



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:06 AM UTC

PDB ID : 8PML / pdb\_00008pml  
Title : Structure of Nall protein , SPIKE allele from japonica rice, construct 46-458  
Authors : Huang, L.Y.; Rety, S.; Xi, X.G.  
Deposited on : 2023-06-29  
Resolution : 2.95 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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)  
Xtrriage (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

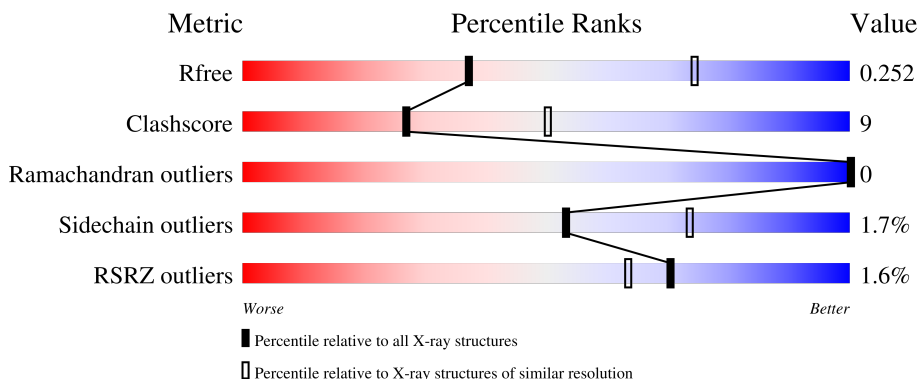
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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.



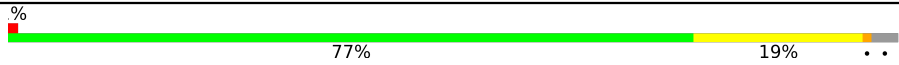
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	413	 2% 80% 17% .
1	B	413	 2% 76% 20% ..
1	C	413	 2% 76% 20% ...
1	D	413	 2% 82% 15% .
1	E	413	 2% 77% 19% ...

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Mol	Chain	Length	Quality of chain
1	F	413	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into segments: a small red segment at the start, followed by a large green segment labeled '77%', then a yellow segment labeled '19%', and finally a small grey segment at the end. Above the bar is a '%' symbol and below it are two dots '••'.</p>

## 2 Entry composition [i](#)

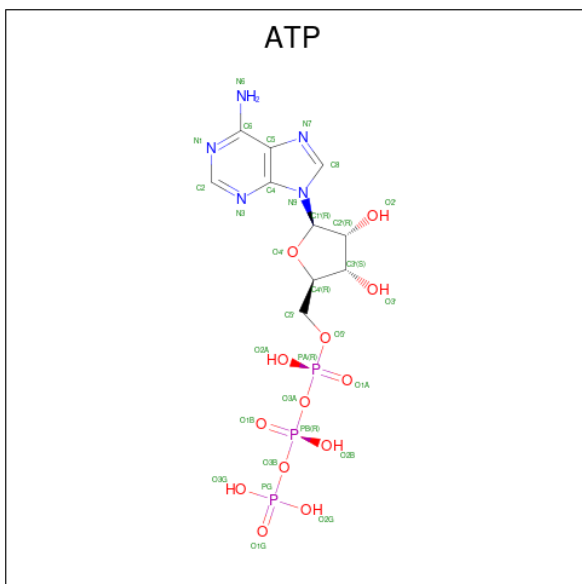
There are 3 unique types of molecules in this entry. The entry contains 18777 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Protein NARROW LEAF 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	401	Total 3090	C 1958	N 542	O 578	S 12	0	0	0
1	B	402	Total 3099	C 1963	N 543	O 581	S 12	0	0	0
1	C	402	Total 3099	C 1963	N 543	O 581	S 12	0	0	0
1	D	402	Total 3099	C 1963	N 543	O 581	S 12	0	0	0
1	E	402	Total 3099	C 1963	N 543	O 581	S 12	0	0	0
1	F	402	Total 3099	C 1963	N 543	O 581	S 12	0	0	0

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

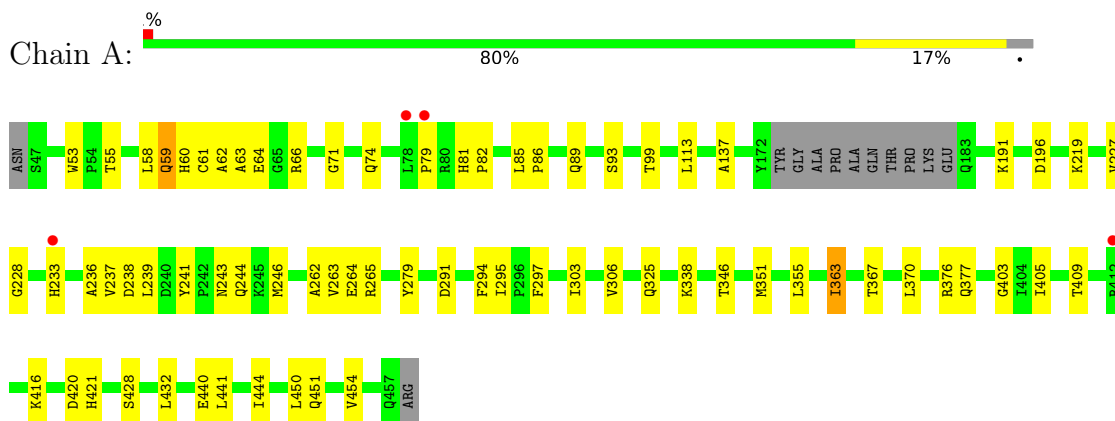
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		

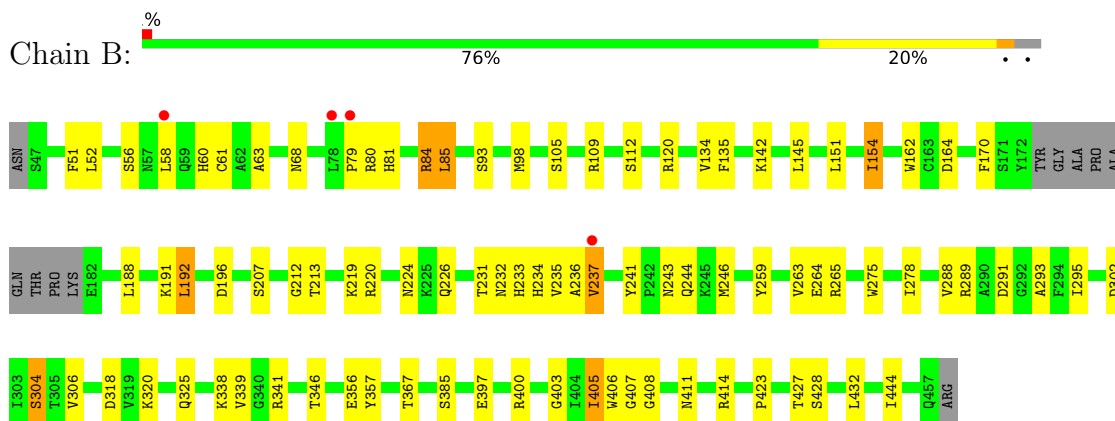
### 3 Residue-property plots [i](#)

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.

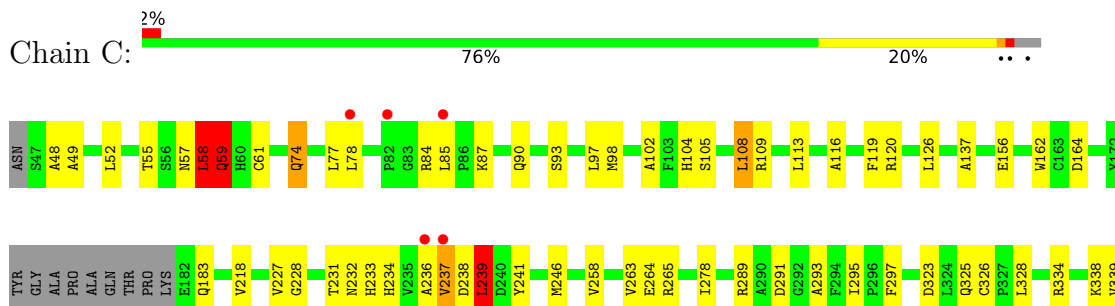
#### • Molecule 1: Protein NARROW LEAF 1

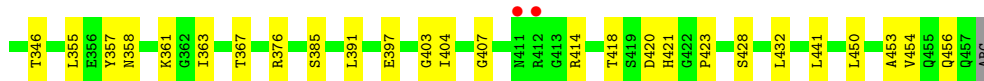


#### • Molecule 1: Protein NARROW LEAF 1

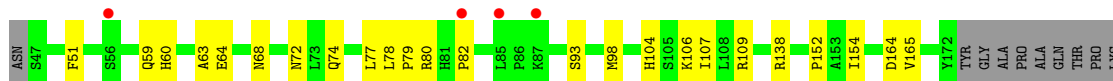
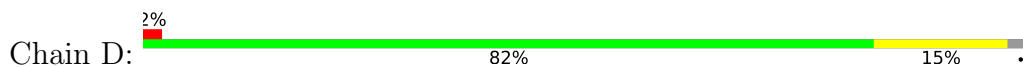


#### • Molecule 1: Protein NARROW LEAF 1

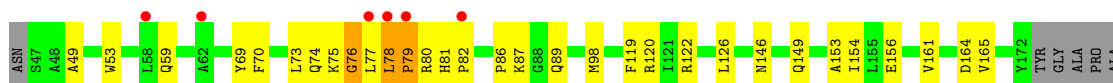
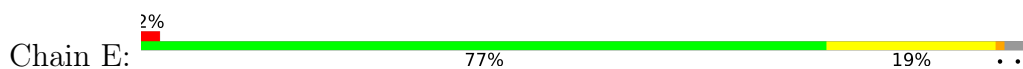




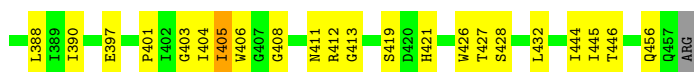
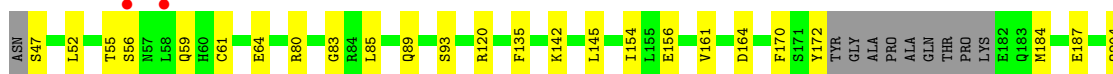
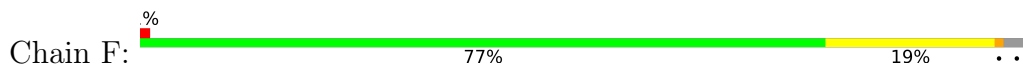
● Molecule 1: Protein NARROW LEAF 1



● Molecule 1: Protein NARROW LEAF 1



● Molecule 1: Protein NARROW LEAF 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	175.43Å 193.36Å 84.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.71 – 2.95 87.71 – 2.95	Depositor EDS
% Data completeness (in resolution range)	77.4 (87.71-2.95) 77.6 (87.71-2.95)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.96Å)	Xtrriage
Refinement program	PHENIX 1.21rc1_4903	Depositor
R, $R_{free}$	0.205 , 0.252 0.205 , 0.252	Depositor DCC
$R_{free}$ test set	2269 reflections (3.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.9	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	18777	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0850e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: MG, ATP

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	0.24	0/3157	0.57	0/4285
1	B	0.27	1/3166 (0.0%)	0.56	1/4297 (0.0%)
1	C	0.25	0/3166	0.64	7/4297 (0.2%)
1	D	0.24	0/3166	0.56	0/4297
1	E	0.25	0/3166	0.65	9/4297 (0.2%)
1	F	0.26	0/3166	0.56	2/4297 (0.0%)
All	All	0.25	1/18987 (0.0%)	0.59	19/25770 (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	3
1	C	0	4
1	E	0	1
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	84	ARG	CB-CG	5.46	1.68	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	75	LYS	CA-C-N	8.04	137.16	121.41
1	E	75	LYS	C-N-CA	8.04	137.16	121.41
1	C	59	GLN	N-CA-C	6.76	125.21	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	78	LEU	N-CA-C	6.75	124.72	109.81
1	C	58	LEU	CA-C-N	6.72	134.37	121.54

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	58	LEU	Peptide
1	A	59	GLN	Peptide
1	A	79	PRO	Peptide
1	C	58	LEU	Peptide
1	C	59	GLN	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	3090	0	3056	45	0
1	B	3099	0	3062	75	0
1	C	3099	0	3062	71	0
1	D	3099	0	3062	46	0
1	E	3099	0	3062	65	0
1	F	3099	0	3062	68	0
2	A	31	0	12	0	0
2	B	31	0	12	0	0
2	C	31	0	12	0	0
2	D	31	0	12	0	0
2	E	31	0	12	2	0
2	F	31	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
All	All	18777	0	18438	344	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 9.

The worst 5 of 344 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:B:105:SER:HB2	1:B:109:ARG:HH12	1.29	0.94
1:E:238:ASP:OD2	1:E:243:ASN:HB2	1.72	0.88
1:F:232:ASN:HD21	1:F:385:SER:HB2	1.37	0.87
1:B:105:SER:HB2	1:B:109:ARG:NH1	1.92	0.85
1:A:238:ASP:OD1	1:A:243:ASN:N	2.08	0.84

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	397/413 (96%)	391 (98%)	6 (2%)	0	100	100
1	B	398/413 (96%)	394 (99%)	4 (1%)	0	100	100
1	C	398/413 (96%)	393 (99%)	5 (1%)	0	100	100
1	D	398/413 (96%)	397 (100%)	1 (0%)	0	100	100
1	E	398/413 (96%)	391 (98%)	7 (2%)	0	100	100
1	F	398/413 (96%)	393 (99%)	5 (1%)	0	100	100
All	All	2387/2478 (96%)	2359 (99%)	28 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	333/342 (97%)	327 (98%)	6 (2%)	51	72
1	B	334/342 (98%)	326 (98%)	8 (2%)	43	67
1	C	334/342 (98%)	328 (98%)	6 (2%)	51	72
1	D	334/342 (98%)	329 (98%)	5 (2%)	57	76
1	E	334/342 (98%)	330 (99%)	4 (1%)	63	79
1	F	334/342 (98%)	329 (98%)	5 (2%)	57	76
All	All	2003/2052 (98%)	1969 (98%)	34 (2%)	53	73

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	306	VAL
1	F	64	GLU
1	F	291	ASP
1	B	306	VAL
1	B	304	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	59	GLN
1	E	456	GLN
1	F	335	GLN
1	F	234	HIS
1	B	421	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	ATP	D	1001	3	32,33,33	1.45	5 (15%)	48,52,52	1.71	7 (14%)
2	ATP	F	1001	3	32,33,33	1.46	5 (15%)	48,52,52	1.75	8 (16%)
2	ATP	A	1001	3	32,33,33	1.48	7 (21%)	48,52,52	1.75	7 (14%)
2	ATP	B	1001	3	32,33,33	1.40	4 (12%)	48,52,52	1.76	8 (16%)
2	ATP	C	1001	3	32,33,33	1.38	5 (15%)	48,52,52	1.77	10 (20%)
2	ATP	E	1001	3	32,33,33	1.37	5 (15%)	48,52,52	2.14	14 (29%)

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	ATP	D	1001	3	-	2/22/38/38	0/3/3/3
2	ATP	F	1001	3	-	2/22/38/38	0/3/3/3
2	ATP	A	1001	3	-	2/22/38/38	0/3/3/3
2	ATP	B	1001	3	-	2/22/38/38	0/3/3/3
2	ATP	C	1001	3	-	2/22/38/38	0/3/3/3
2	ATP	E	1001	3	-	2/22/38/38	0/3/3/3

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1001	ATP	C5-C4	4.84	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1001	ATP	C5-C4	4.80	1.47	1.39
2	A	1001	ATP	C5-C4	4.78	1.47	1.39
2	E	1001	ATP	C5-C4	4.65	1.47	1.39
2	B	1001	ATP	C5-C4	4.65	1.47	1.39

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1001	ATP	O3A-PB-O1B	-7.48	88.21	110.70
2	F	1001	ATP	C5-C4-N3	-6.07	118.36	126.72
2	A	1001	ATP	C5-C4-N3	-6.06	118.37	126.72
2	B	1001	ATP	C5-C4-N3	-6.03	118.41	126.72
2	D	1001	ATP	C5-C4-N3	-5.92	118.57	126.72

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

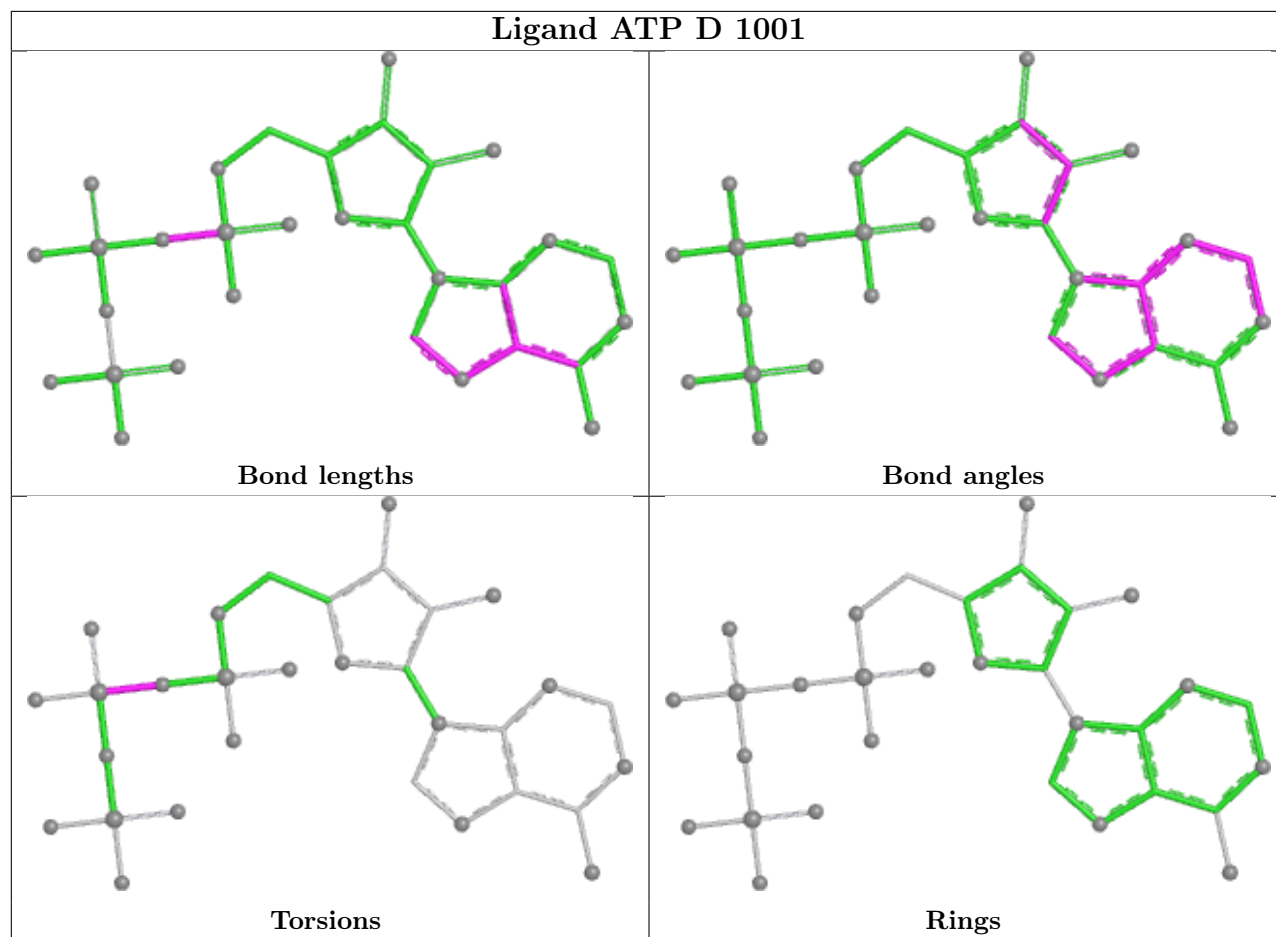
Mol	Chain	Res	Type	Atoms
2	A	1001	ATP	PA-O3A-PB-O2B
2	C	1001	ATP	PA-O3A-PB-O2B
2	D	1001	ATP	PA-O3A-PB-O2B
2	E	1001	ATP	PA-O3A-PB-O2B
2	B	1001	ATP	PA-O3A-PB-O2B

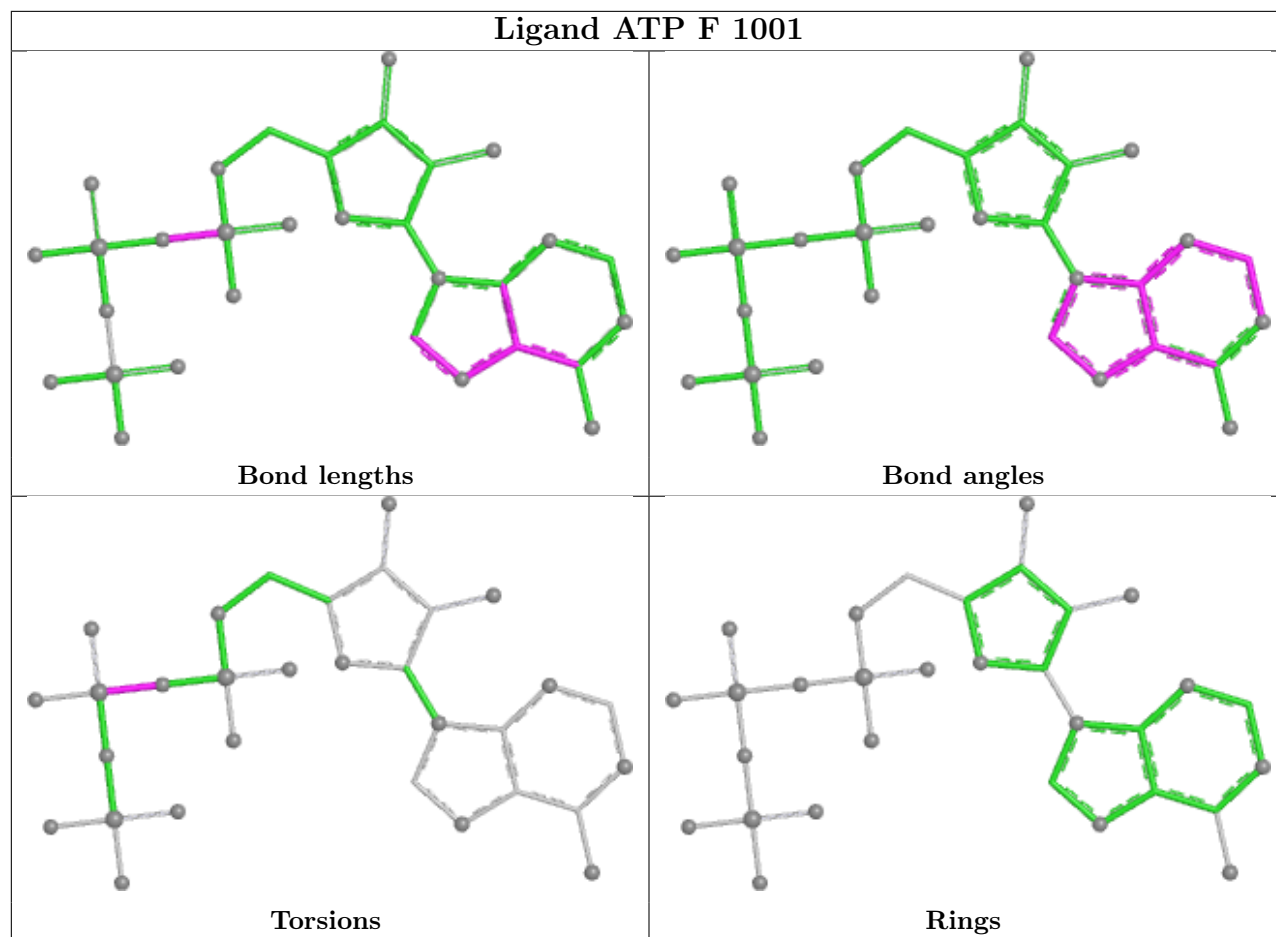
There are no ring outliers.

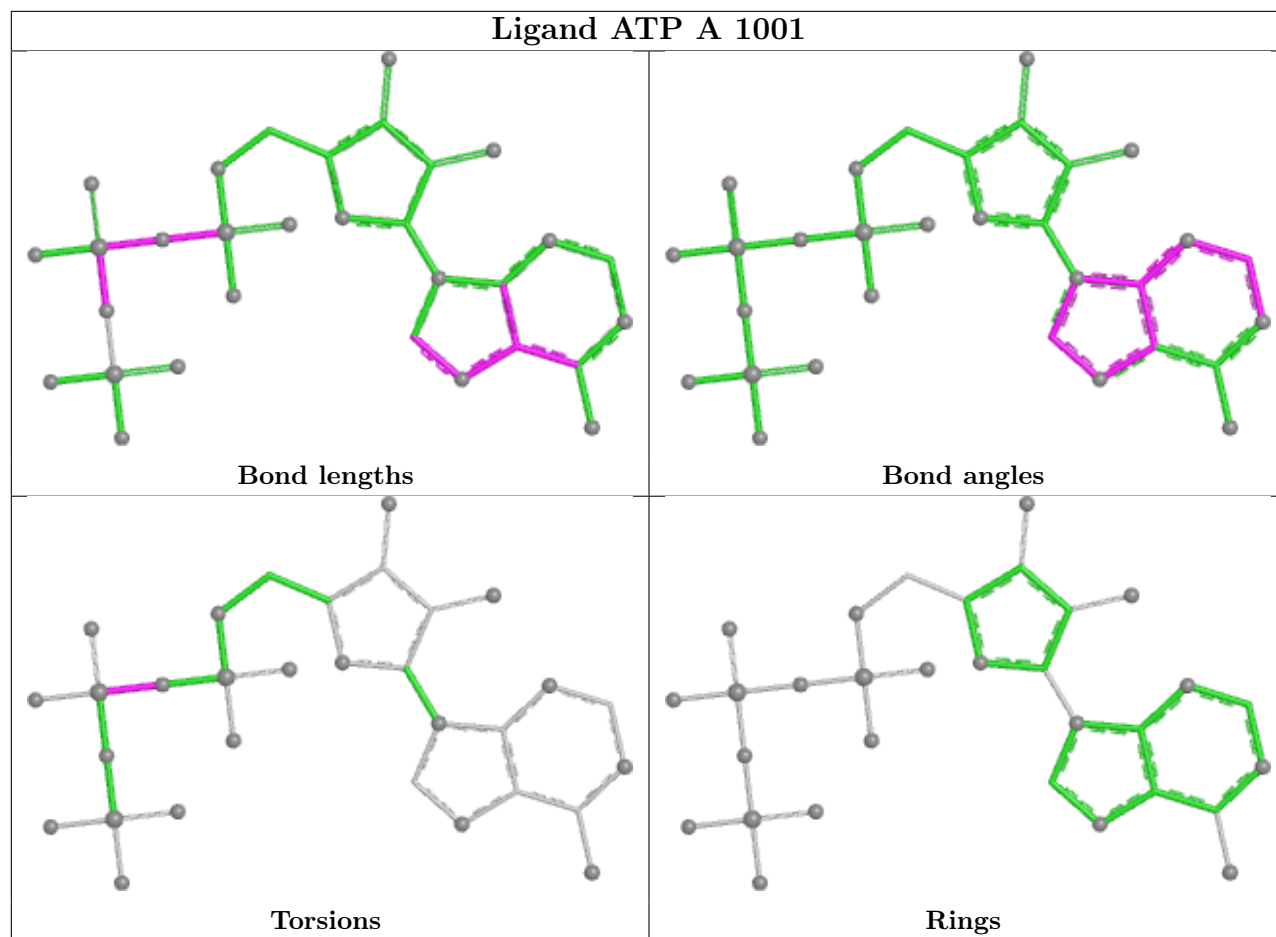
1 monomer is involved in 2 short contacts:

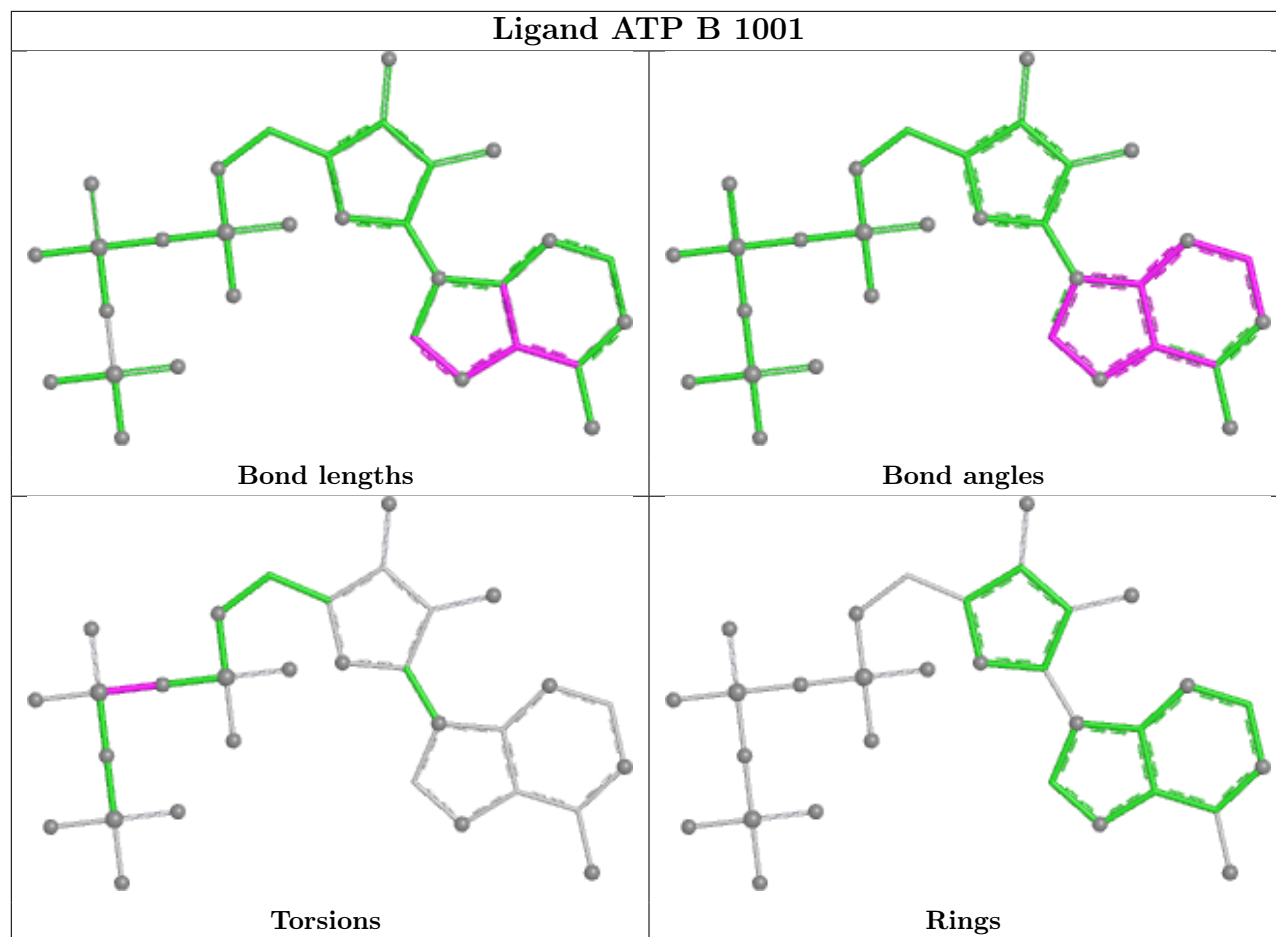
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1001	ATP	2	0

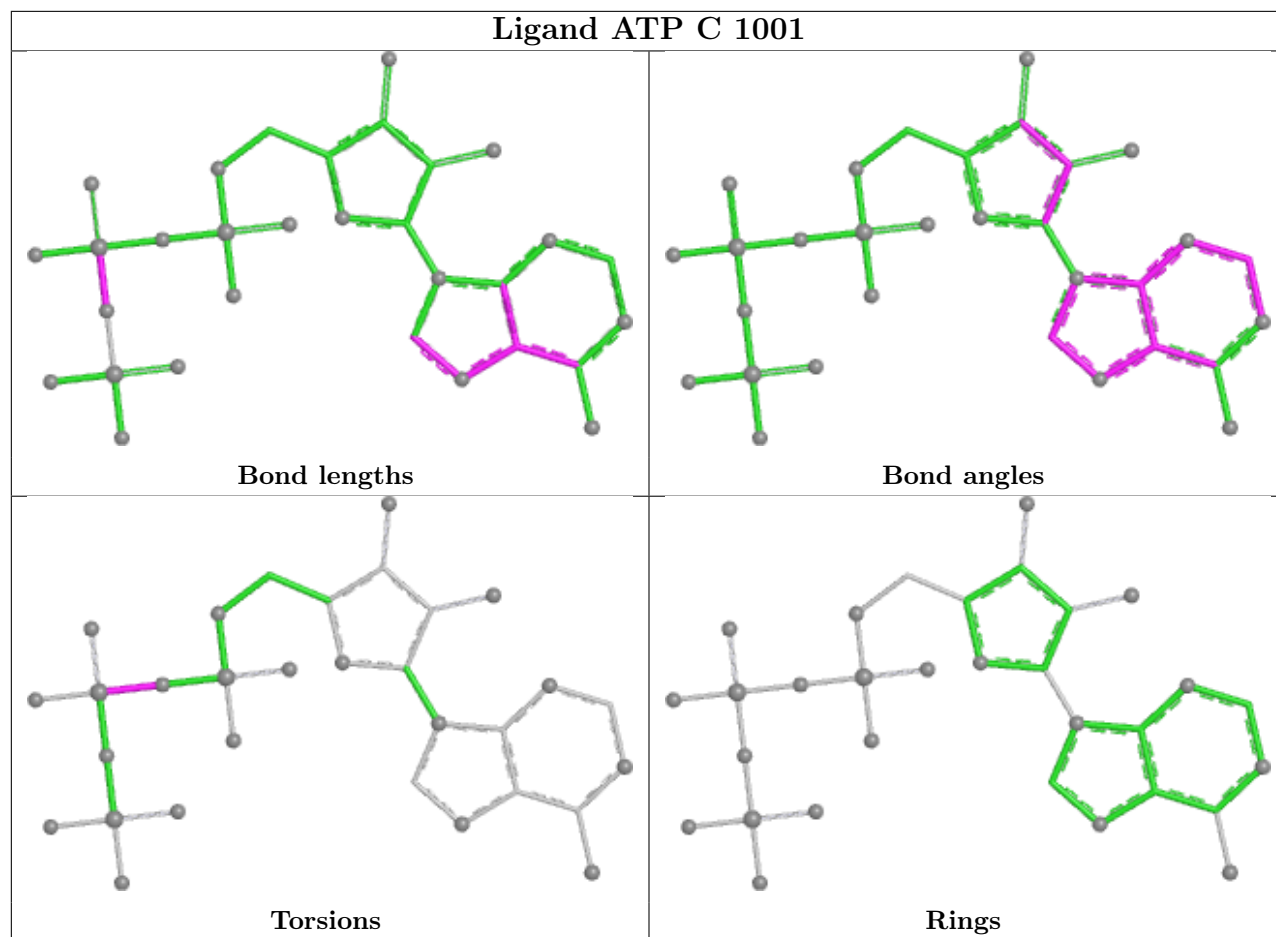
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

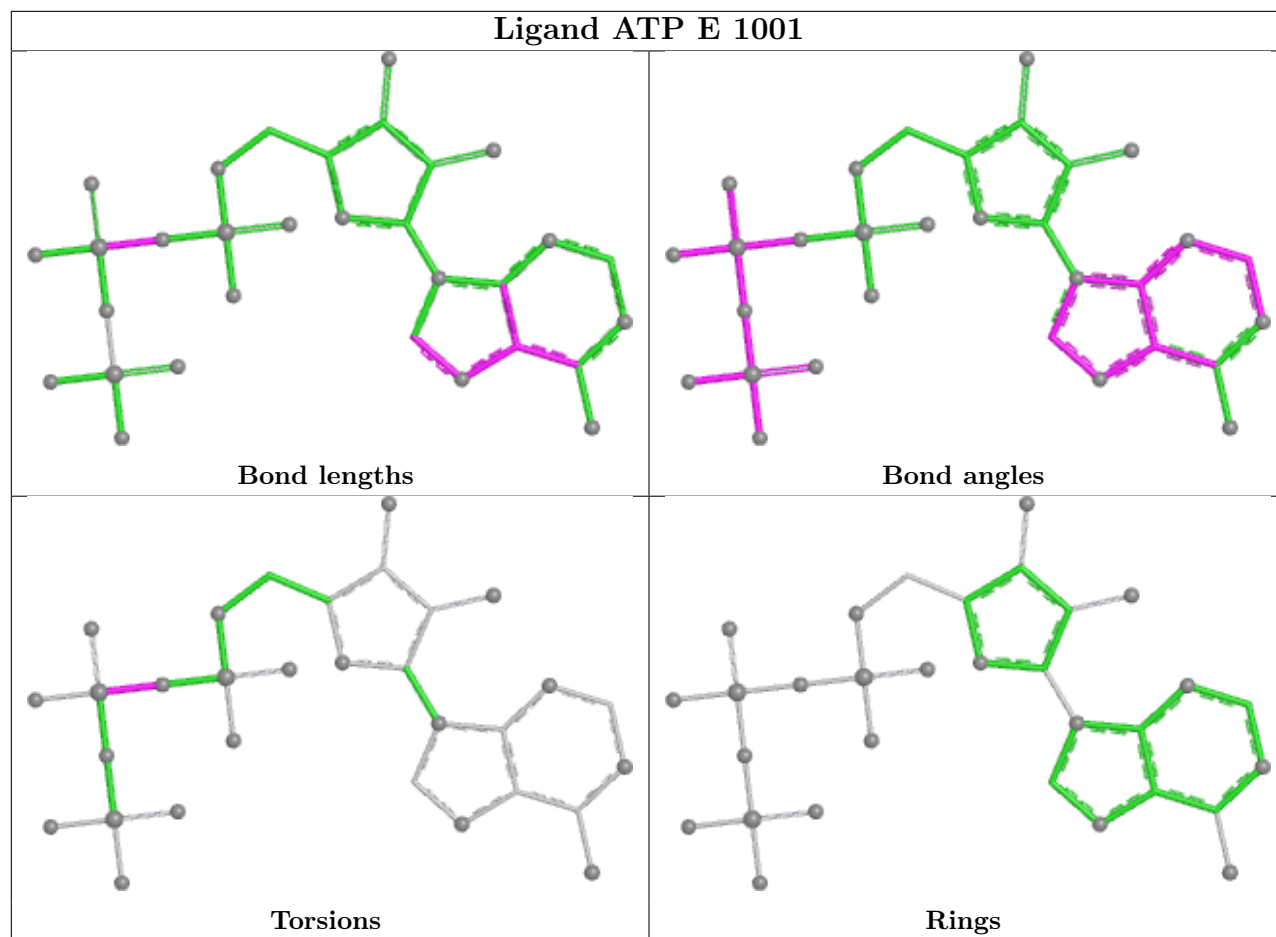












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	401/413 (97%)	-0.14	4 (0%) 79 74	38, 64, 116, 191	0
1	B	402/413 (97%)	-0.25	4 (0%) 79 74	37, 60, 106, 160	0
1	C	402/413 (97%)	-0.11	7 (1%) 69 62	38, 68, 116, 157	0
1	D	402/413 (97%)	-0.16	9 (2%) 62 54	39, 63, 114, 188	0
1	E	402/413 (97%)	-0.11	10 (2%) 58 50	43, 68, 120, 189	0
1	F	402/413 (97%)	-0.27	4 (0%) 79 74	36, 59, 104, 150	0
All	All	2411/2478 (97%)	-0.17	38 (1%) 70 63	36, 63, 115, 191	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	236	ALA	4.3
1	B	78	LEU	4.1
1	C	236	ALA	3.9
1	D	241	TYR	3.8
1	C	237	VAL	3.5

### 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

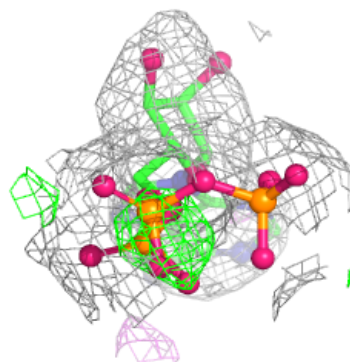
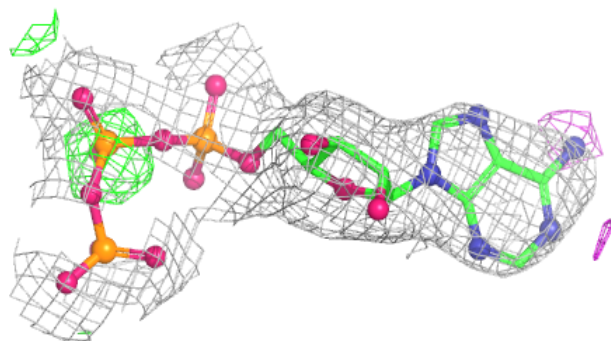
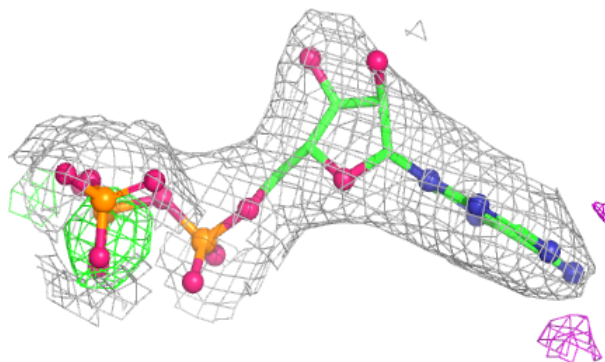
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	ATP	B	1001	31/31	0.95	0.07	41,51,64,84	0
2	ATP	C	1001	31/31	0.95	0.07	51,65,77,87	0
2	ATP	F	1001	31/31	0.95	0.07	44,53,65,72	0
2	ATP	E	1001	31/31	0.96	0.07	48,63,73,89	0
2	ATP	A	1001	31/31	0.96	0.07	39,50,67,75	0
2	ATP	D	1001	31/31	0.97	0.06	40,51,64,69	0
3	MG	A	1002	1/1	0.98	0.10	55,55,55,55	0
3	MG	C	1002	1/1	0.98	0.06	49,49,49,49	0
3	MG	B	1002	1/1	0.99	0.08	48,48,48,48	0
3	MG	D	1002	1/1	0.99	0.09	48,48,48,48	0
3	MG	E	1002	1/1	0.99	0.05	54,54,54,54	0
3	MG	F	1002	1/1	0.99	0.07	49,49,49,49	0

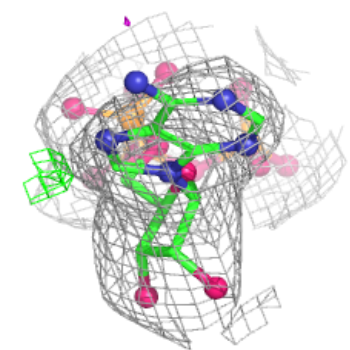
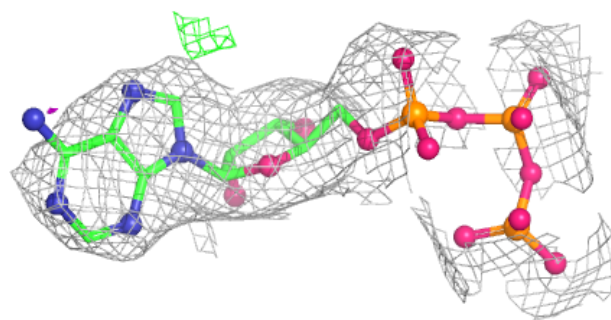
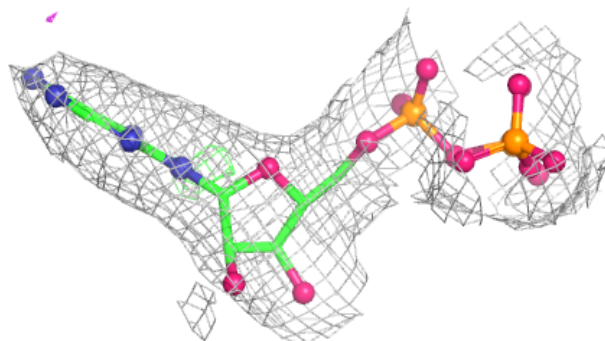
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around ATP 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)

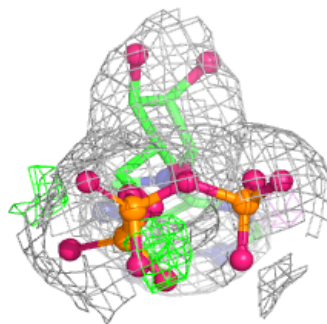
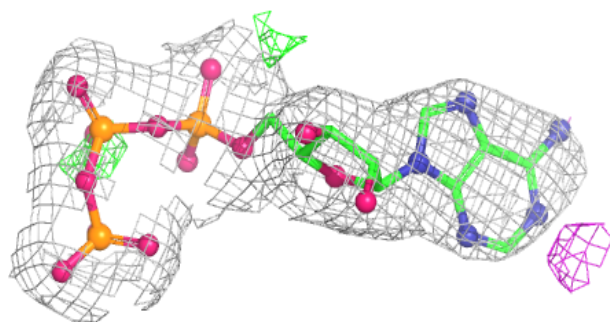
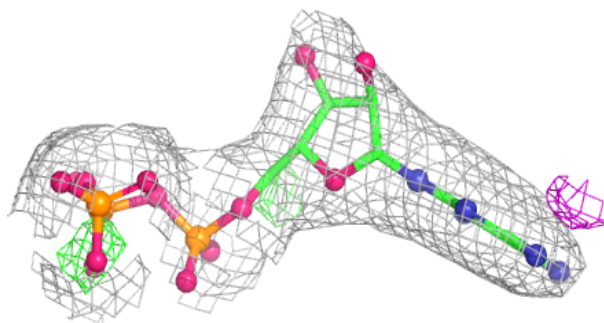
**Electron density around ATP C 1001:**

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

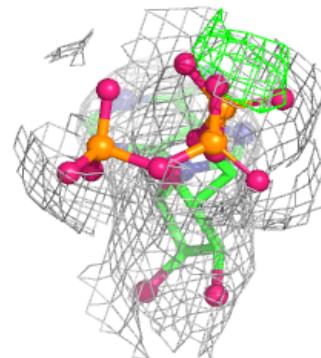
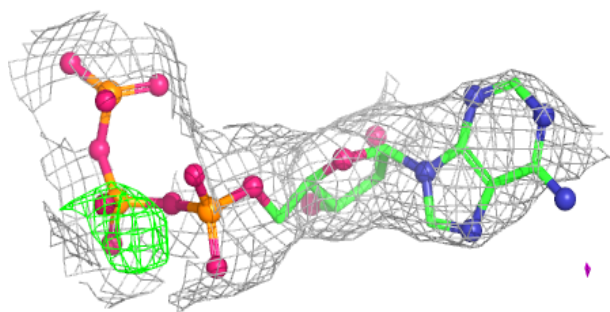
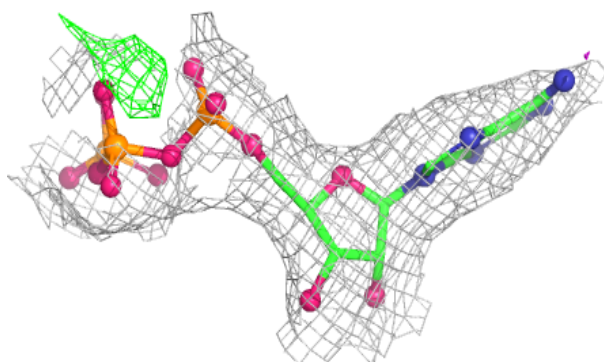


**Electron density around ATP F 1001:**

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

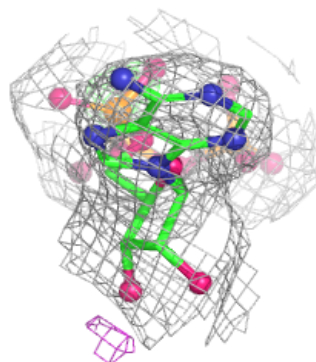
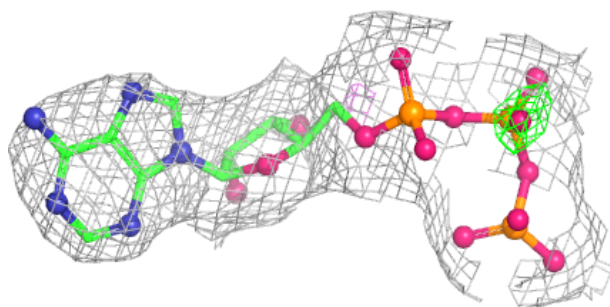
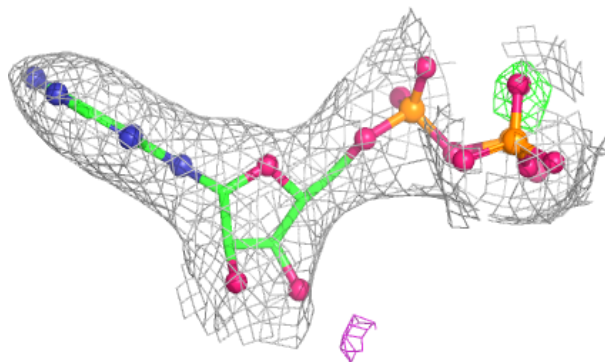
**Electron density around ATP E 1001:**

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

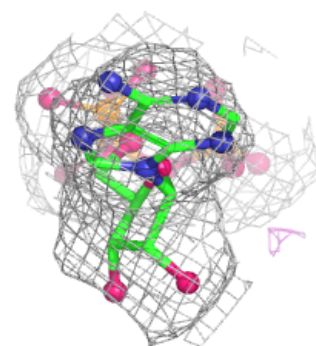
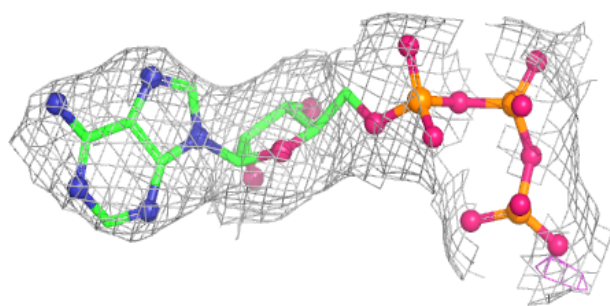
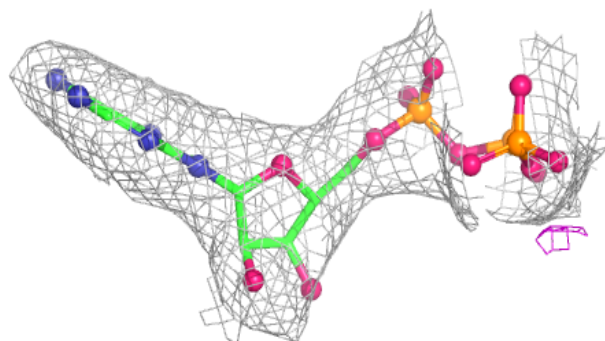


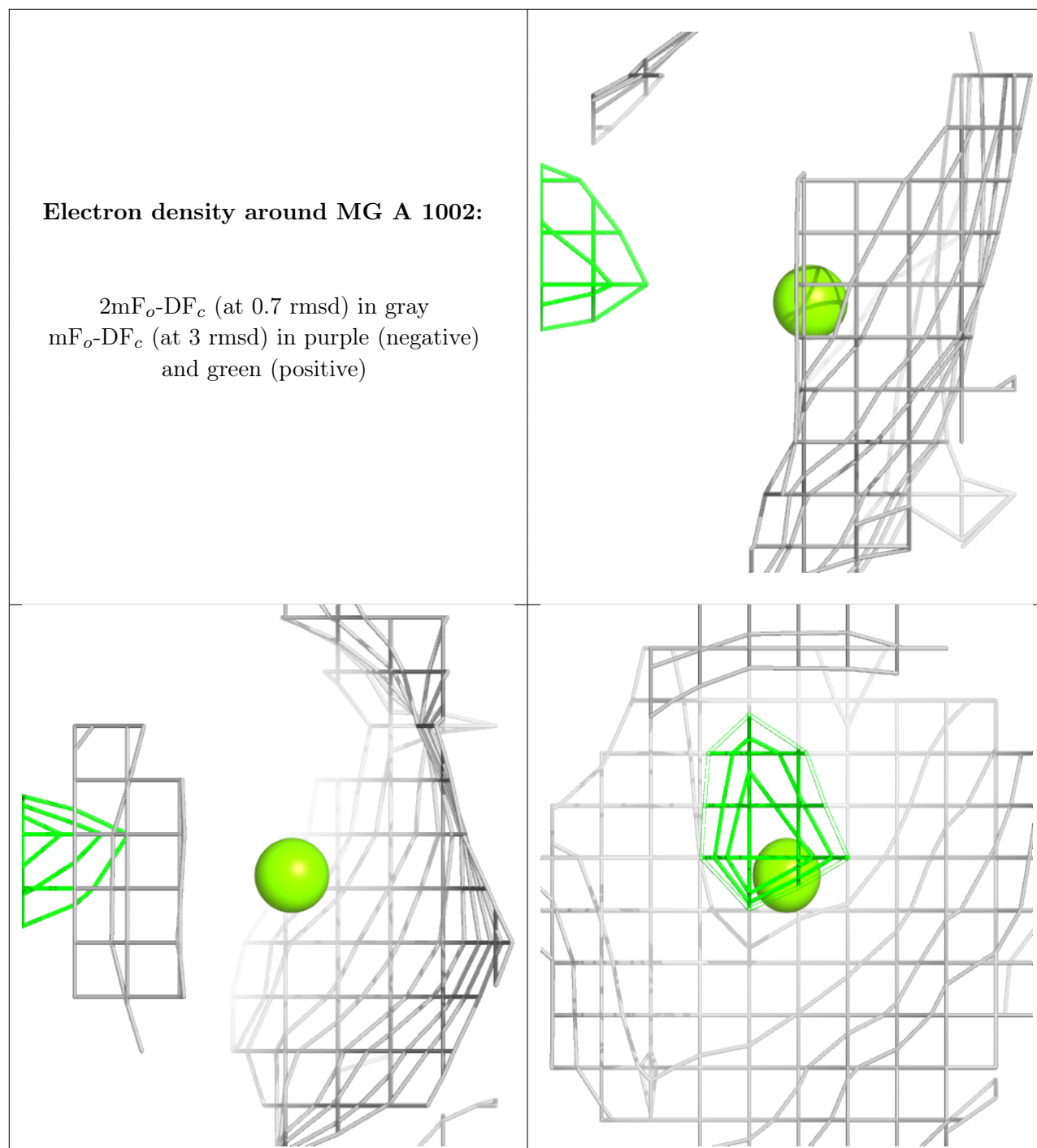
**Electron density around ATP A 1001:**

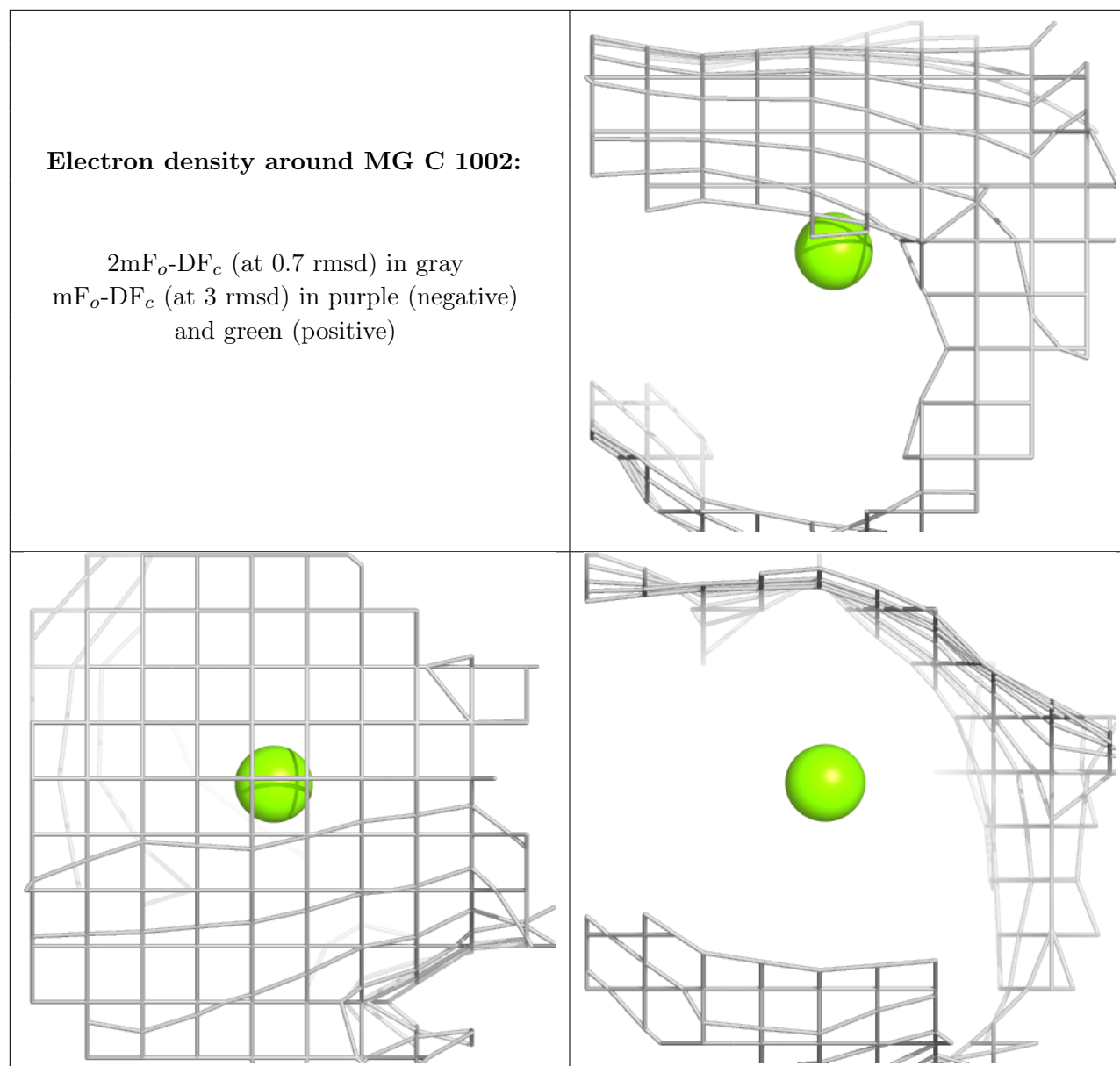
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

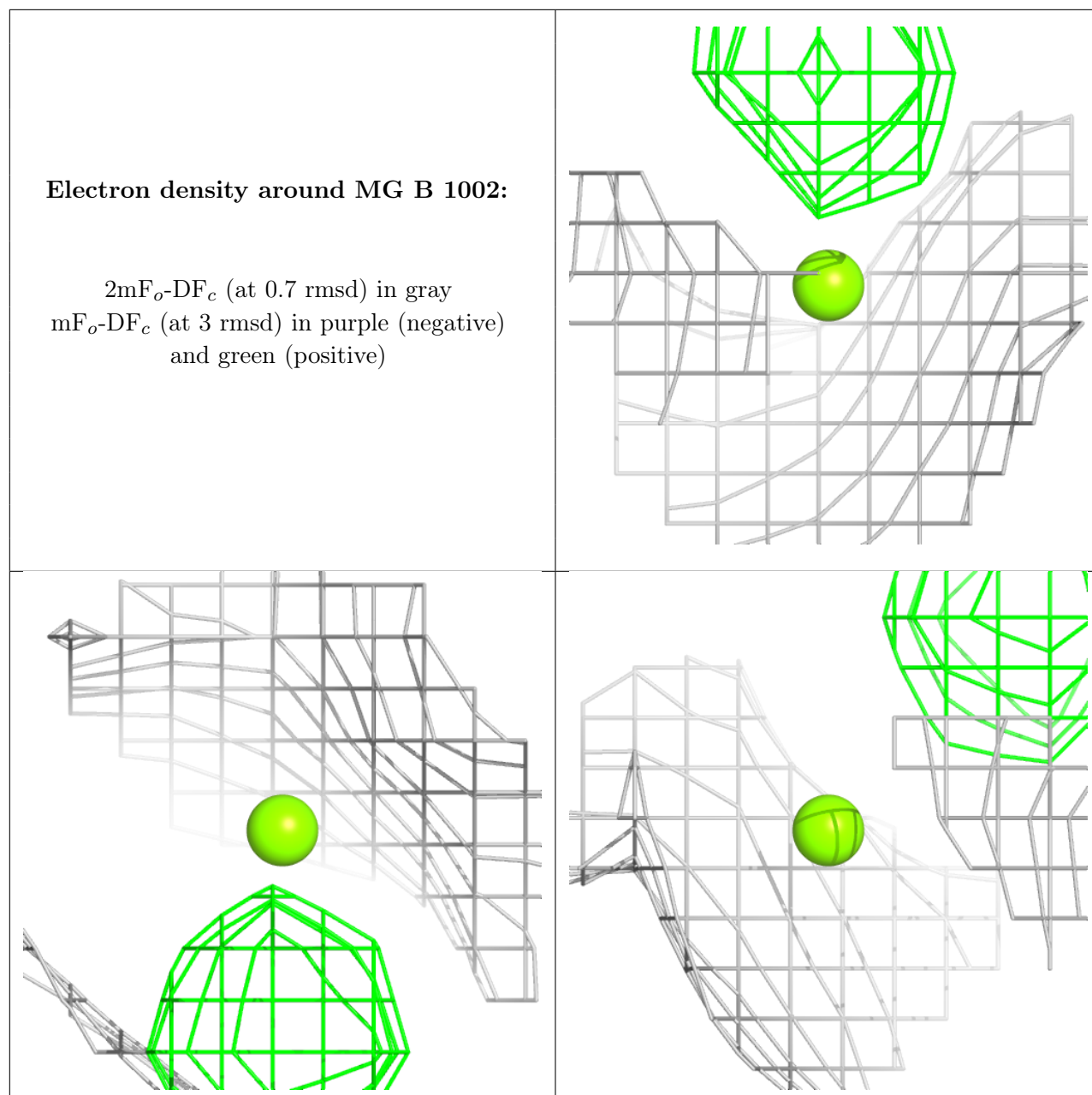
**Electron density around ATP D 1001:**

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



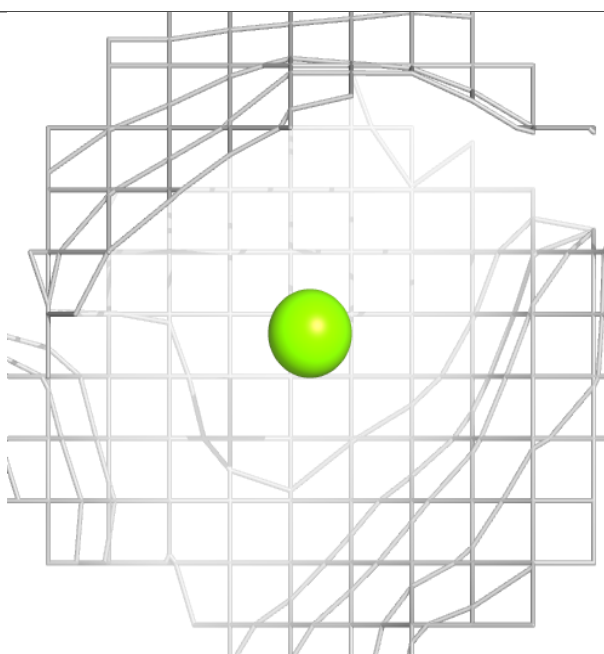
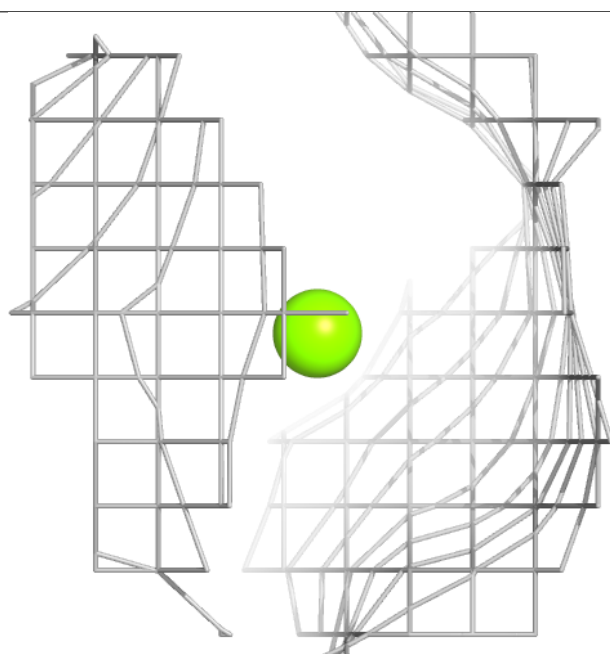
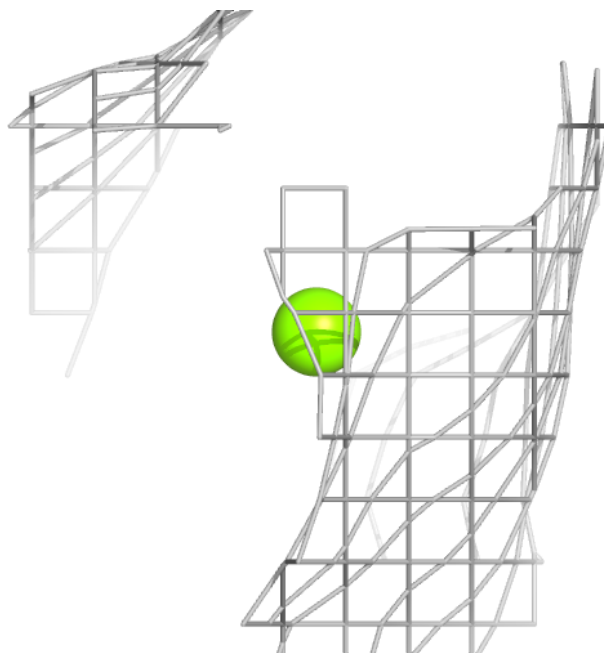


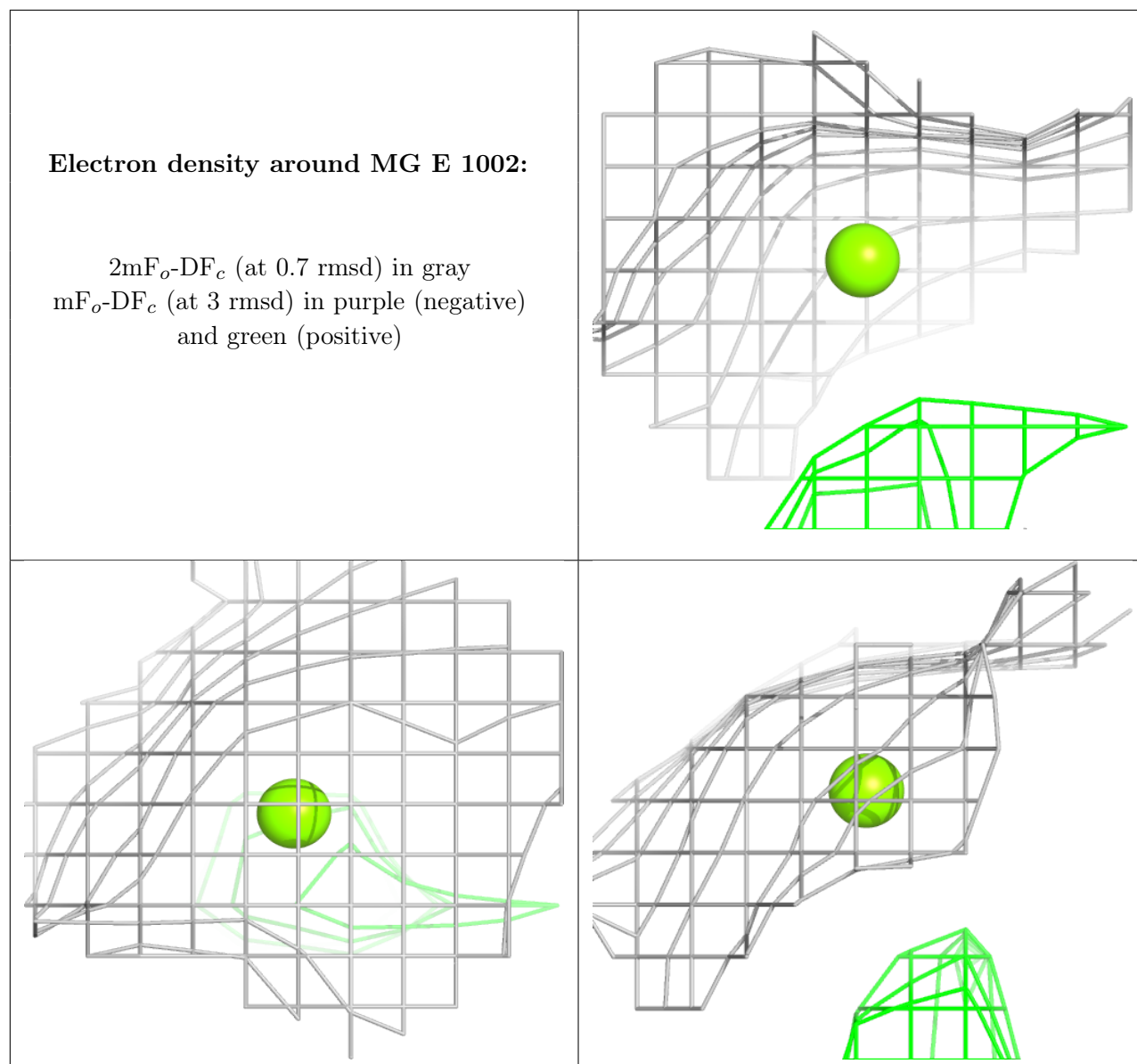


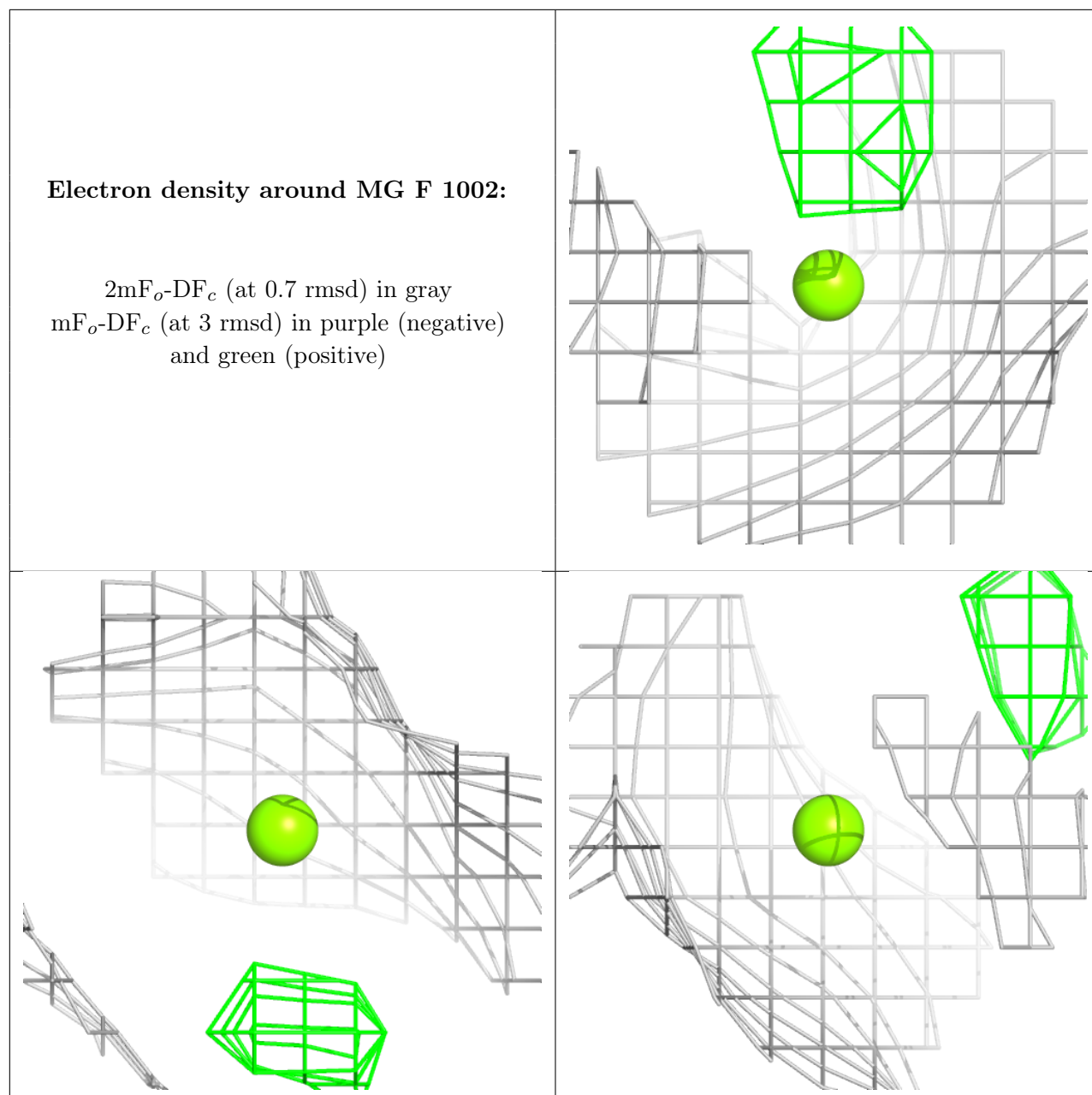


**Electron density around MG D 1002:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.