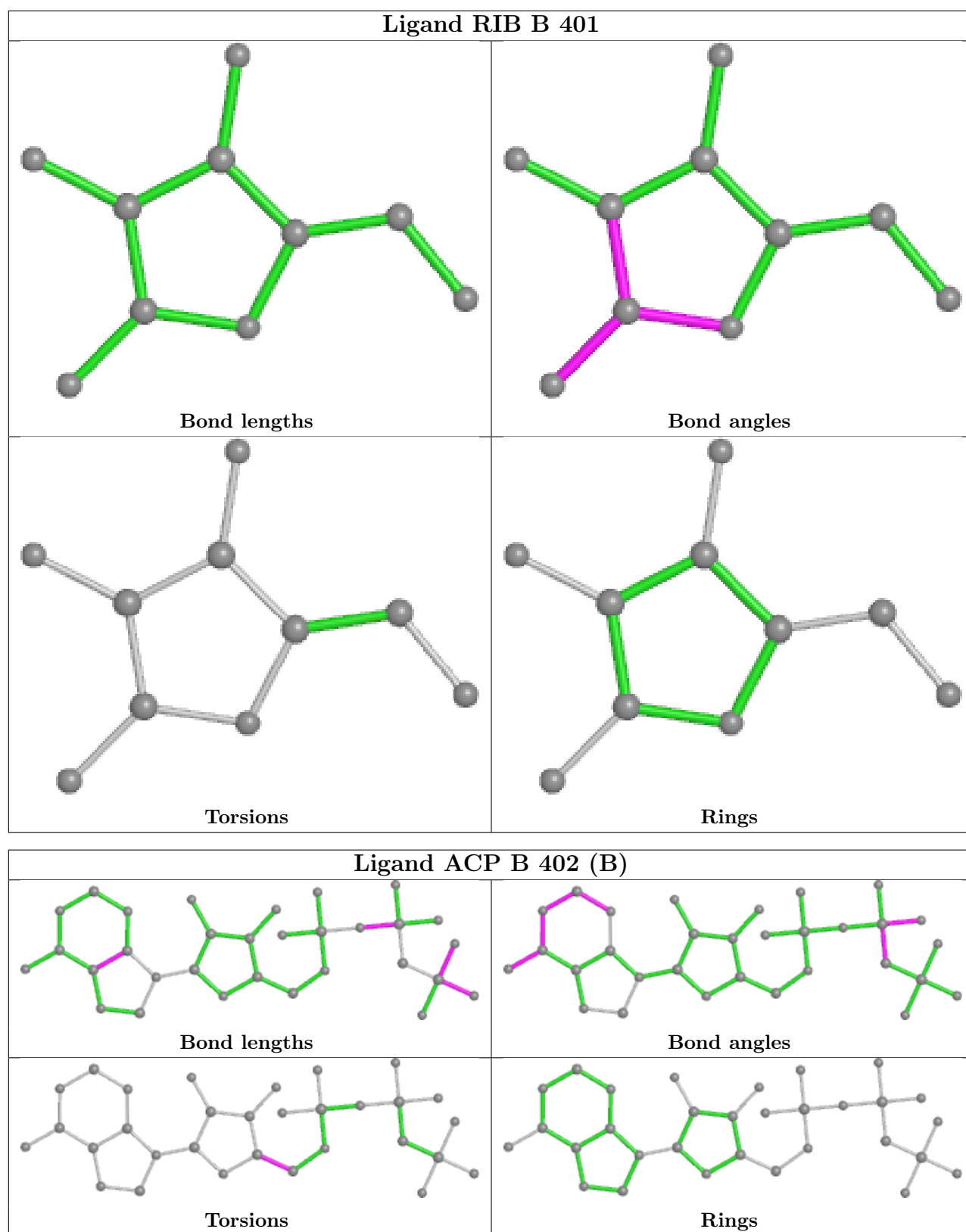
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	317/317 (100%)	-0.50	0 100 100	20, 30, 54, 80	0
1	B	311/317 (98%)	-0.57	0 100 100	23, 34, 57, 70	0
1	C	317/317 (100%)	-0.45	0 100 100	22, 35, 61, 86	0
1	D	316/317 (99%)	0.25	20 (6%) 20 19	36, 57, 102, 121	0
All	All	1261/1268 (99%)	-0.32	20 (1%) 72 70	20, 38, 78, 121	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	215	ALA	5.1
1	D	203	ALA	4.7
1	D	209	LEU	4.0
1	D	211	VAL	3.8
1	D	207	THR	3.8

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

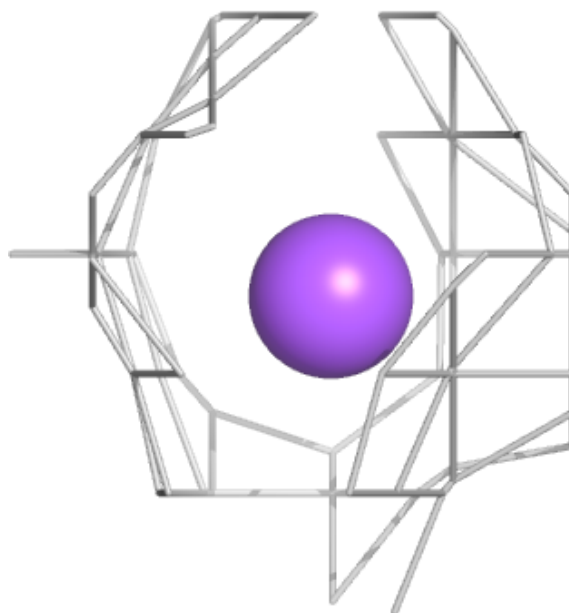
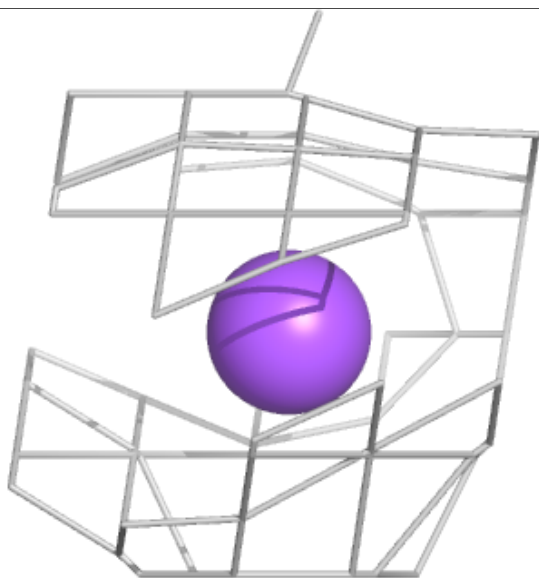
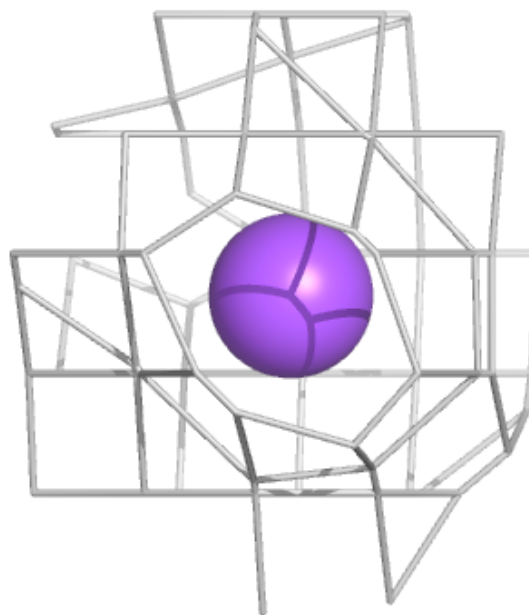
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
3	NA	D	402	1/1	0.79	0.09	55,55,55,55	0
3	NA	B	404	1/1	0.91	0.08	48,48,48,48	0
2	ACP	D	401	31/31	0.94	0.11	54,70,79,92	0
3	NA	D	403	1/1	0.95	0.05	54,54,54,54	0
2	ACP	A	401	31/31	0.96	0.08	21,27,40,47	0
2	ACP	B	402[A]	31/31	0.96	0.10	25,28,38,42	31
3	NA	C	403	1/1	0.96	0.04	30,30,30,30	0
2	ACP	B	402[B]	31/31	0.96	0.10	25,28,40,51	31
2	ACP	C	402	31/31	0.96	0.09	24,29,48,48	0
4	RIB	B	401	10/10	0.96	0.08	23,26,30,33	0
4	RIB	C	401	10/10	0.96	0.08	25,29,31,31	0
3	NA	B	403	1/1	0.98	0.07	26,26,26,26	0
3	NA	C	404	1/1	0.98	0.04	34,34,34,34	0
3	NA	A	402	1/1	0.99	0.03	26,26,26,26	0
3	NA	A	403	1/1	0.99	0.06	29,29,29,29	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.

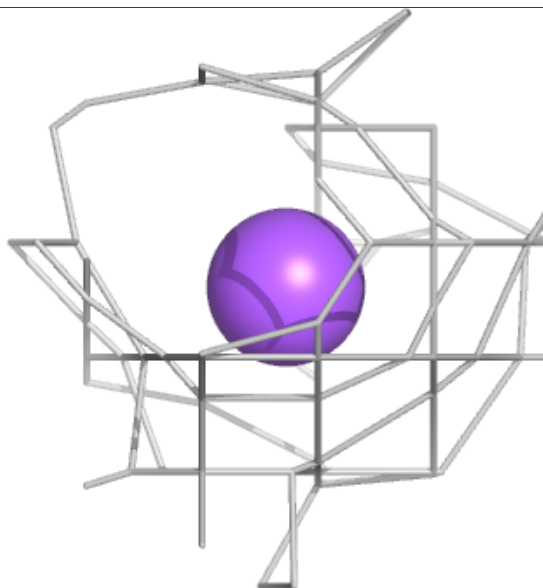
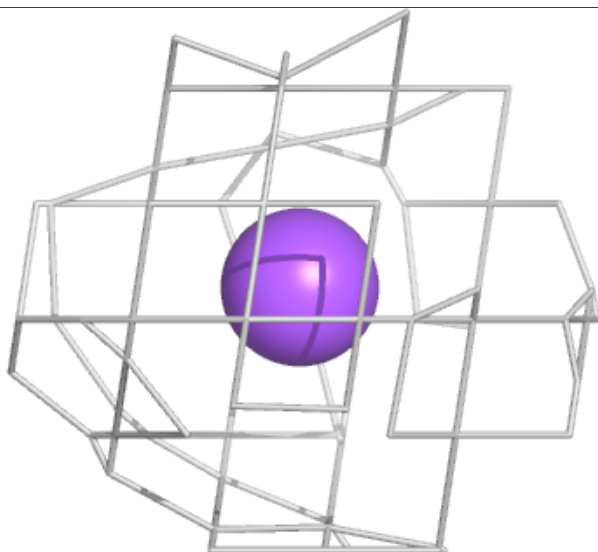
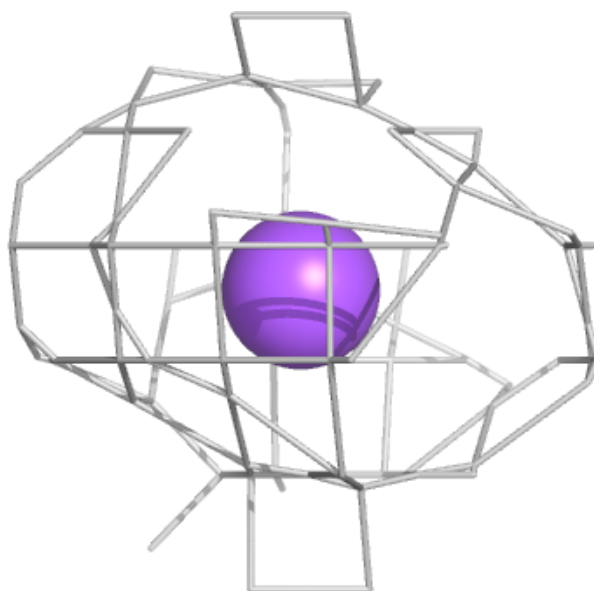
**Electron density around NA D 402:**

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



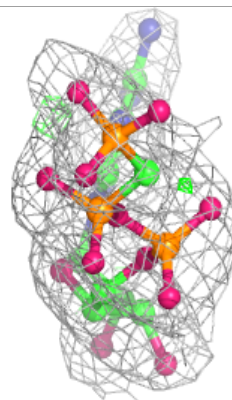
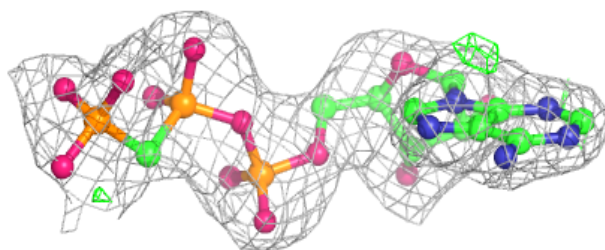
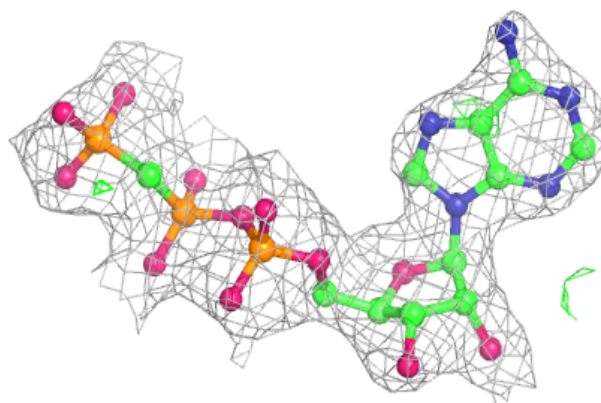
**Electron density around NA B 404:**

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



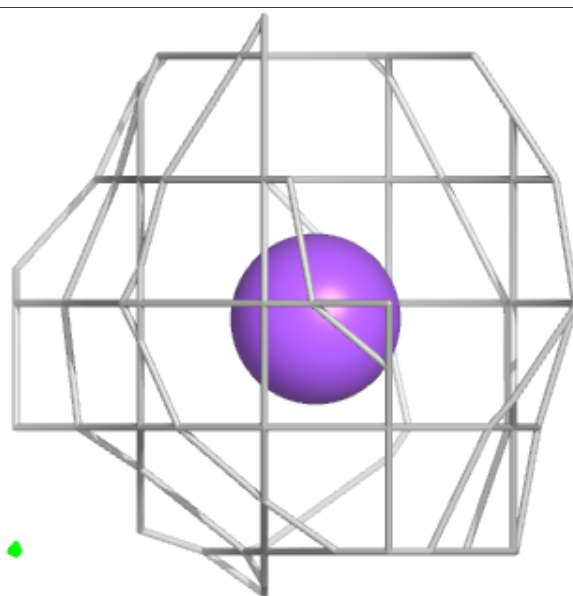
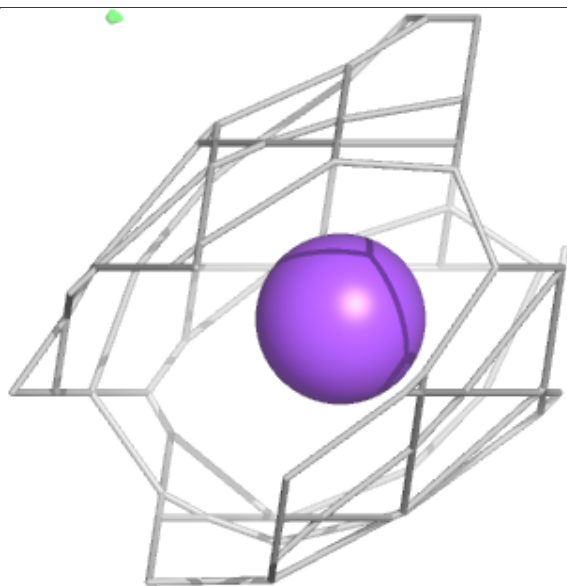
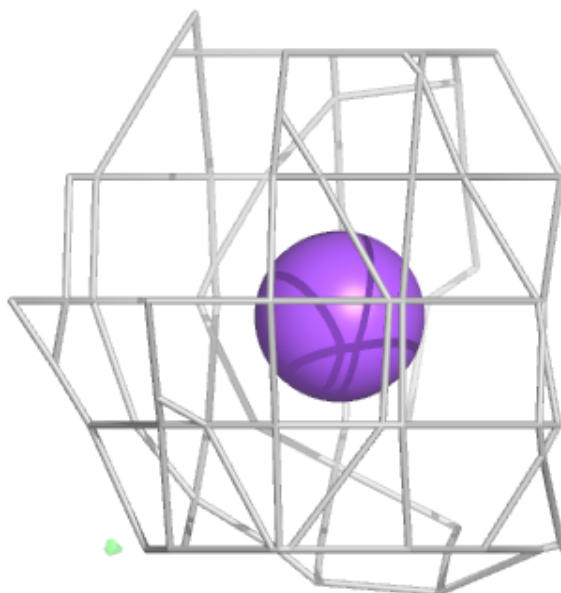
**Electron density around ACP D 401:**

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



**Electron density around NA D 403:**

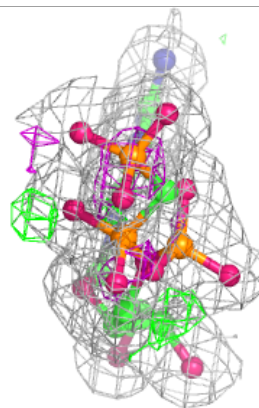
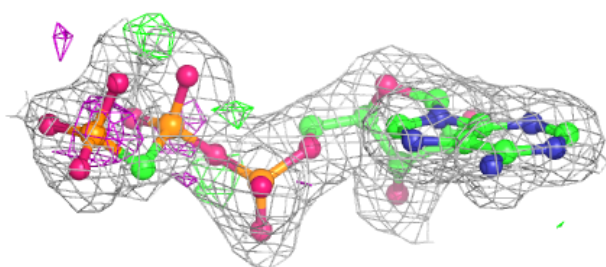
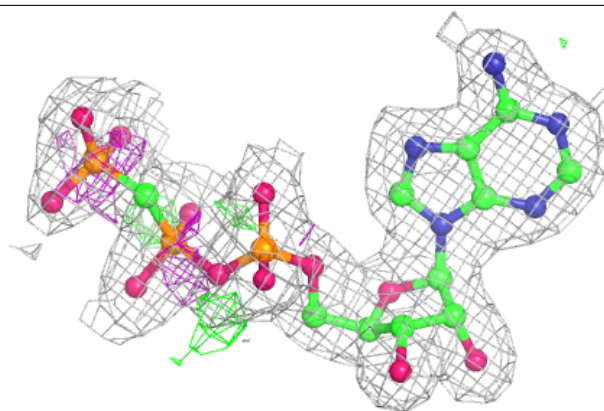
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



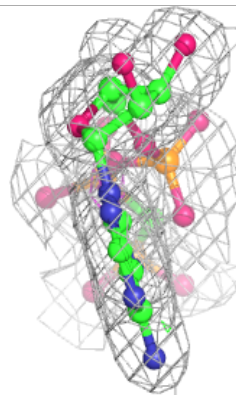
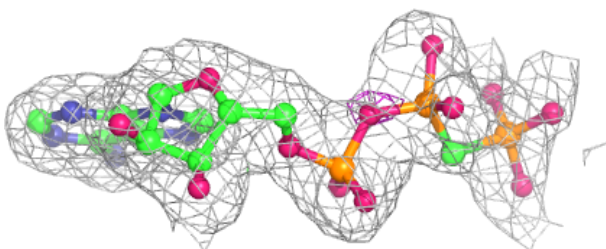
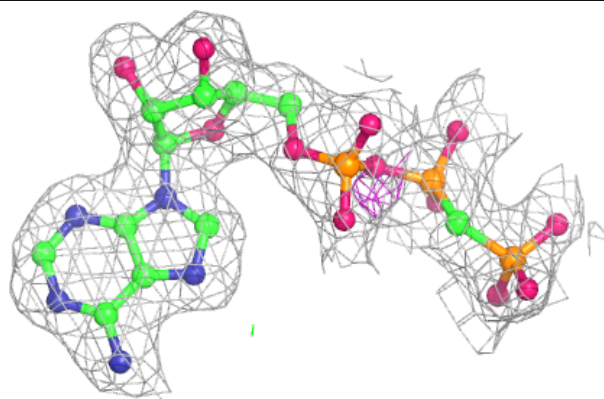


**Electron density around ACP A 401:**

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

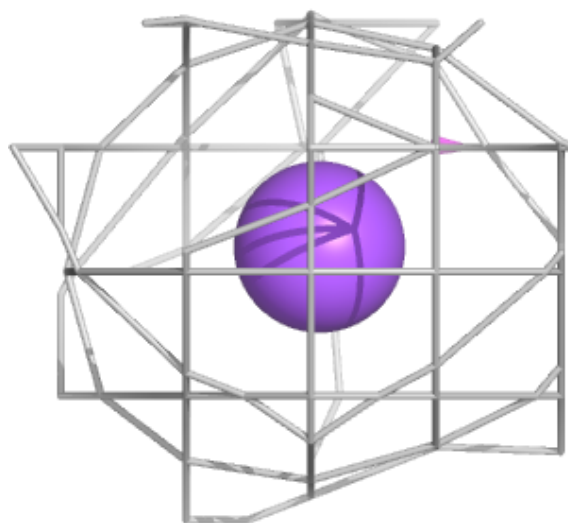
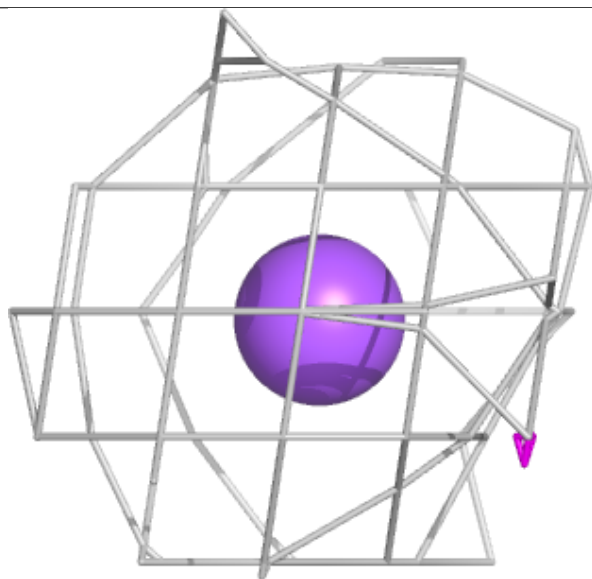
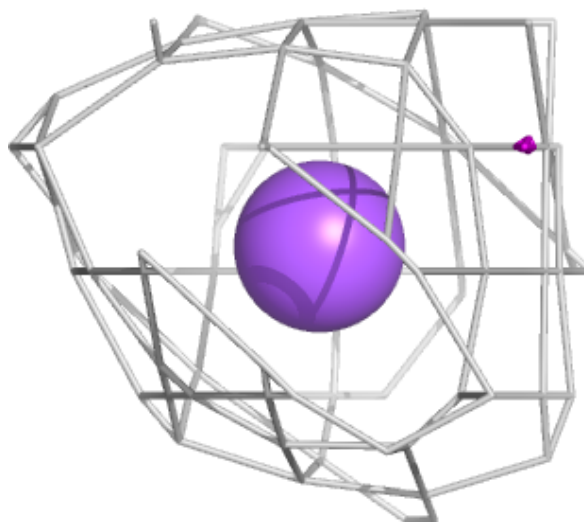
**Electron density around ACP B 402 (A):**

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and green (positive)



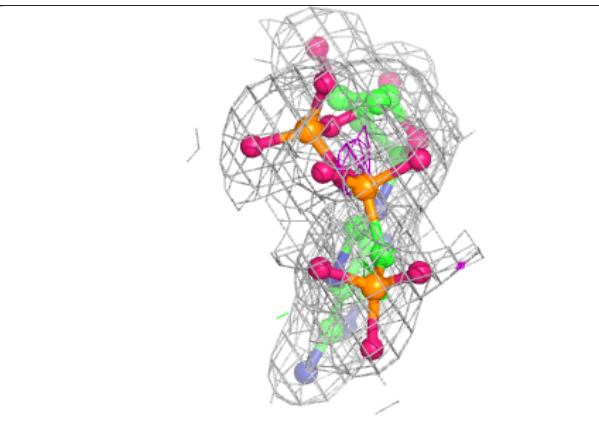
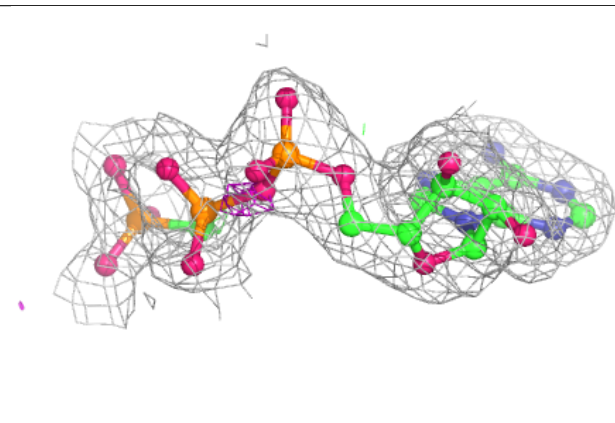
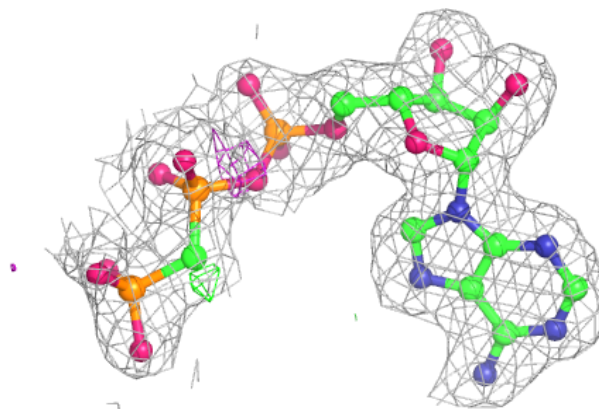
**Electron density around NA C 403:**

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and green (positive)

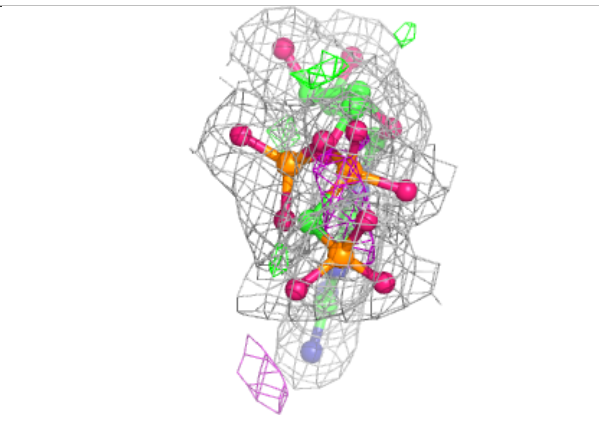
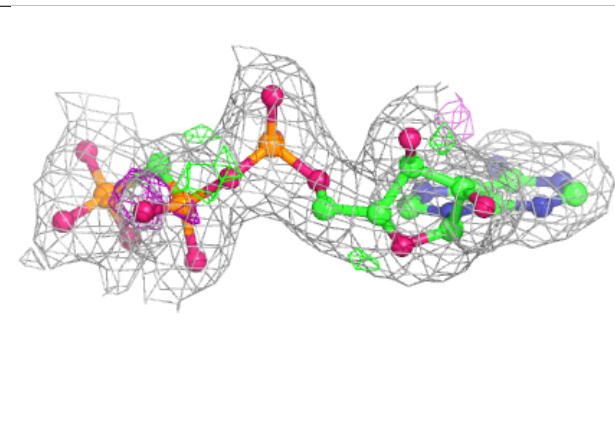
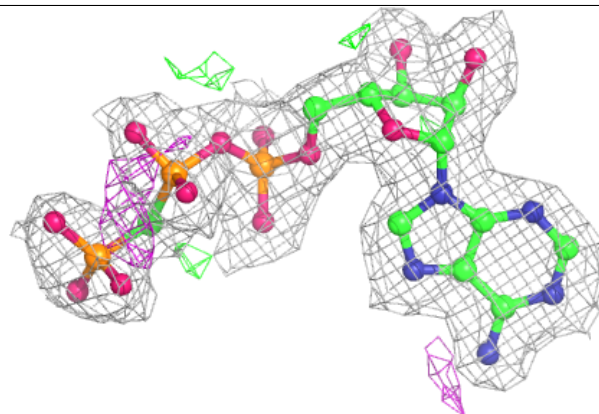


**Electron density around ACP B 402 (B):**

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and green (positive)

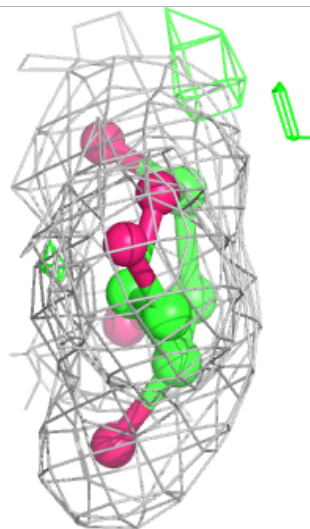
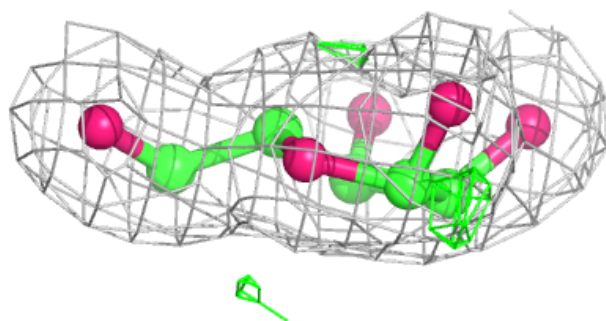
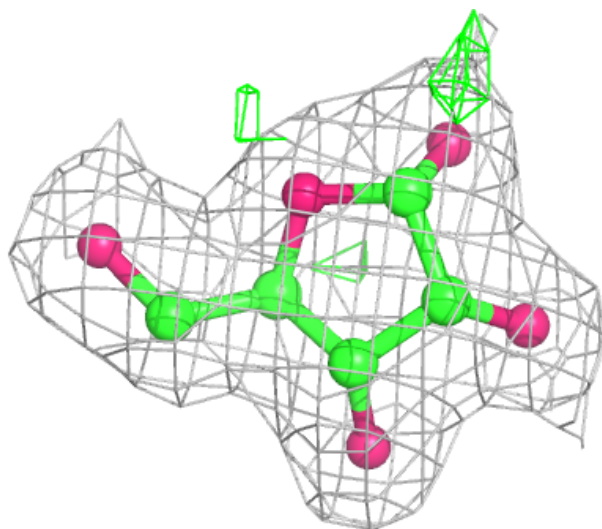
**Electron density around ACP C 402:**

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



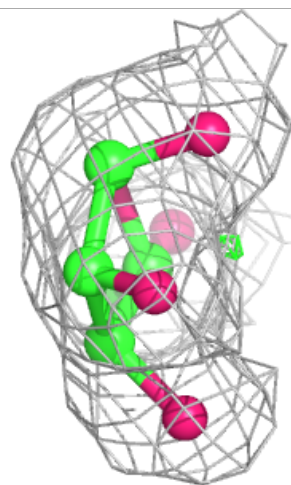
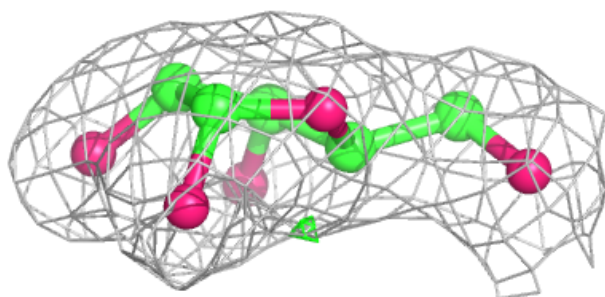
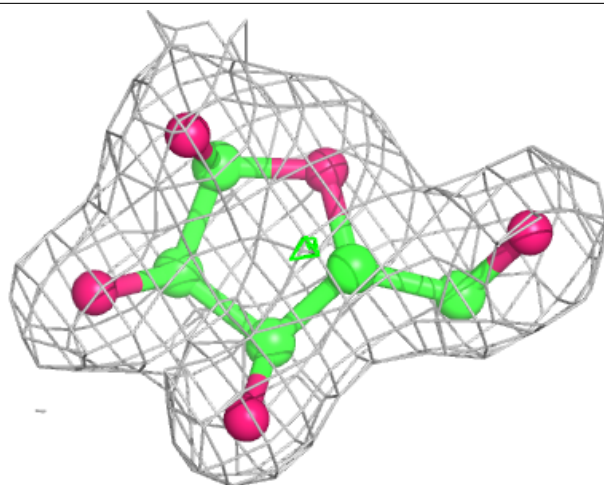
**Electron density around RIB B 401:**

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



**Electron density around RIB C 401:**

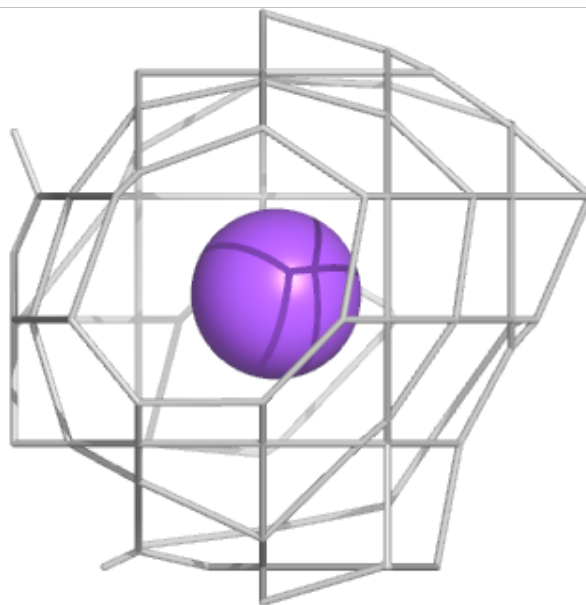
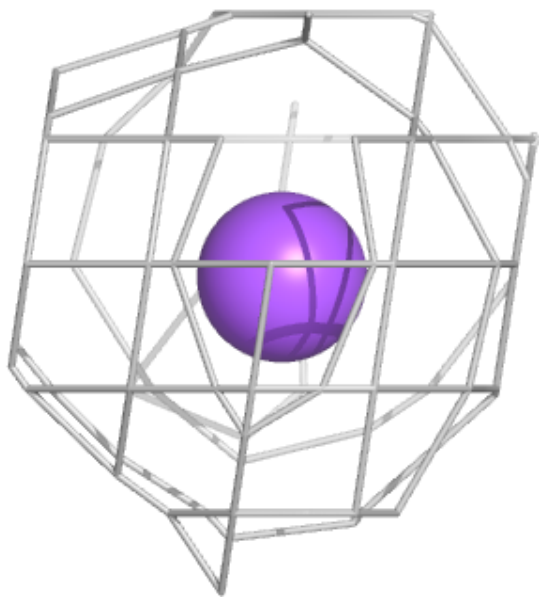
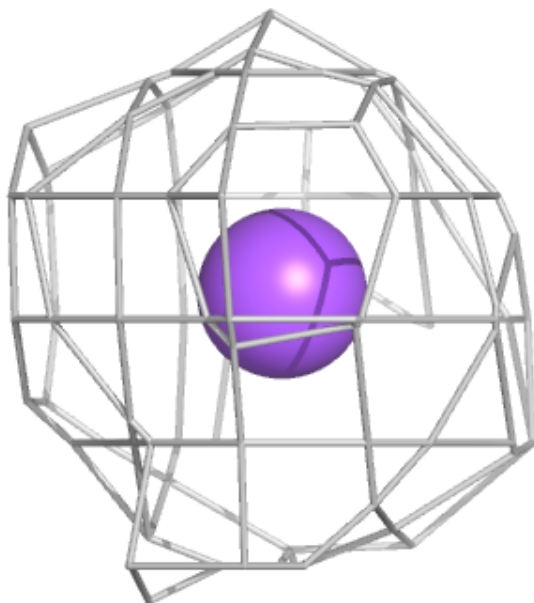
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





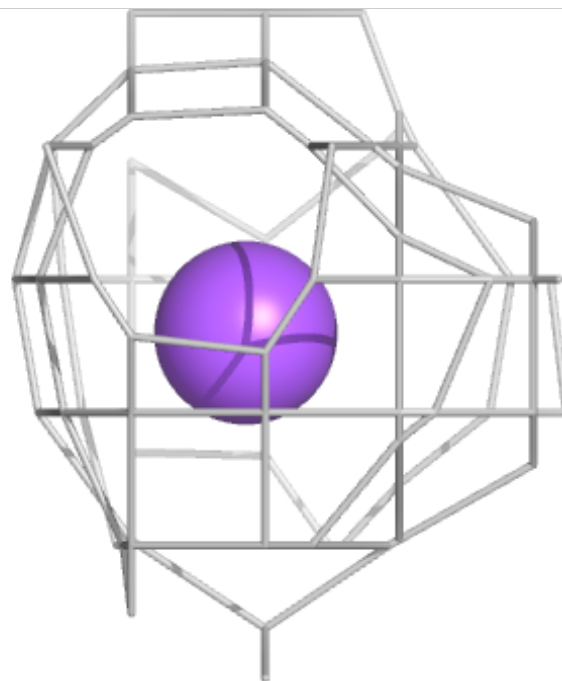
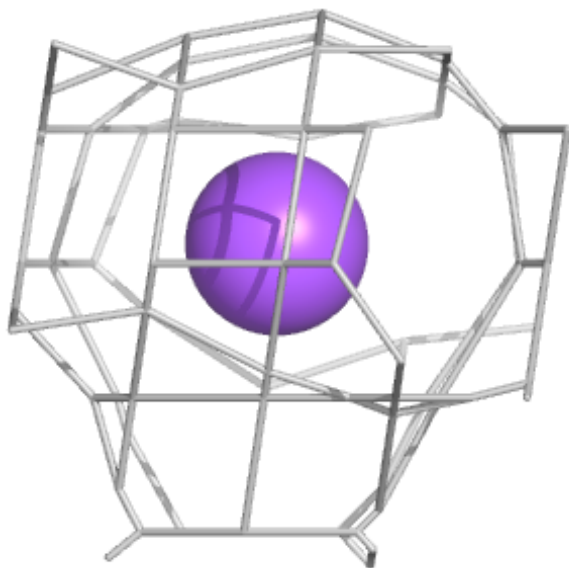
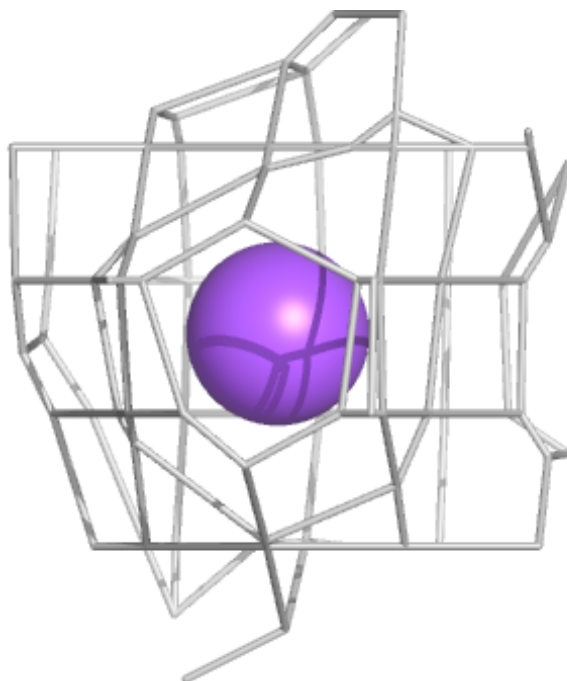
**Electron density around NA B 403:**

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



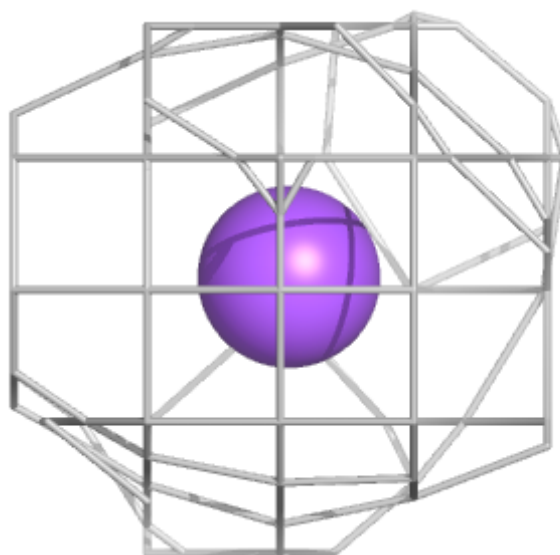
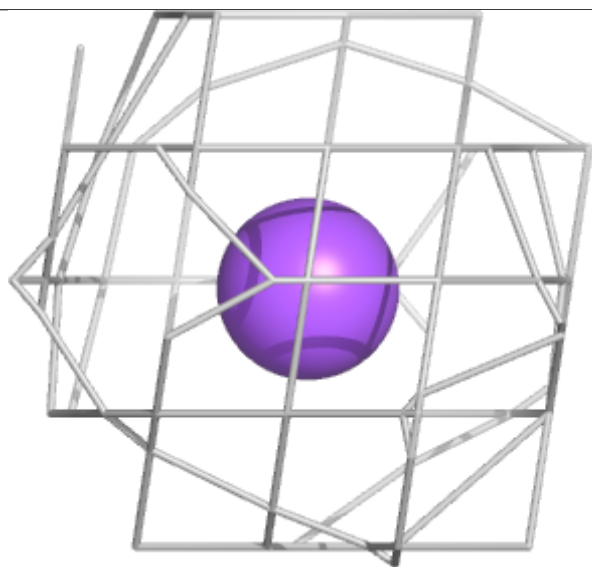
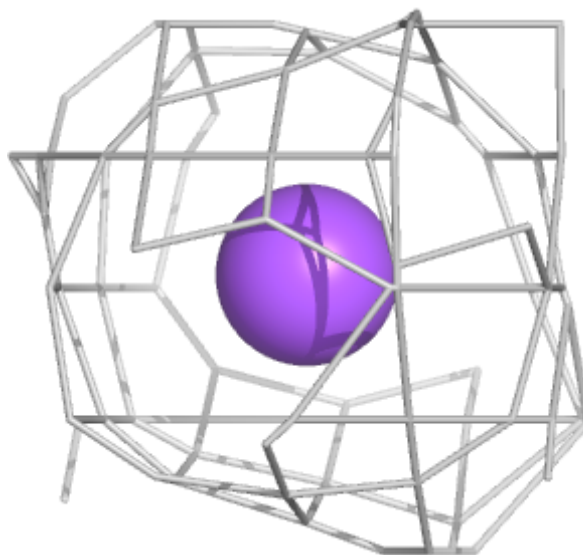
**Electron density around NA C 404:**

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and green (positive)



**Electron density around NA A 402:**

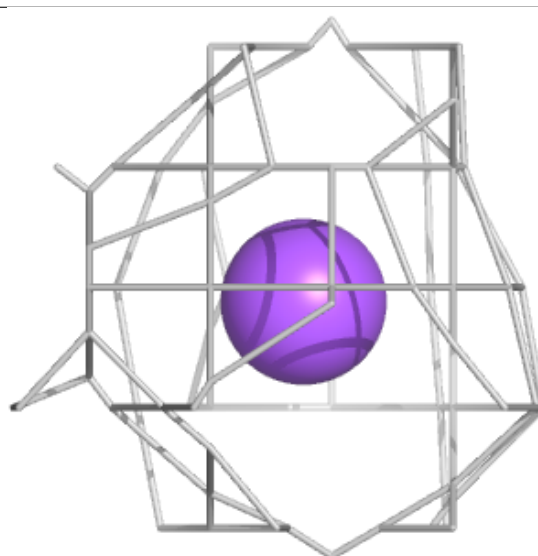
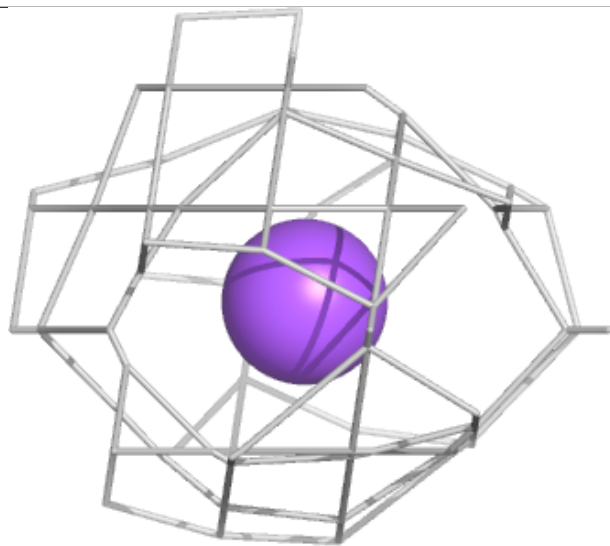
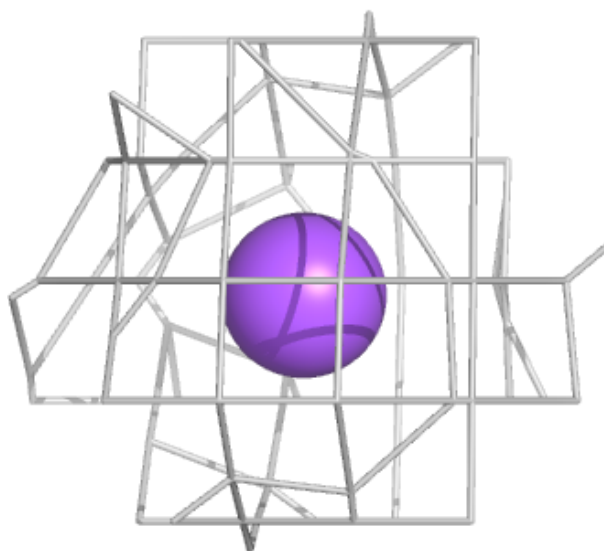
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around NA A 403:**

$2mF_o-DF_c$  (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.