



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 23, 2025 – 01:49 am BST

PDB ID : 9I16 / pdb_00009i16
Title : Structure of RecQL-dsDNA-ADP-AlF₄ complex from Bos taurus
Authors : Song, Z.Y.; Liu, N.N.; Ai, X.; Rety, S.; Xi, X.G.
Deposited on : 2025-01-16
Resolution : 2.82 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

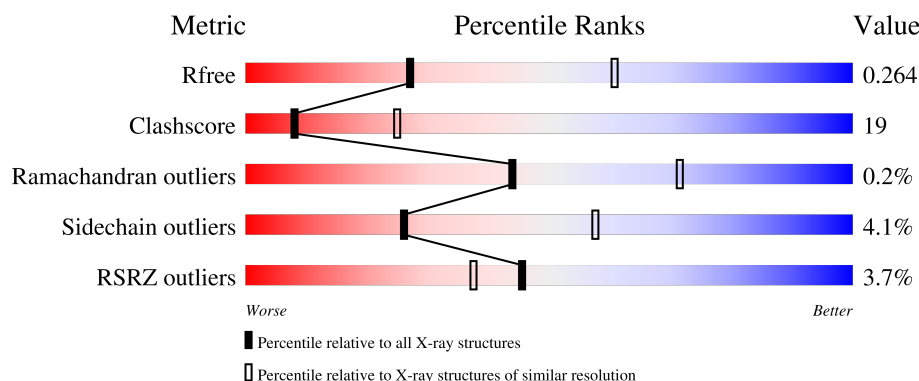
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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}	164625	4293 (2.84-2.80)
Clashscore	180529	4801 (2.84-2.80)
Ramachandran outliers	177936	4739 (2.84-2.80)
Sidechain outliers	177891	4741 (2.84-2.80)
RSRZ outliers	164620	4295 (2.84-2.80)

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	531	<div> <div>2%</div> <div>69%</div> <div>30%</div> <div>.</div> </div>
1	B	531	<div> <div>%</div> <div>72%</div> <div>27%</div> <div>.</div> </div>
1	C	531	<div> <div>%</div> <div>76%</div> <div>24%</div> <div>.</div> </div>
1	E	531	<div> <div>8%</div> <div>52%</div> <div>45%</div> <div>.</div> </div>
1	F	531	<div> <div>3%</div> <div>57%</div> <div>39%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	531	
3	G	21	
3	I	21	
3	K	21	
4	H	15	
4	J	15	
4	L	15	

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
8	PO4	F	1003	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 27673 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 ATP-dependent DNA helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	531	Total	C	N	O	S	0	0	0
			4237	2704	727	770	36			
1	B	531	Total	C	N	O	S	0	0	0
			4237	2704	727	770	36			
1	C	531	Total	C	N	O	S	0	0	0
			4237	2704	727	770	36			
1	E	531	Total	C	N	O	S	0	0	0
			4237	2704	727	770	36			
1	F	531	Total	C	N	O	S	0	0	0
			4237	2704	727	770	36			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	MET	-	initiating methionine	UNP A0JN36
B	62	MET	-	initiating methionine	UNP A0JN36
C	62	MET	-	initiating methionine	UNP A0JN36
E	62	MET	-	initiating methionine	UNP A0JN36
F	62	MET	-	initiating methionine	UNP A0JN36

- Molecule 2 is a protein called ATP-dependent DNA helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	531	Total	C	N	O	S	0	0	0
			4237	2703	727	772	35			

- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*TP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	18	Total	C	N	O	P	0	0	0
			362	172	62	110	18			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	18	Total	C	N	O	P	0	0	0
			362	172	62	110	18			
3	K	18	Total	C	N	O	P	0	0	0
			362	172	62	110	18			

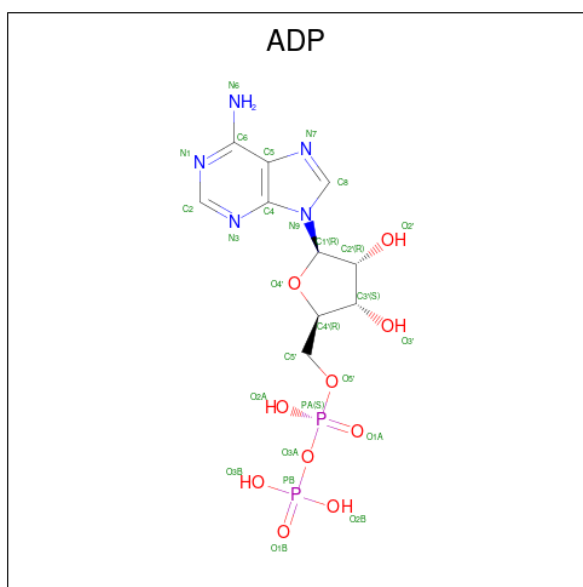
- Molecule 4 is a DNA chain called DNA (5'-D(P*AP*GP*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	15	Total	C	N	O	P	0	0	0
			310	146	61	88	15			
4	J	15	Total	C	N	O	P	0	0	0
			310	146	61	88	15			
4	L	15	Total	C	N	O	P	0	0	0
			310	146	61	88	15			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		
5	C	1	Total	Zn	0	0
			1	1		
5	D	1	Total	Zn	0	0
			1	1		
5	E	1	Total	Zn	0	0
			1	1		
5	F	1	Total	Zn	0	0
			1	1		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	0	0
			1	1		
7	B	1	Total	Mg	0	0
			1	1		
7	C	2	Total	Mg	0	0
			2	2		

- Molecule 8 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	P	0	0
			5	4	1		
8	A	1	Total	O	P	0	0
			5	4	1		
8	A	1	Total	O	P	0	0
			5	4	1		
8	A	1	Total	O	P	0	0
			5	4	1		
8	B	1	Total	O	P	0	0
			5	4	1		
8	B	1	Total	O	P	0	0
			5	4	1		
8	C	1	Total	O	P	0	0
			5	4	1		
8	C	1	Total	O	P	0	0
			5	4	1		
8	E	1	Total	O	P	0	0
			5	4	1		
8	F	1	Total	O	P	0	0
			5	4	1		
8	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 9 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	2	Total	K	0	0
			2	2		

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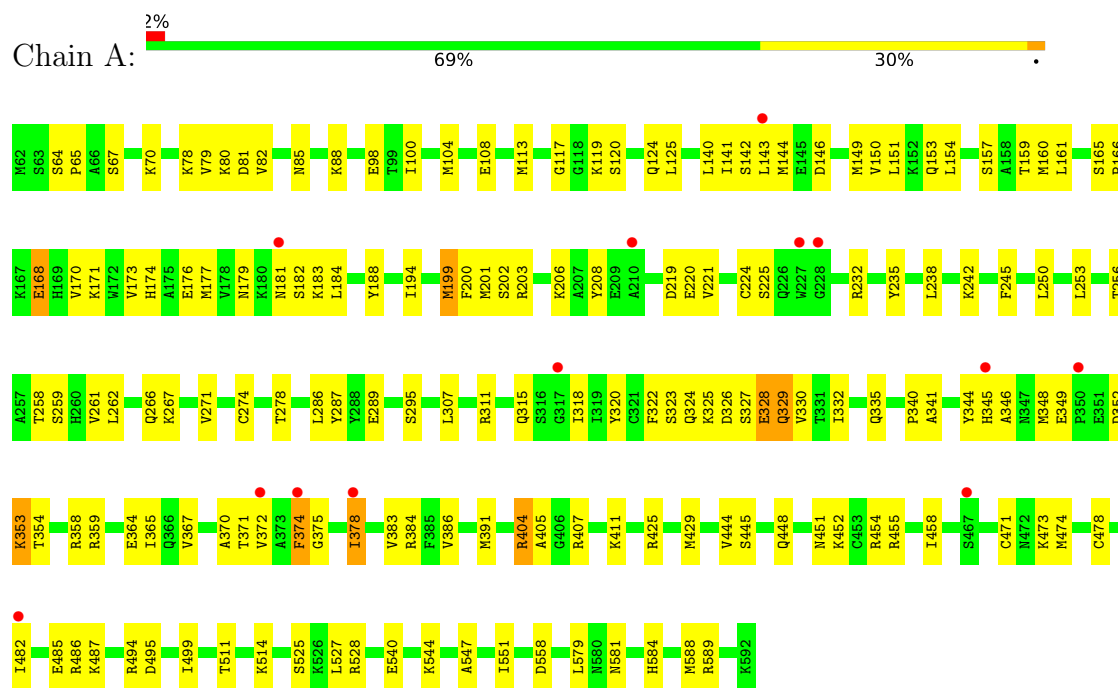
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	4	Total 4	K 4	0	0
9	C	1	Total 1	K 1	0	0
9	G	1	Total 1	K 1	0	0

3 Residue-property plots

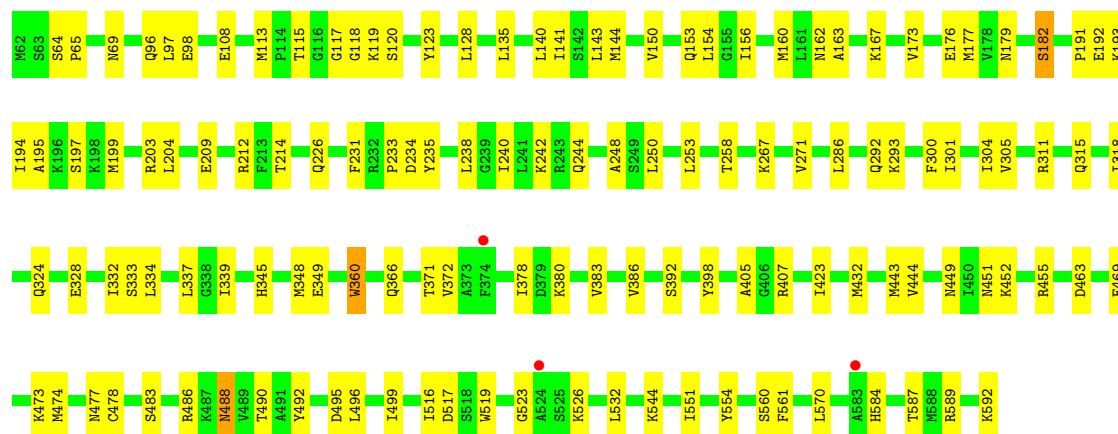
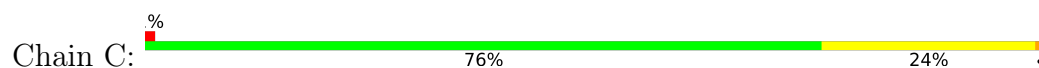
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: ATP-dependent DNA helicase

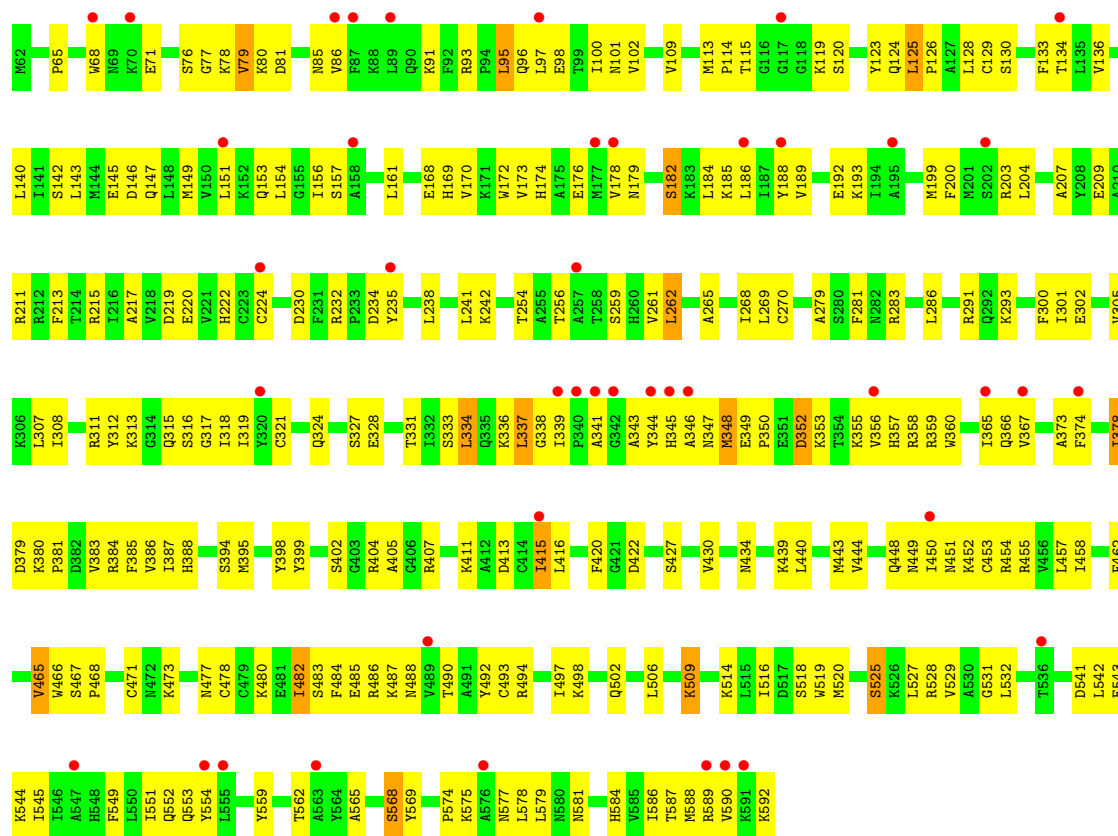




• Molecule 1: ATP-dependent DNA helicase

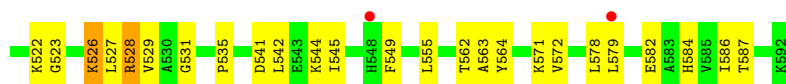


• Molecule 1: ATP-dependent DNA helicase

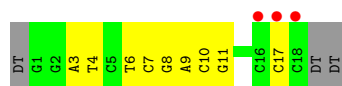
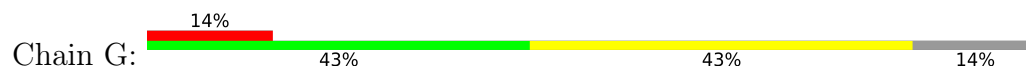


• Molecule 1: ATP-dependent DNA helicase





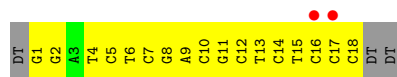
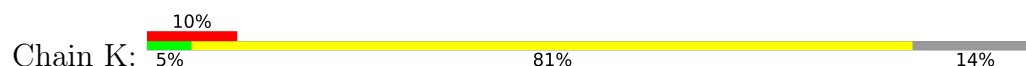
- Molecule 3: DNA (5'-D(P*GP*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*TP*C P*CP*C)-3')



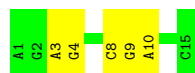
- Molecule 3: DNA (5'-D(P*GP*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*TP*C P*CP*C)-3')



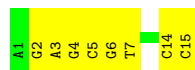
- Molecule 3: DNA (5'-D(P*GP*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*TP*C P*CP*C)-3')



- Molecule 4: DNA (5'-D(P*AP*GP*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*C)-3')



- Molecule 4: DNA (5'-D(P*AP*GP*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*C)-3')



- Molecule 4: DNA (5'-D(P*AP*GP*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*C)-3')





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	117.56Å 112.08Å 181.79Å 90.00° 92.73° 90.00°	Depositor
Resolution (Å)	29.89 – 2.82 29.89 – 2.82	Depositor EDS
% Data completeness (in resolution range)	69.2 (29.89-2.82) 69.1 (29.89-2.82)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.80Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.218 , 0.265 0.218 , 0.264	Depositor DCC
R_{free} test set	3927 reflections (3.45%)	wwPDB-VP
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 66.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	27673	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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: PO4, MG, ZN, K, ADP

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	0.28	0/4325	0.61	10/5830 (0.2%)
1	B	0.21	0/4325	0.45	2/5830 (0.0%)
1	C	0.16	0/4325	0.44	3/5830 (0.1%)
1	E	0.24	0/4325	0.57	2/5830 (0.0%)
1	F	0.30	2/4325 (0.0%)	0.58	5/5830 (0.1%)
2	D	0.54	6/4325 (0.1%)	1.00	35/5831 (0.6%)
3	G	0.26	0/403	0.55	0/618
3	I	0.30	0/403	0.66	0/618
3	K	0.33	0/403	0.66	0/618
4	H	0.22	0/348	0.44	0/535
4	J	0.33	0/348	0.50	0/535
4	L	0.35	0/348	0.56	0/535
All	All	0.31	8/28203 (0.0%)	0.63	57/38440 (0.1%)

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
1	B	0	4
1	C	0	1
1	E	0	1
1	F	0	2
2	D	0	4
All	All	0	13

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	132	GLY	C-O	-16.47	1.15	1.24
2	D	401	GLU	CD-OE2	11.49	1.47	1.25
2	D	183	LYS	CD-CE	7.17	1.74	1.52
2	D	404	ARG	CA-CB	5.89	1.63	1.53
1	F	381	PRO	CA-CB	-5.78	1.44	1.53

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	192	GLU	CG-CD-OE1	19.04	162.18	118.40
2	D	192	GLU	CB-CG-CD	-18.93	80.42	112.60
2	D	192	GLU	OE1-CD-OE2	-16.01	84.47	122.90
2	D	192	GLU	CG-CD-OE2	-14.47	85.12	118.40
1	A	199	MET	CB-CG-SD	-12.57	74.98	112.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	404	ARG	Sidechain
1	B	229	HIS	Peptide
1	B	265	ALA	Peptide
1	B	425	ARG	Sidechain
1	B	70	LYS	Peptide

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	4237	0	4295	137	0
1	B	4237	0	4295	119	0
1	C	4237	0	4295	86	0
1	E	4237	0	4294	244	0
1	F	4237	0	4295	175	0
2	D	4237	0	4290	246	0
3	G	362	0	203	14	0
3	I	362	0	203	15	0
3	K	362	0	203	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	310	0	168	4	0
4	J	310	0	168	7	0
4	L	310	0	168	12	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
6	A	27	0	12	0	0
6	B	27	0	12	0	0
6	C	27	0	12	0	0
6	D	27	0	12	1	0
6	E	27	0	12	3	0
6	F	27	0	12	1	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	2	0	0	0	0
8	A	20	0	0	0	0
8	B	10	0	0	1	0
8	C	10	0	0	1	0
8	E	5	0	0	0	0
8	F	10	0	0	2	0
9	A	2	0	0	0	0
9	B	4	0	0	0	0
9	C	1	0	0	0	0
9	G	1	0	0	0	0
All	All	27673	0	26949	1045	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 19.

The worst 5 of 1045 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:D:359:ARG:O	2:D:365:ILE:HD12	1.47	1.16
2:D:398:TYR:CA	2:D:401:GLU:HG3	1.77	1.13
2:D:398:TYR:HA	2:D:401:GLU:CG	1.79	1.13
1:A:140:LEU:HB2	1:A:143:LEU:HD13	1.43	0.98
1:F:565:ALA:HB1	3:K:16:DC:H41	1.33	0.94

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	529/531 (100%)	528 (100%)	1 (0%)	0	100	100
1	B	529/531 (100%)	524 (99%)	5 (1%)	0	100	100
1	C	529/531 (100%)	528 (100%)	1 (0%)	0	100	100
1	E	529/531 (100%)	523 (99%)	5 (1%)	1 (0%)	44	71
1	F	529/531 (100%)	520 (98%)	4 (1%)	5 (1%)	14	39
2	D	529/531 (100%)	522 (99%)	6 (1%)	1 (0%)	44	71
All	All	3174/3186 (100%)	3145 (99%)	22 (1%)	7 (0%)	44	71

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	335	GLN
1	F	482	ILE
1	E	348	MET
1	F	346	ALA
1	F	348	MET

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	469/469 (100%)	451 (96%)	18 (4%)	28	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	469/469 (100%)	456 (97%)	13 (3%)	38	71
1	C	469/469 (100%)	455 (97%)	14 (3%)	36	69
1	E	469/469 (100%)	446 (95%)	23 (5%)	21	50
1	F	469/469 (100%)	447 (95%)	22 (5%)	22	52
2	D	469/469 (100%)	445 (95%)	24 (5%)	20	49
All	All	2814/2814 (100%)	2700 (96%)	114 (4%)	26	57

5 of 114 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	365	ILE
1	F	478	CYS
1	E	95	LEU
1	F	450	ILE
1	F	198	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	366	GLN
1	F	438	GLN
1	F	577	ASN
1	C	292	GLN
1	C	226	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 35 ligands modelled in this entry, 18 are monoatomic - leaving 17 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	ADP	E	1002	-	24,29,29	0.94	1 (4%)	29,45,45	1.44	4 (13%)
8	PO4	B	1004	-	4,4,4	0.92	0	6,6,6	0.40	0
8	PO4	A	1007	-	4,4,4	0.92	0	6,6,6	0.48	0
8	PO4	A	1004	-	4,4,4	0.88	0	6,6,6	0.44	0
8	PO4	E	1003	-	4,4,4	0.92	0	6,6,6	0.43	0
6	ADP	D	1002	-	24,29,29	0.97	1 (4%)	29,45,45	1.35	4 (13%)
6	ADP	A	1002	-	24,29,29	0.97	1 (4%)	29,45,45	1.42	4 (13%)
6	ADP	F	1002	-	24,29,29	0.96	1 (4%)	29,45,45	1.47	4 (13%)
8	PO4	A	1005	-	4,4,4	0.93	0	6,6,6	0.41	0
8	PO4	C	1004	-	4,4,4	0.91	0	6,6,6	0.44	0
8	PO4	F	1004	-	4,4,4	0.91	0	6,6,6	0.43	0
8	PO4	A	1006	-	4,4,4	0.89	0	6,6,6	0.45	0
8	PO4	F	1003	-	4,4,4	0.93	0	6,6,6	0.41	0
6	ADP	C	1002	-	24,29,29	0.93	1 (4%)	29,45,45	1.38	4 (13%)
6	ADP	B	1002	-	24,29,29	0.95	1 (4%)	29,45,45	1.40	4 (13%)
8	PO4	C	1005	-	4,4,4	1.02	0	6,6,6	0.54	0
8	PO4	B	1005	-	4,4,4	0.99	0	6,6,6	0.48	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
6	ADP	E	1002	-	-	0/12/32/32	0/3/3/3
6	ADP	D	1002	-	-	4/12/32/32	0/3/3/3
6	ADP	A	1002	-	-	3/12/32/32	0/3/3/3
6	ADP	F	1002	-	-	3/12/32/32	0/3/3/3
6	ADP	C	1002	-	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	ADP	B	1002	-	-	3/12/32/32	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	1002	ADP	C5-C4	2.51	1.47	1.40
6	A	1002	ADP	C5-C4	2.51	1.47	1.40
6	F	1002	ADP	C5-C4	2.47	1.47	1.40
6	C	1002	ADP	C5-C4	2.46	1.47	1.40
6	B	1002	ADP	C5-C4	2.46	1.47	1.40

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1002	ADP	N3-C2-N1	-3.35	123.45	128.68
6	B	1002	ADP	PA-O3A-PB	-3.34	121.38	132.83
6	A	1002	ADP	PA-O3A-PB	-3.32	121.43	132.83
6	F	1002	ADP	PA-O3A-PB	-3.32	121.45	132.83
6	F	1002	ADP	C3'-C2'-C1'	3.27	105.91	100.98

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

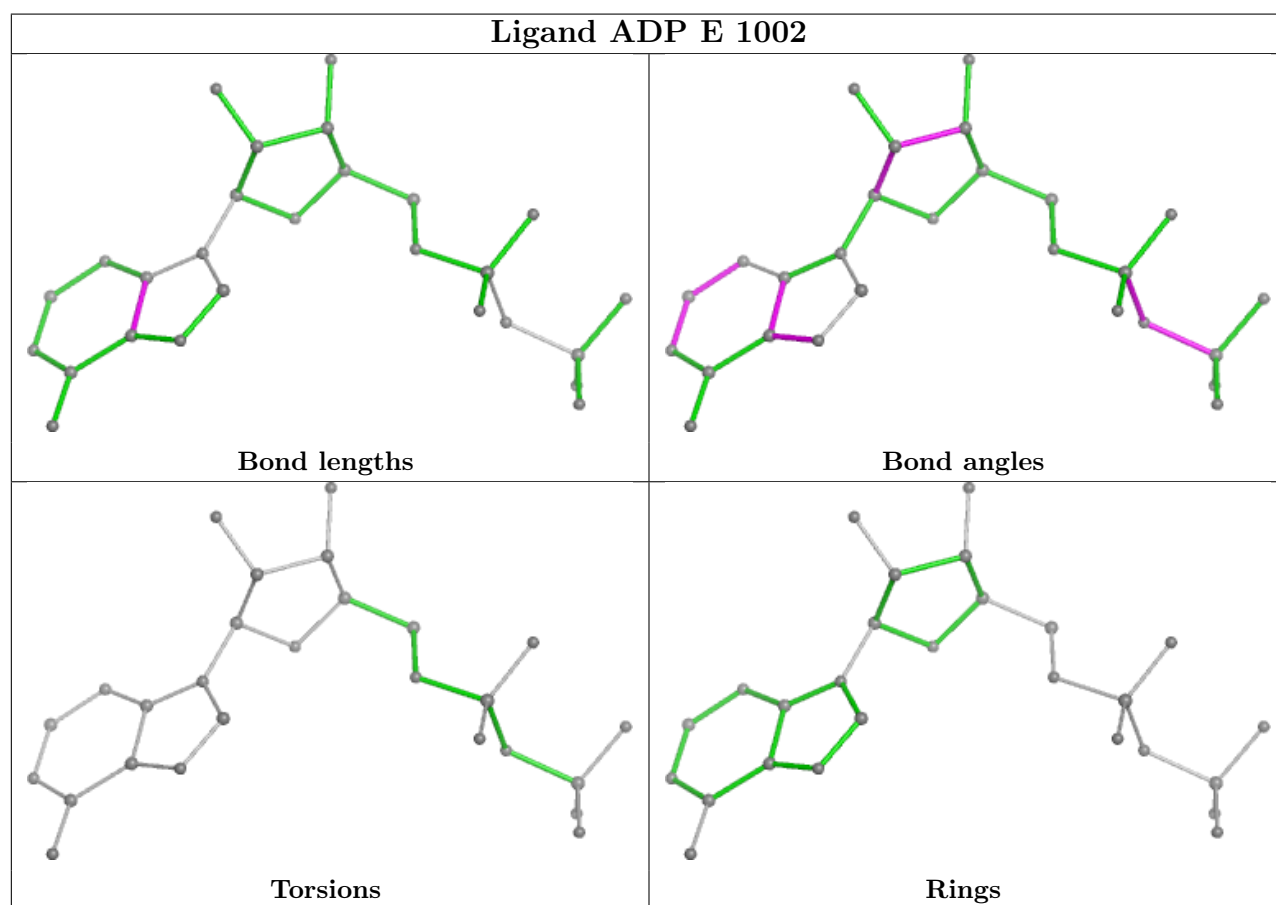
Mol	Chain	Res	Type	Atoms
6	A	1002	ADP	C5'-O5'-PA-O1A
6	A	1002	ADP	C5'-O5'-PA-O2A
6	B	1002	ADP	C5'-O5'-PA-O1A
6	B	1002	ADP	C5'-O5'-PA-O2A
6	C	1002	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

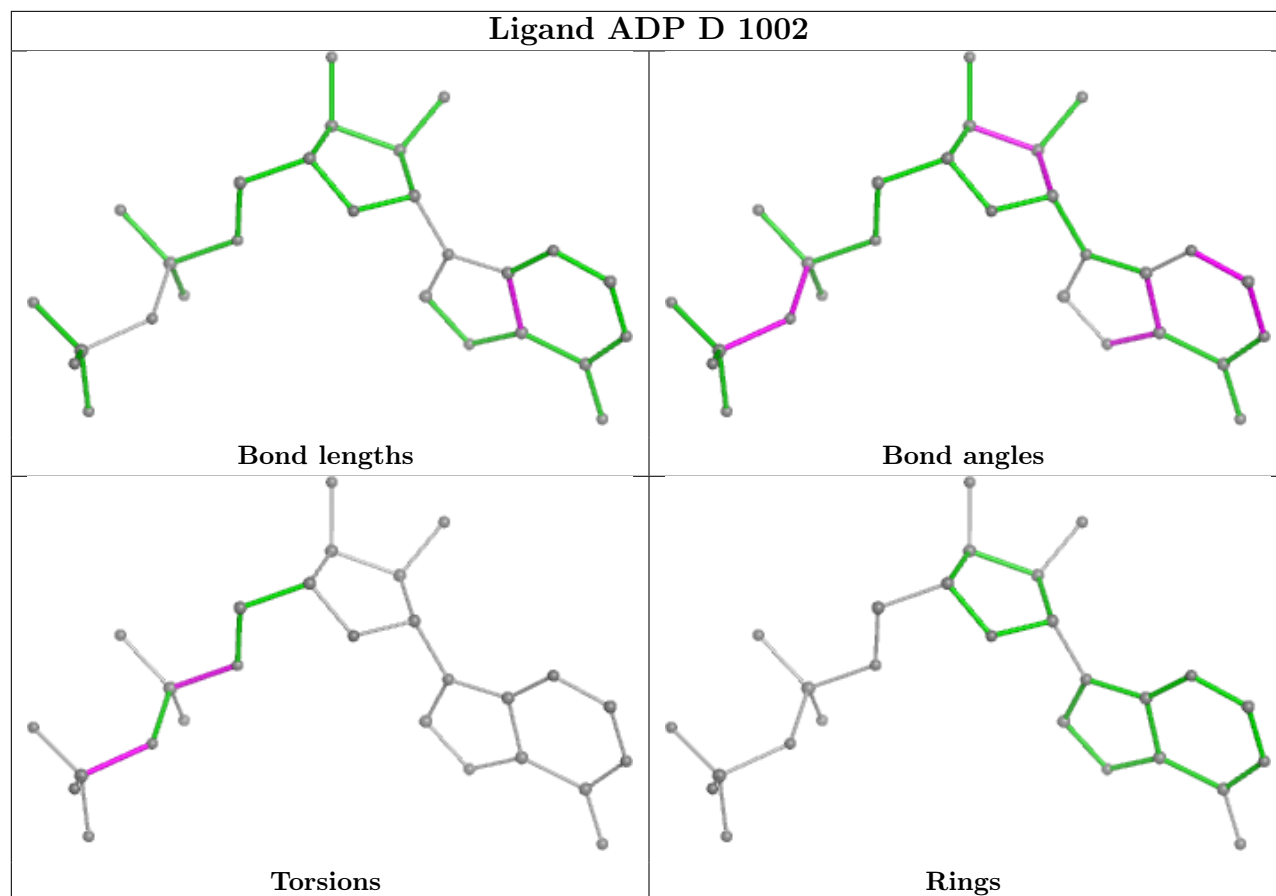
6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	1002	ADP	3	0
6	D	1002	ADP	1	0
6	F	1002	ADP	1	0
8	F	1003	PO4	2	0
8	C	1005	PO4	1	0
8	B	1005	PO4	1	0

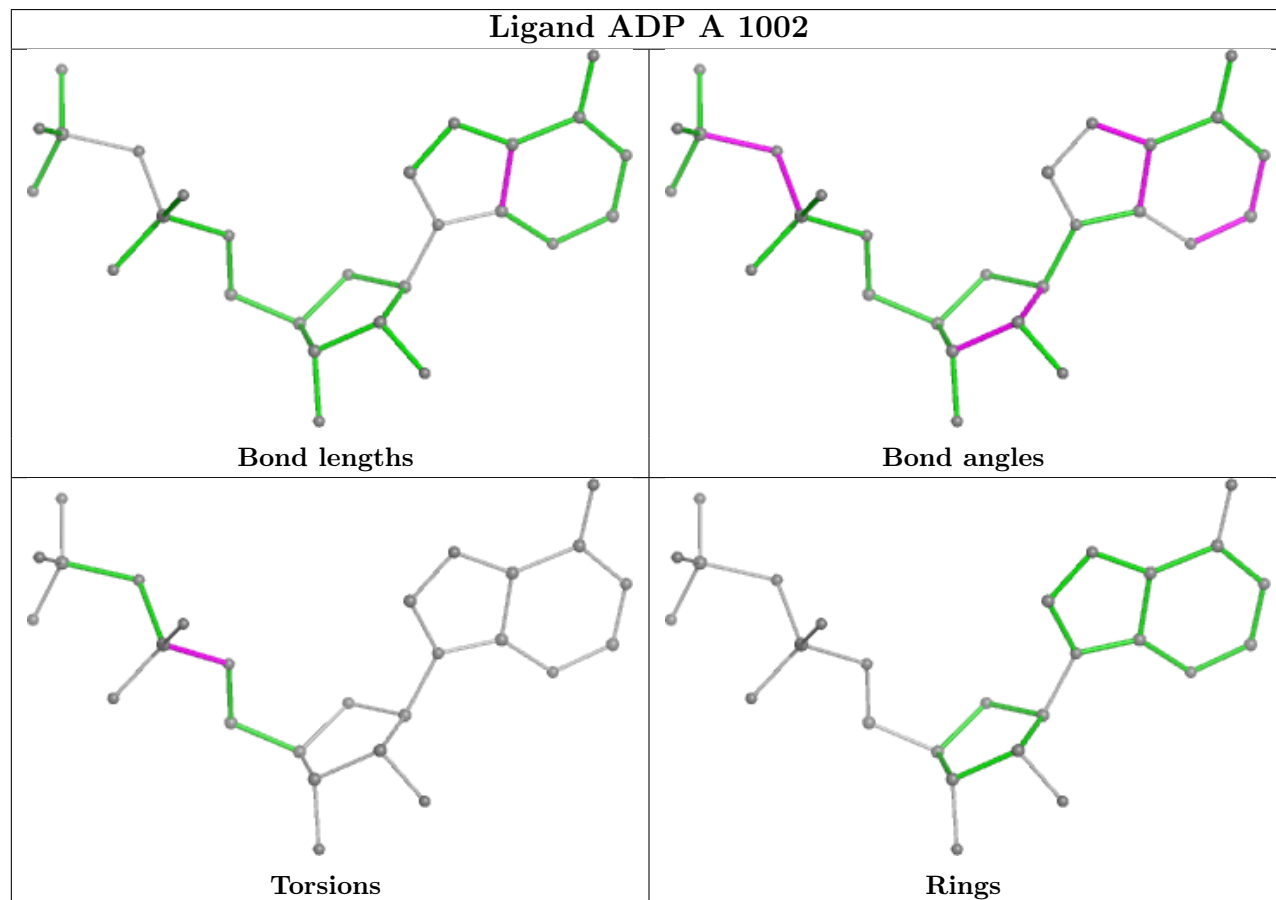
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

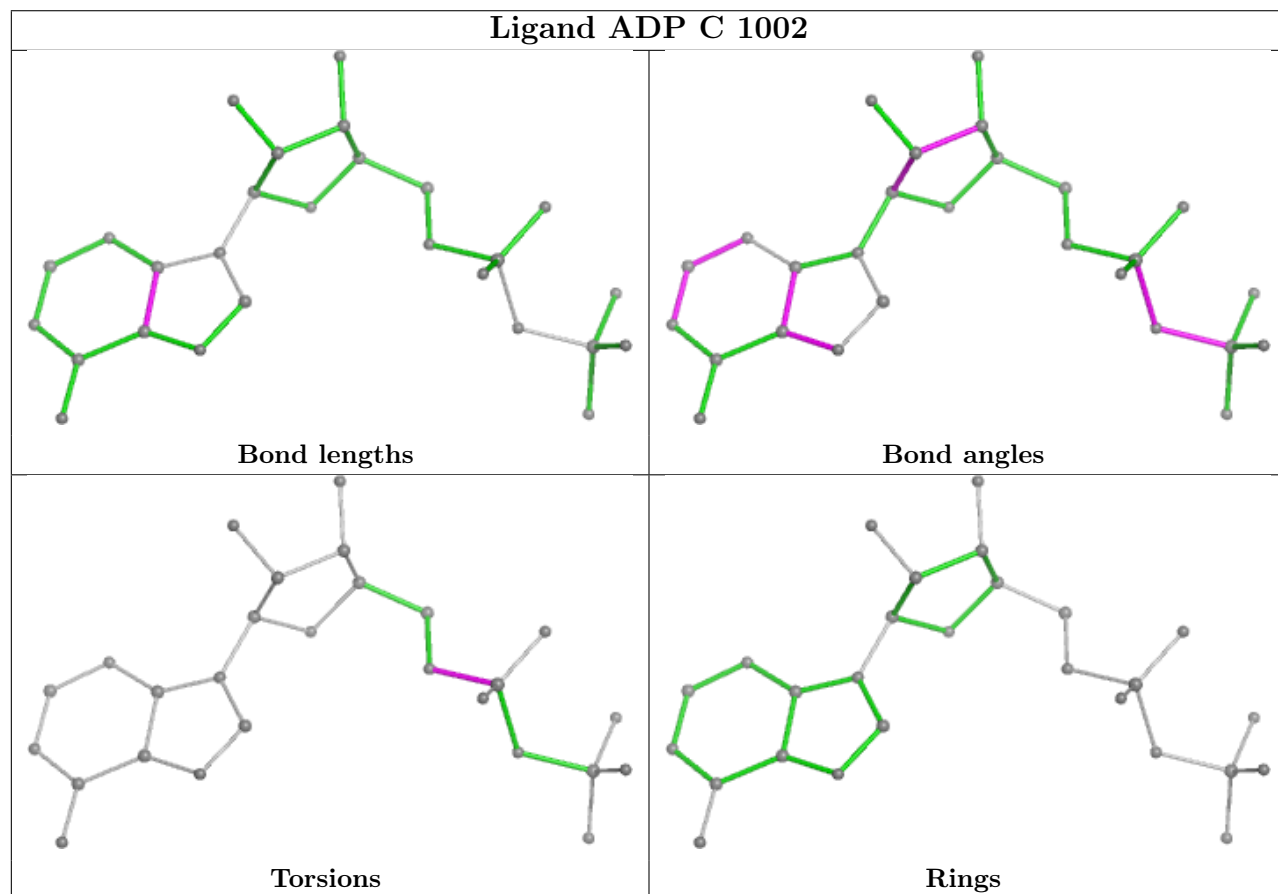
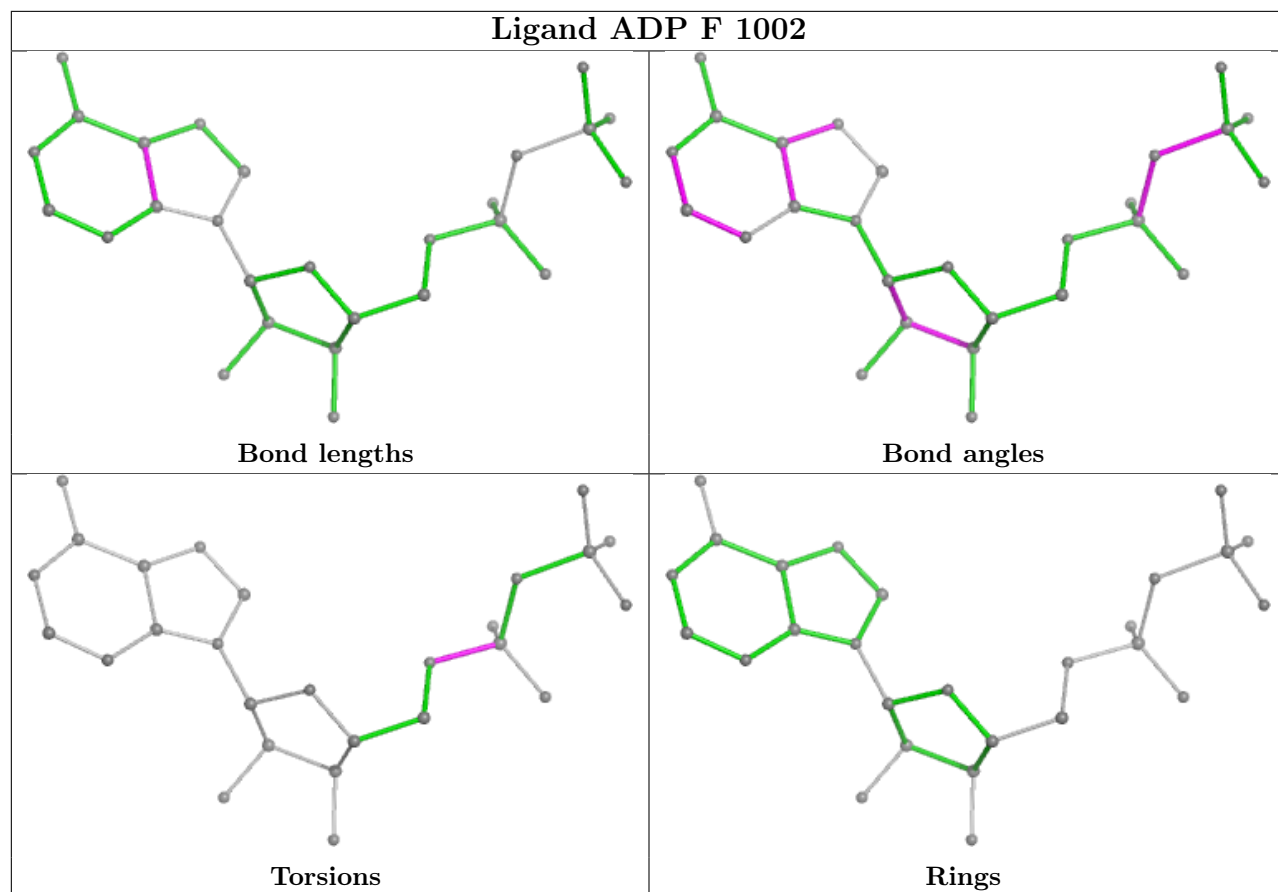


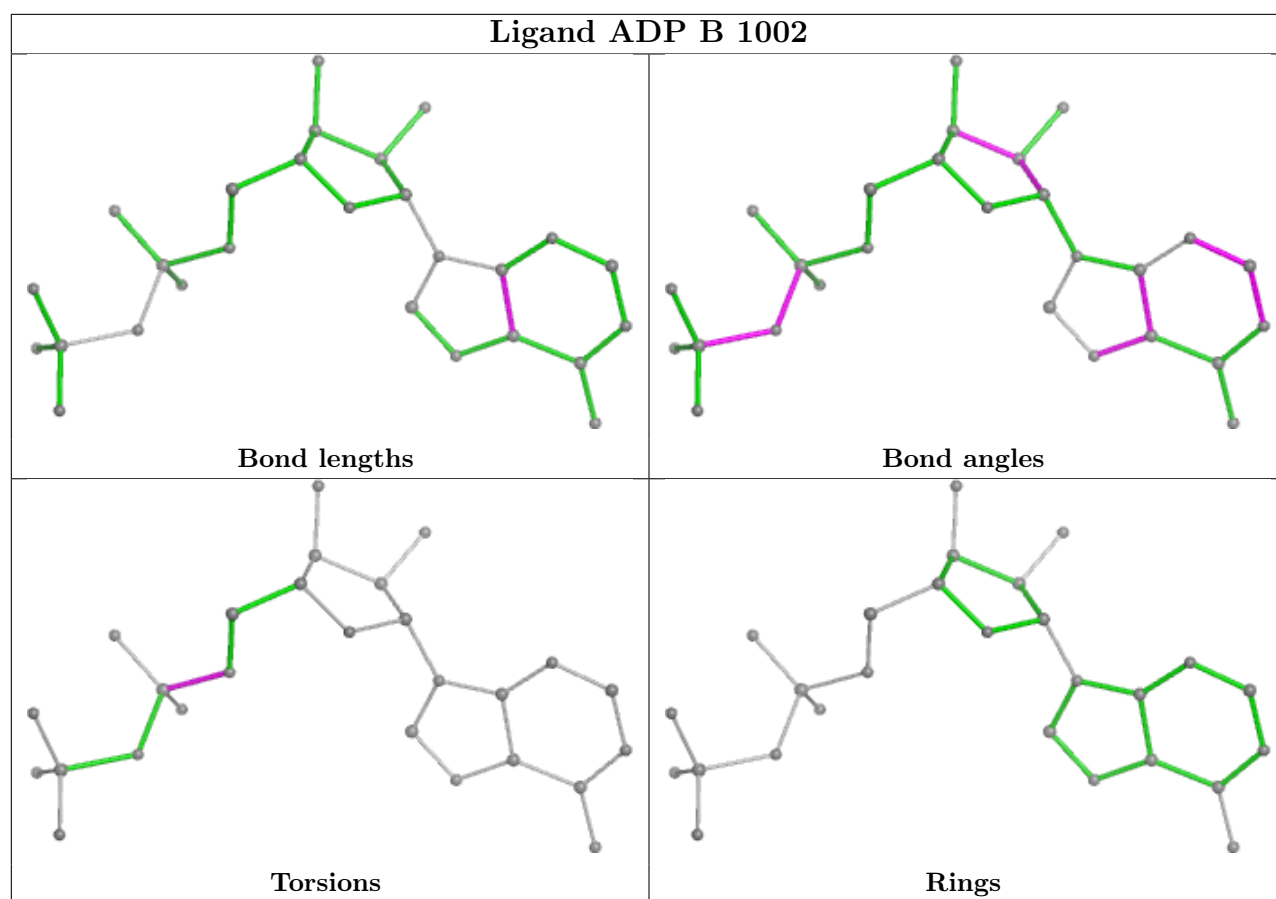
Ligand ADP D 1002



Ligand ADP A 1002







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	531/531 (100%)	-0.10	13 (2%) 59 52	29, 59, 107, 157	0
1	B	531/531 (100%)	-0.21	3 (0%) 85 81	37, 62, 91, 129	0
1	C	531/531 (100%)	-0.41	3 (0%) 85 81	26, 57, 100, 168	0
1	E	531/531 (100%)	0.63	43 (8%) 19 15	86, 127, 172, 227	0
1	F	531/531 (100%)	0.05	16 (3%) 52 44	38, 86, 135, 221	0
2	D	531/531 (100%)	0.62	34 (6%) 27 20	83, 131, 178, 270	0
3	G	18/21 (85%)	0.43	3 (16%) 5 5	78, 104, 230, 249	0
3	I	18/21 (85%)	0.57	1 (5%) 31 24	83, 142, 206, 298	0
3	K	18/21 (85%)	0.67	2 (11%) 12 9	123, 172, 245, 293	0
4	H	15/15 (100%)	0.06	0 100 100	72, 102, 133, 141	0
4	J	15/15 (100%)	0.32	0 100 100	100, 134, 157, 174	0
4	L	15/15 (100%)	0.98	2 (13%) 8 7	130, 167, 194, 235	0
All	All	3285/3294 (99%)	0.11	120 (3%) 45 37	26, 84, 161, 298	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	392	SER	5.1
1	F	356	VAL	5.1
1	E	177	MET	4.3
1	C	374	PHE	4.2
2	D	403	GLY	4.1

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
8	PO4	E	1003	5/5	0.62	0.13	102,113,121,126	0
8	PO4	C	1004	5/5	0.77	0.08	108,146,166,182	0
6	ADP	D	1002	27/27	0.80	0.11	116,135,157,167	0
8	PO4	A	1005	5/5	0.82	0.16	95,106,138,139	0
8	PO4	A	1006	5/5	0.82	0.25	97,106,107,130	0
8	PO4	F	1003	5/5	0.82	0.27	88,119,124,136	0
8	PO4	F	1004	5/5	0.82	0.19	93,97,121,125	0
8	PO4	C	1005	5/5	0.83	0.28	89,112,117,120	0
6	ADP	E	1002	27/27	0.83	0.12	111,149,164,168	0
8	PO4	B	1004	5/5	0.84	0.17	71,85,119,124	0
9	K	B	1008	1/1	0.86	0.10	84,84,84,84	0
8	PO4	B	1005	5/5	0.87	0.28	107,116,130,163	0
8	PO4	A	1004	5/5	0.88	0.13	56,66,97,118	0
7	MG	C	1007	1/1	0.89	0.10	52,52,52,52	0
9	K	B	1006	1/1	0.89	0.07	70,70,70,70	0
8	PO4	A	1007	5/5	0.89	0.26	87,102,128,136	0
9	K	B	1009	1/1	0.89	0.10	68,68,68,68	0
9	K	C	1006	1/1	0.89	0.07	58,58,58,58	0
9	K	A	1008	1/1	0.90	0.08	65,65,65,65	0
9	K	G	101	1/1	0.91	0.09	91,91,91,91	0
9	K	B	1007	1/1	0.93	0.07	62,62,62,62	0
7	MG	C	1003	1/1	0.94	0.06	57,57,57,57	0
5	ZN	D	1001	1/1	0.94	0.07	149,149,149,149	0
6	ADP	B	1002	27/27	0.95	0.07	41,57,70,81	0
7	MG	B	1003	1/1	0.96	0.06	53,53,53,53	0
6	ADP	A	1002	27/27	0.96	0.06	37,52,67,72	0
6	ADP	C	1002	27/27	0.96	0.07	34,48,61,69	0
6	ADP	F	1002	27/27	0.96	0.06	53,67,78,89	0
7	MG	A	1003	1/1	0.96	0.12	79,79,79,79	0
9	K	A	1009	1/1	0.96	0.09	60,60,60,60	0
5	ZN	E	1001	1/1	0.97	0.05	122,122,122,122	0
5	ZN	F	1001	1/1	0.99	0.03	80,80,80,80	0

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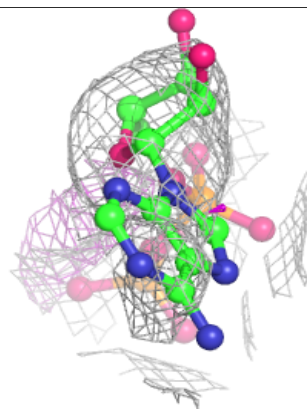
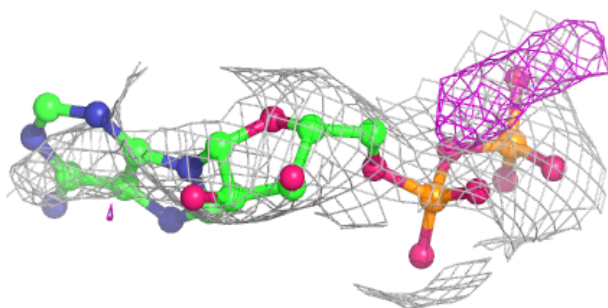
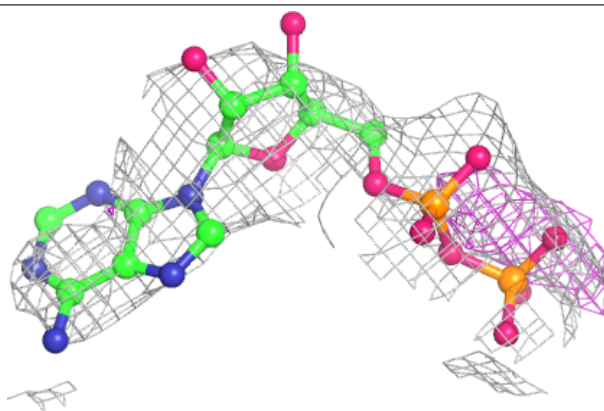
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	ZN	B	1001	1/1	0.99	0.07	66,66,66,66	0
5	ZN	C	1001	1/1	0.99	0.09	60,60,60,60	0
5	ZN	A	1001	1/1	1.00	0.12	53,53,53,53	0

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.

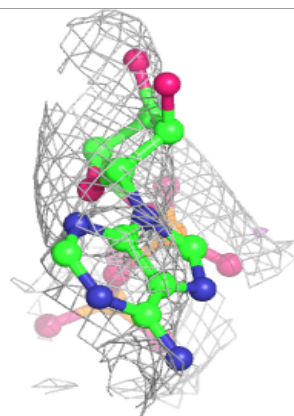
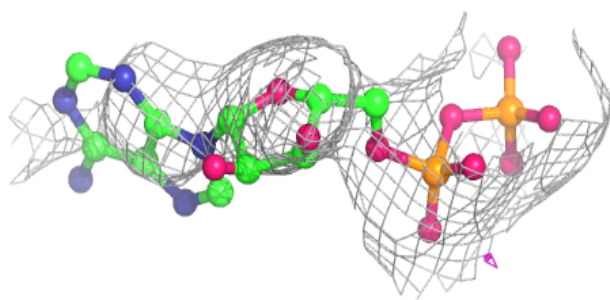
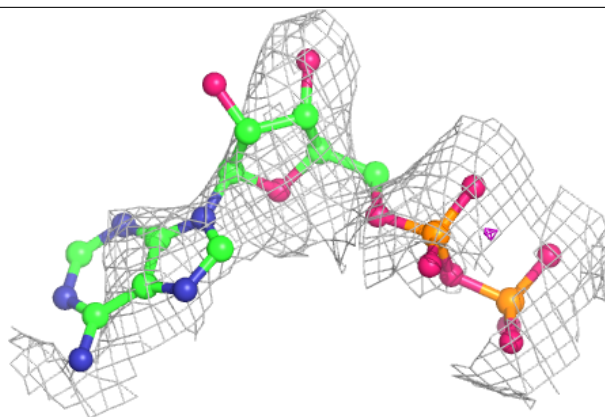
Electron density around ADP D 1002:

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



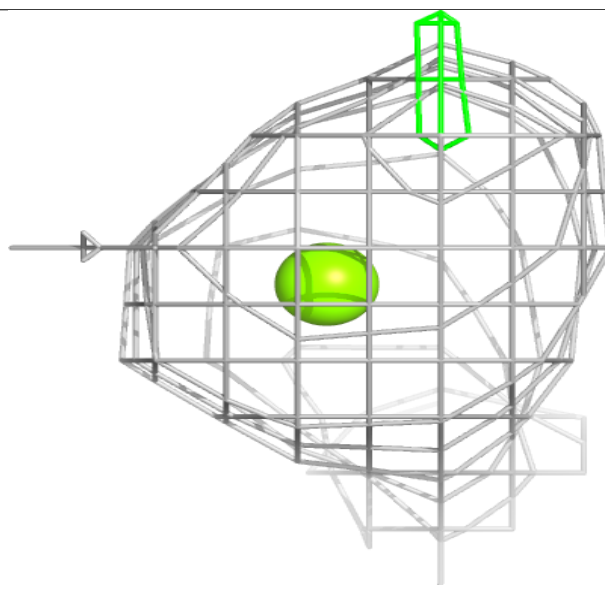
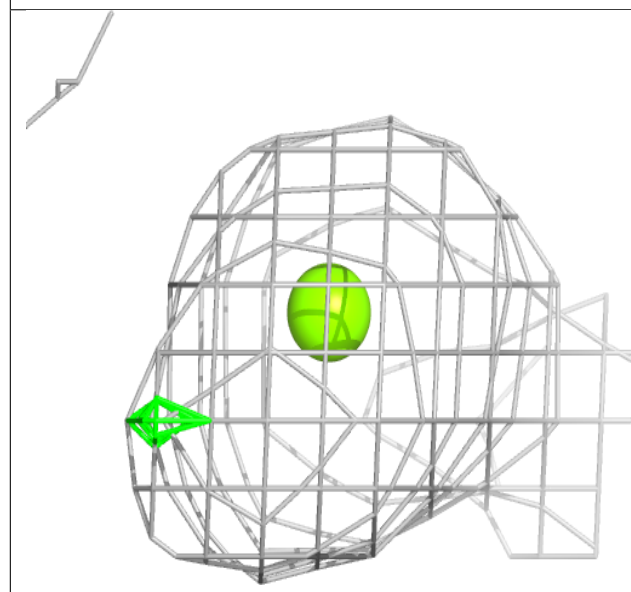
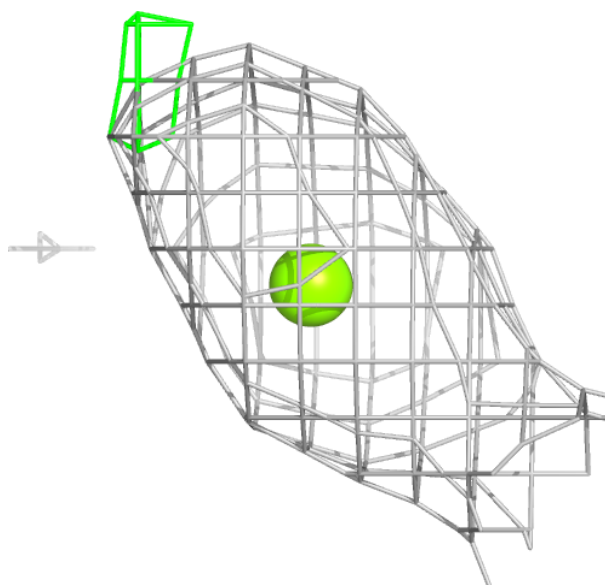
Electron density around ADP E 1002:

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



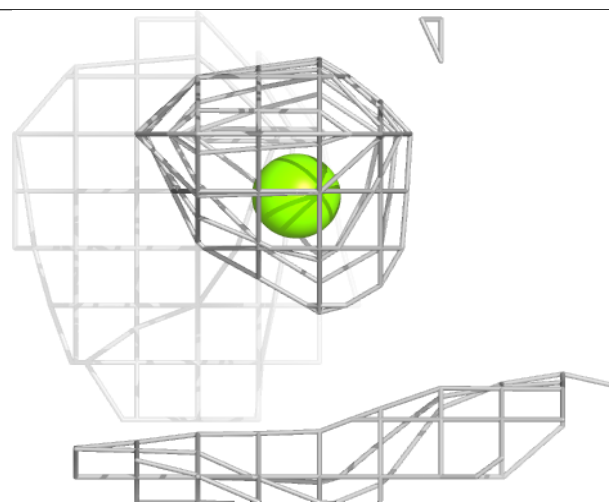
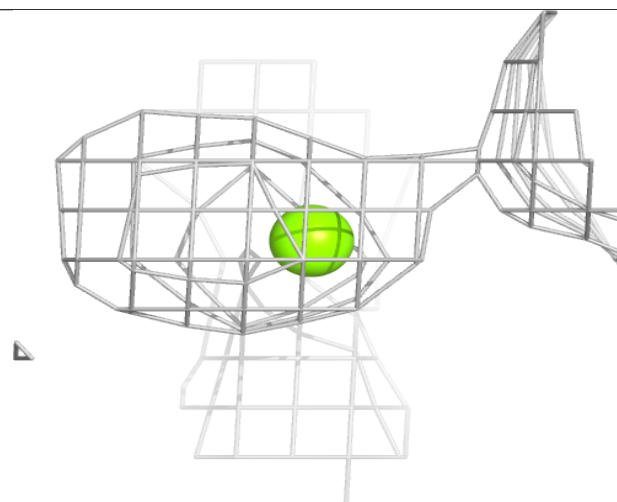
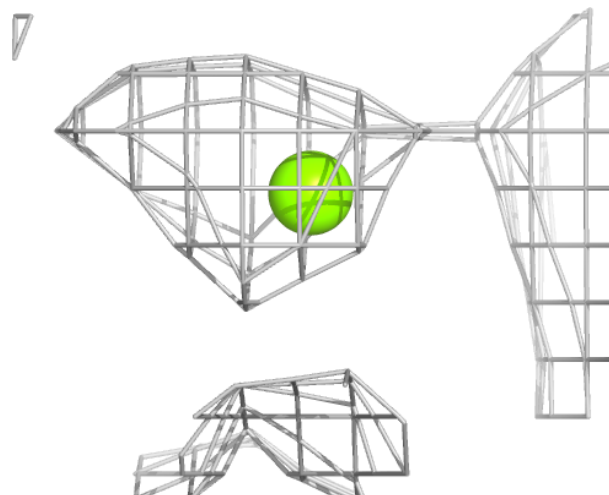
Electron density around MG C 1007:

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



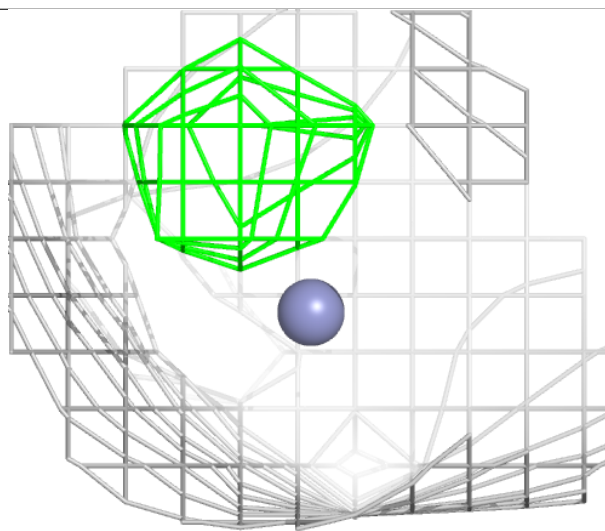
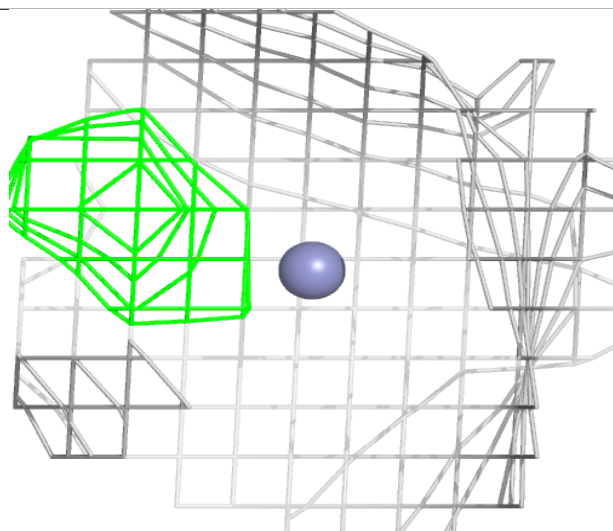
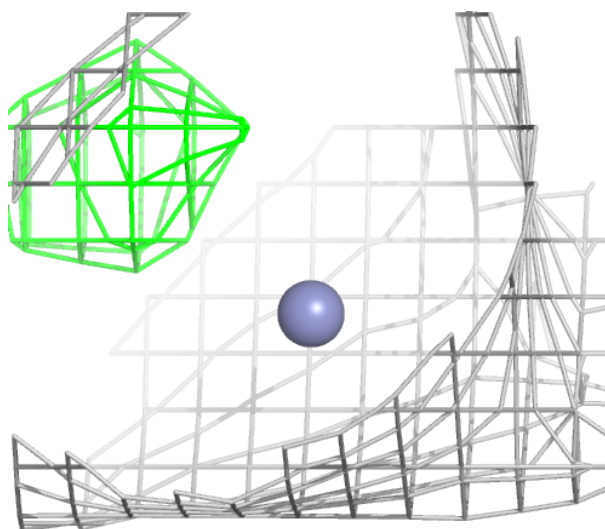
Electron density around MG C 1003:

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



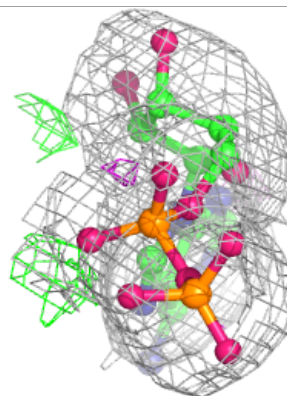
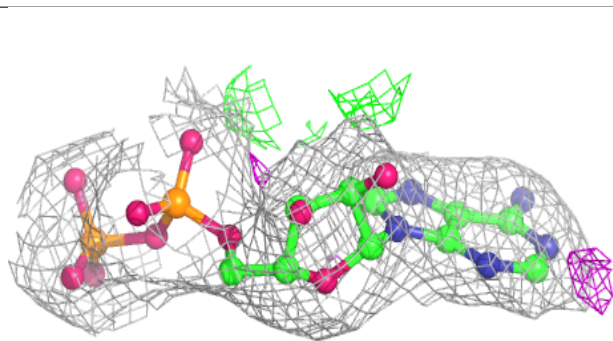
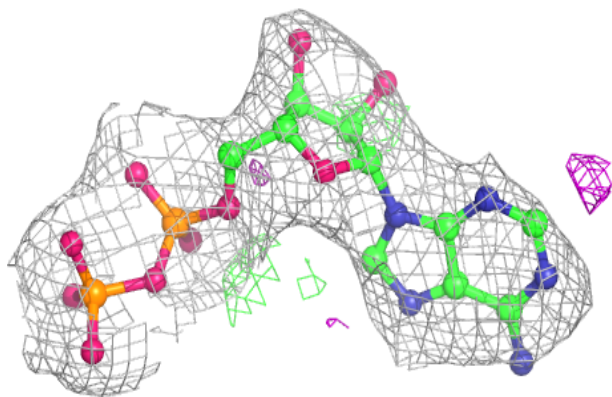
Electron density around ZN D 1001:

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



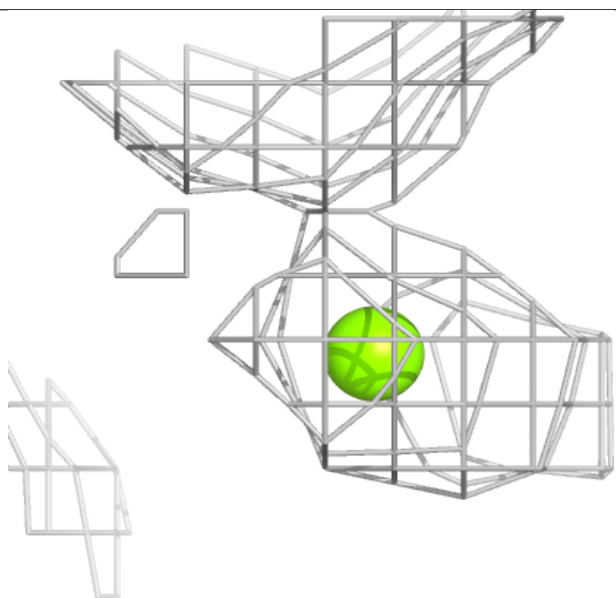
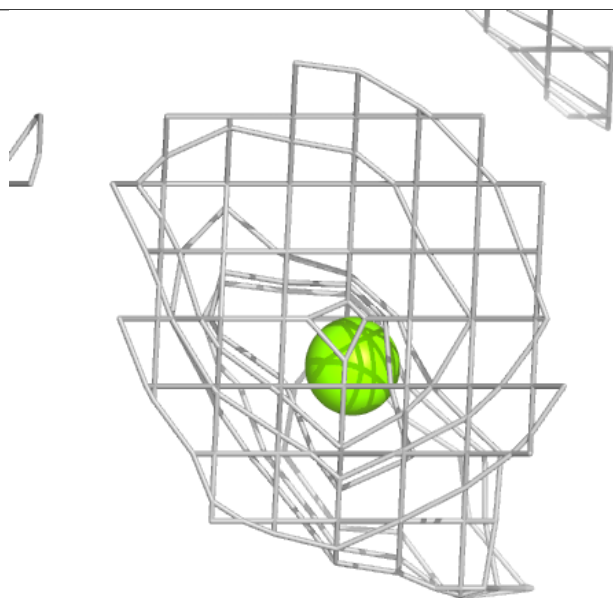
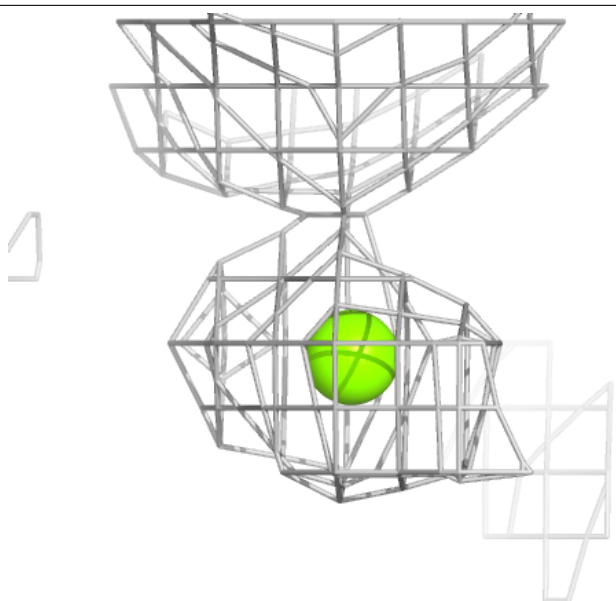
Electron density around ADP B 1002:

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



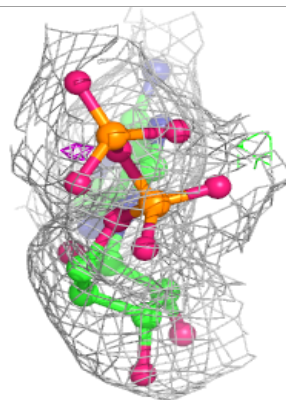
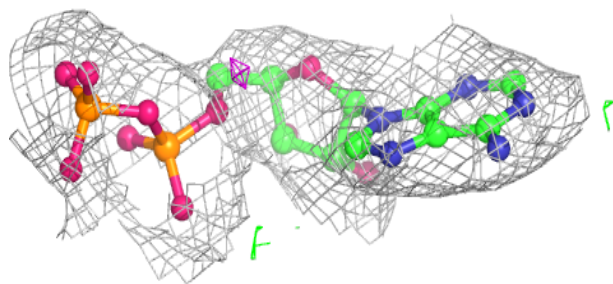
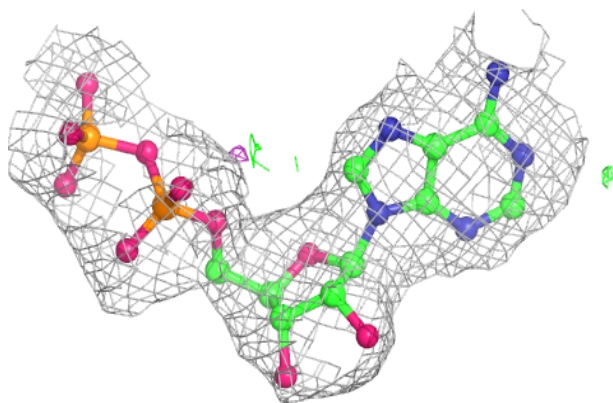
Electron density around MG B 1003:

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

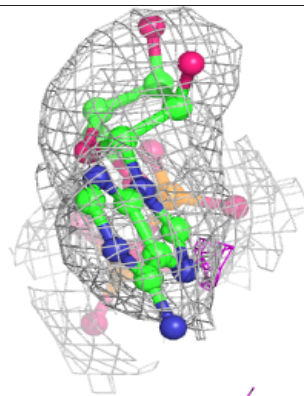
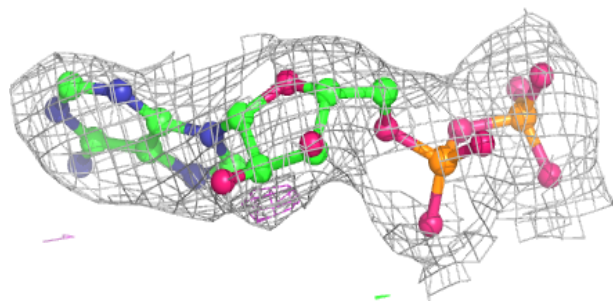
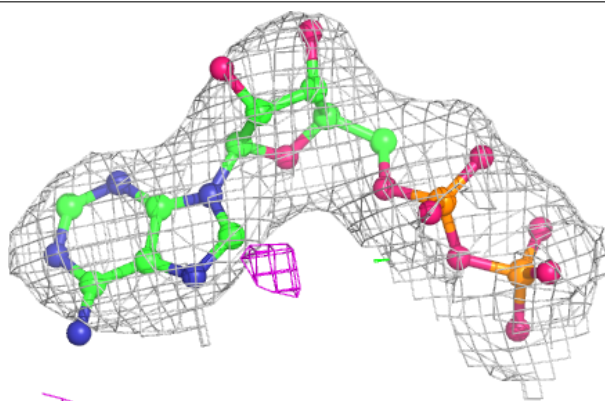


Electron density around ADP A 1002:

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

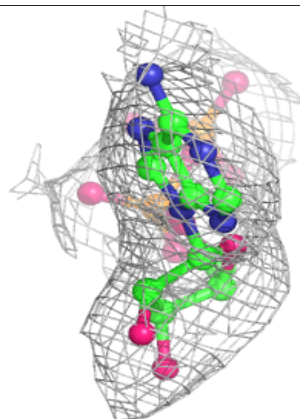
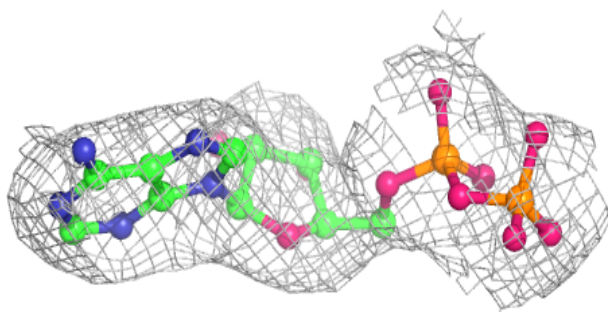
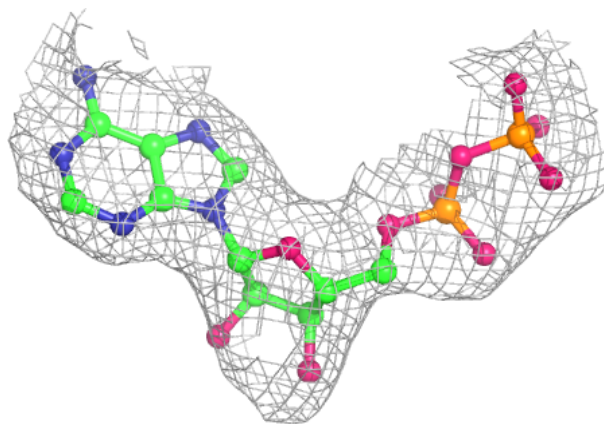
**Electron density around ADP C 1002:**

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



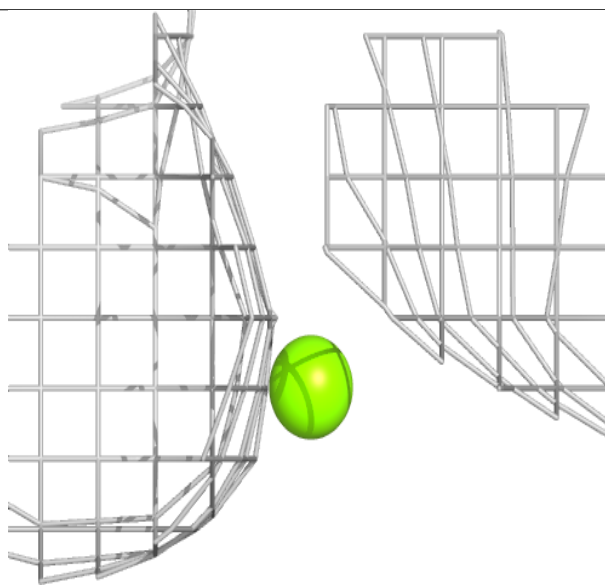
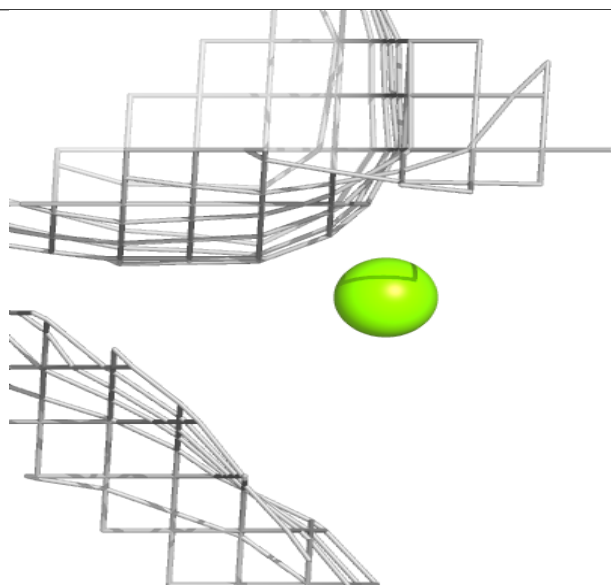
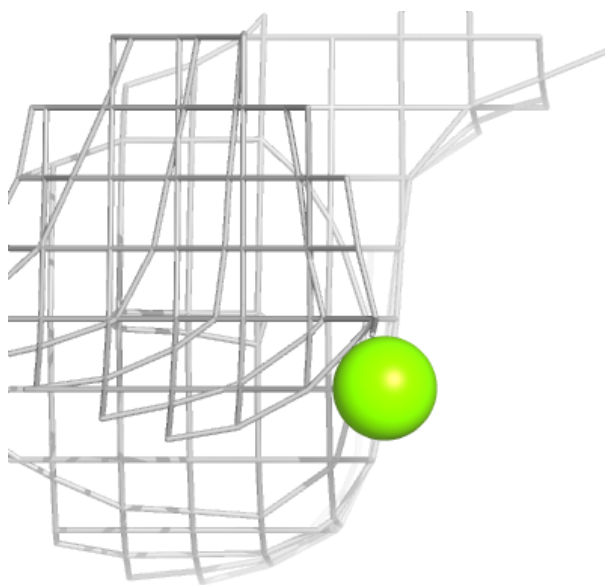
Electron density around ADP F 1002:

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



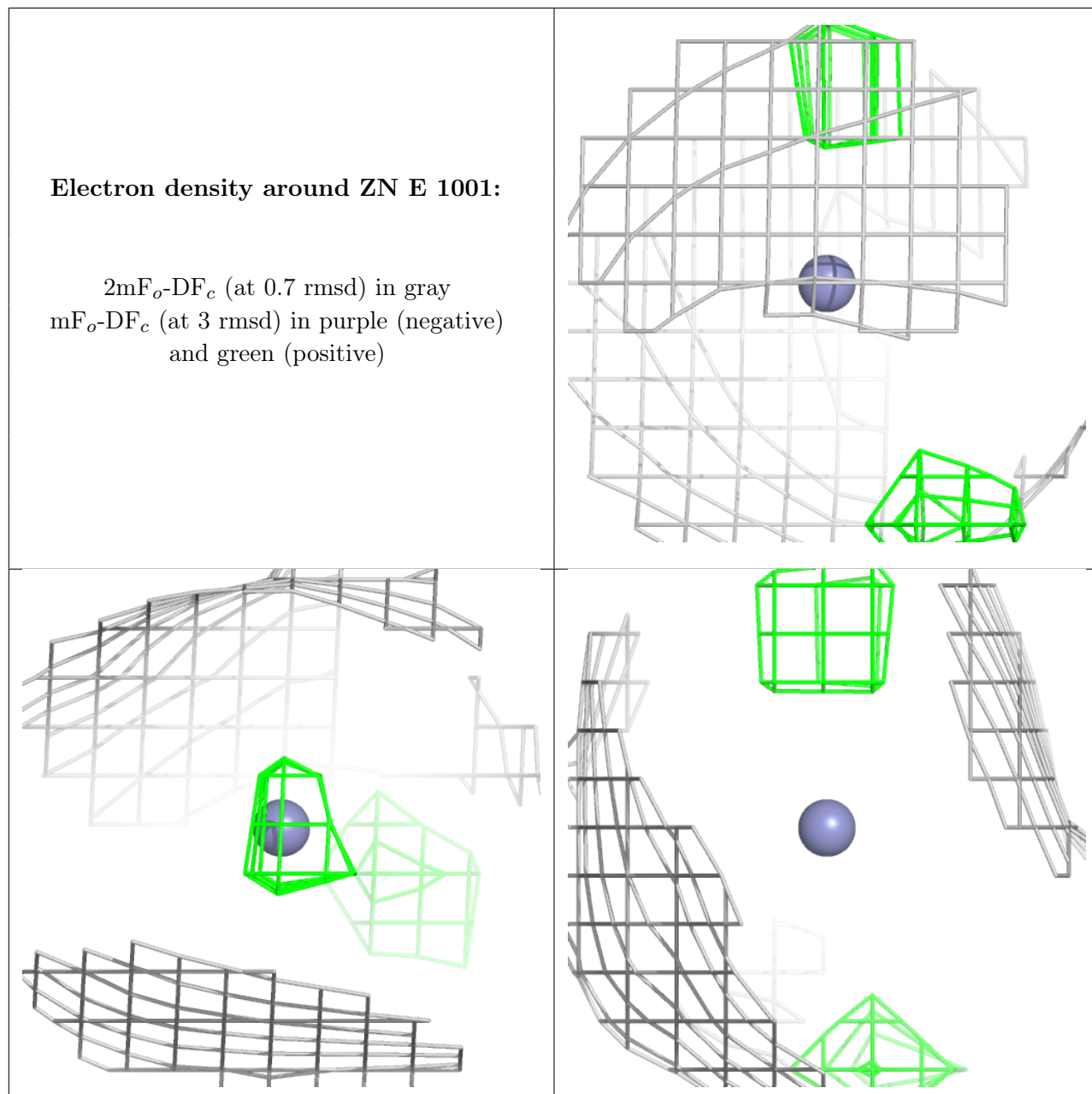
Electron density around MG A 1003:

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



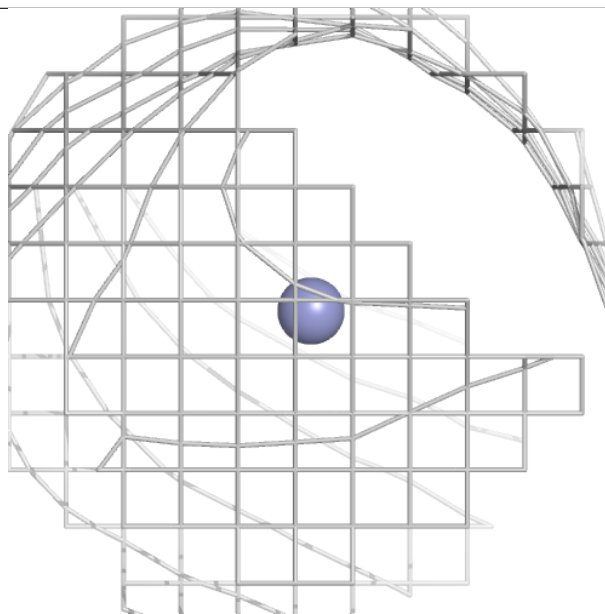
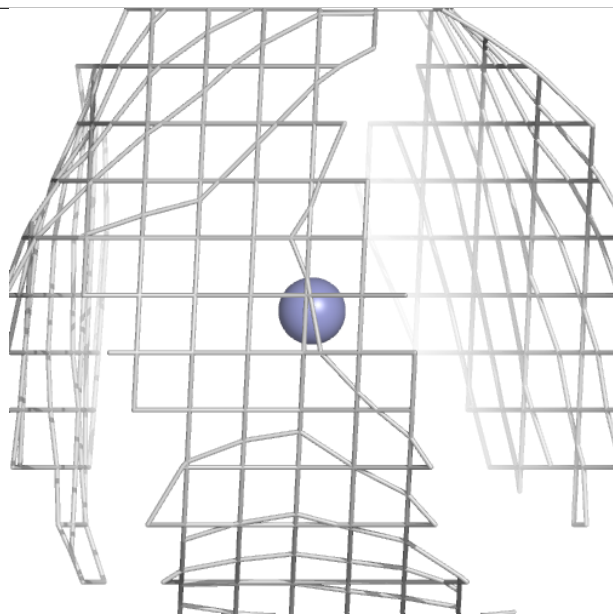
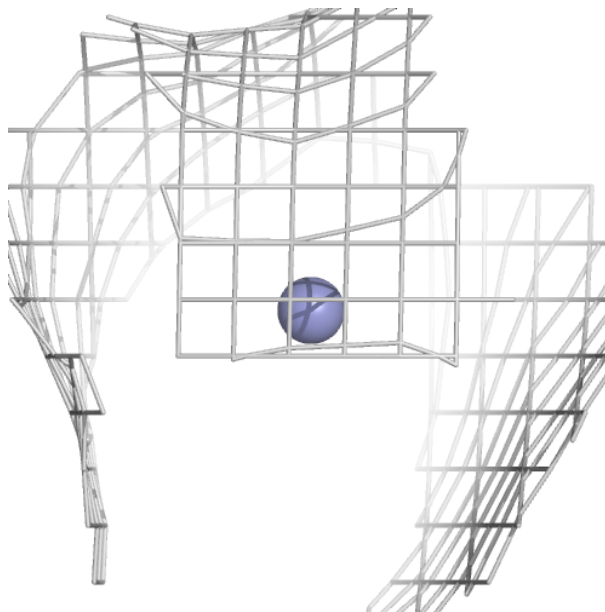
Electron density around ZN E 1001:

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



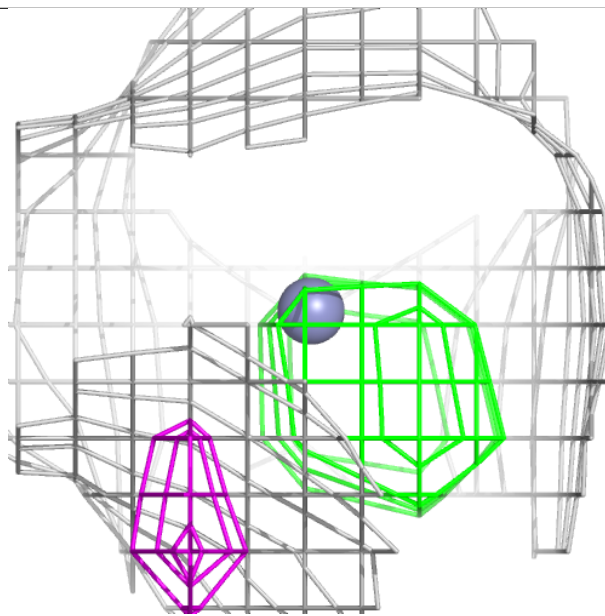
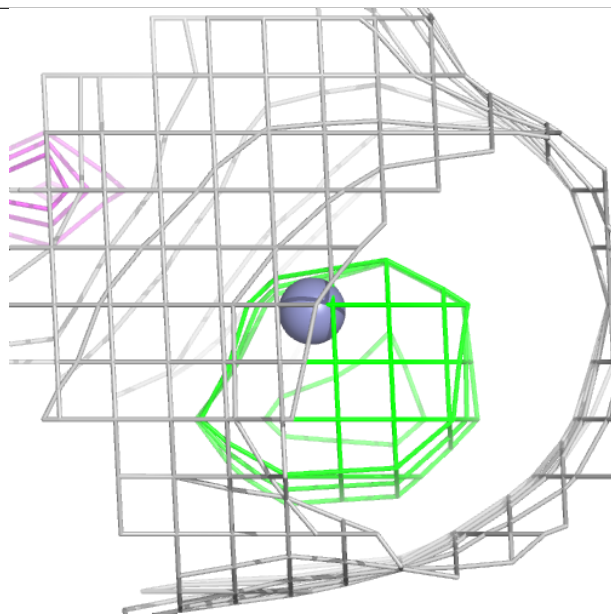
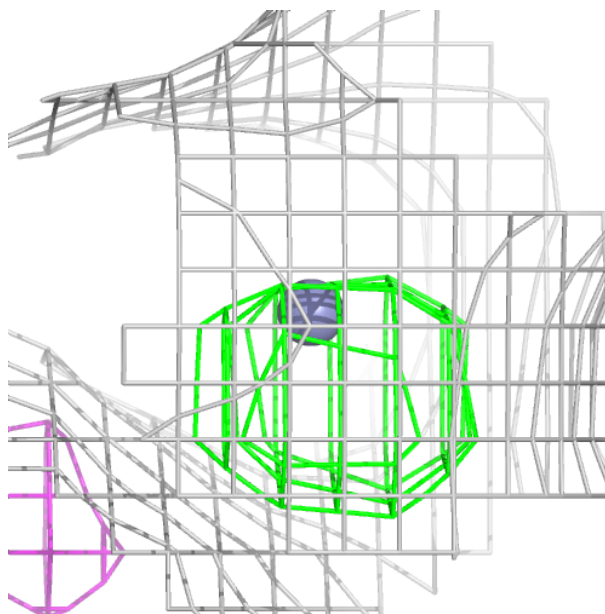
Electron density around ZN F 1001:

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



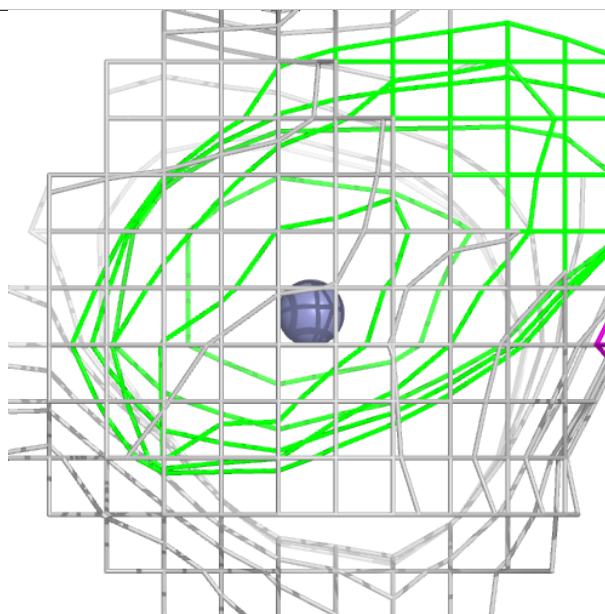
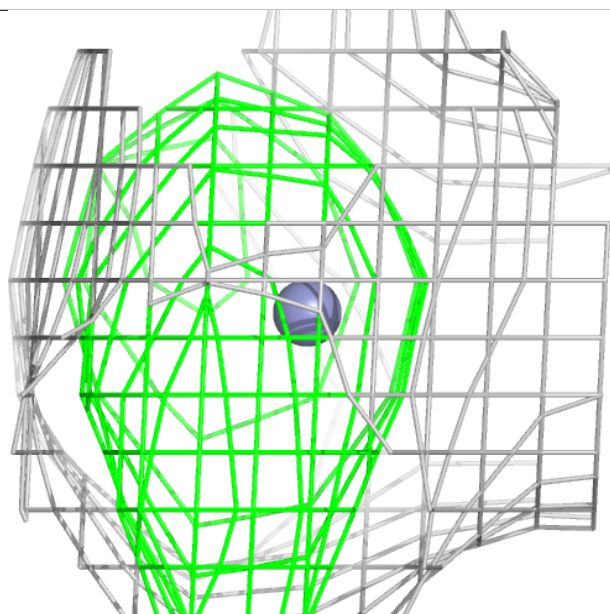
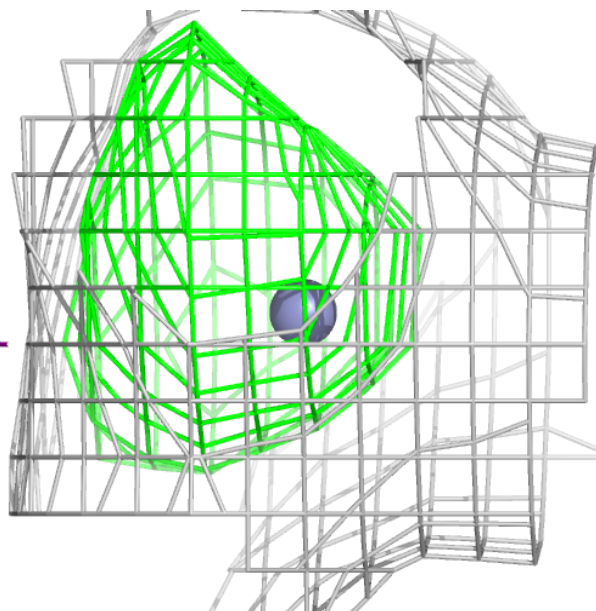
Electron density around ZN B 1001:

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



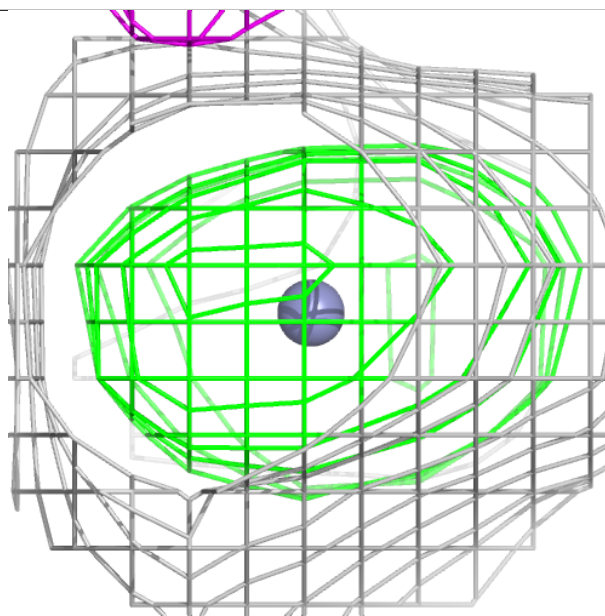
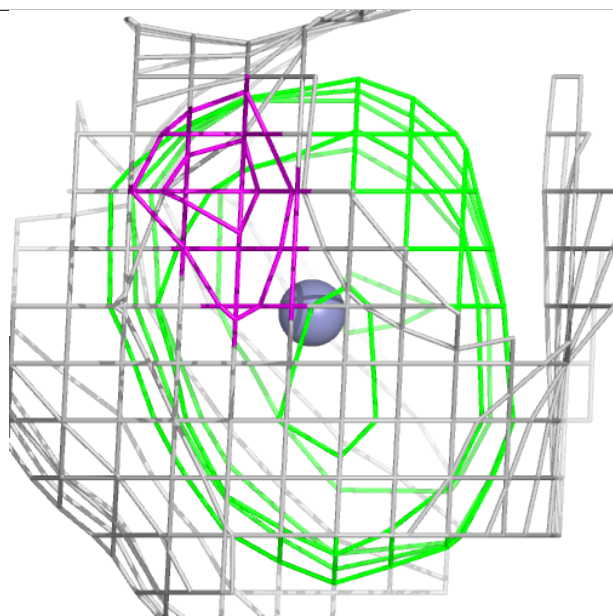
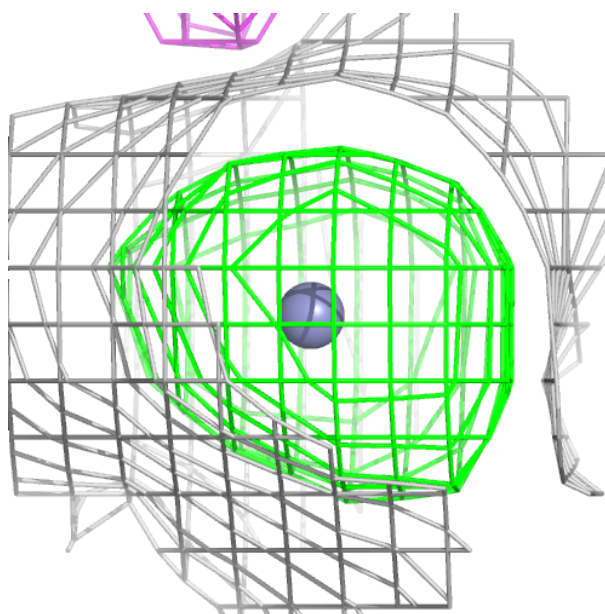
Electron density around ZN C 1001:

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



Electron density around ZN A 1001:

$2mF_o-DF_c$ (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.