



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2023 – 07:47 AM EDT

PDB ID : 7N1R  
Title : A novel and unique ATP hydrolysis to AMP by a human Hsp70 BiP  
Authors : Yang, J.; Musayev, F.; Liu, Q.  
Deposited on : 2021-05-28  
Resolution : 2.03 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

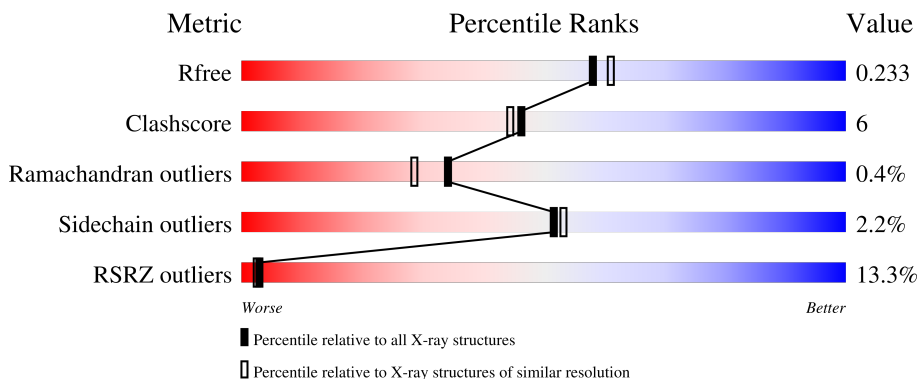
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.03 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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	606	
1	B	606	

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
4	PO4	A	709	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10811 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 Endoplasmic reticulum chaperone BiP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	606	4769	2994	812	951	12	0	9	0
1	B	606	4771	2996	811	952	12	0	9	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	SER	-	expression tag	UNP P11021
A	453	VAL	THR	conflict	UNP P11021
A	454	GLY	ALA	conflict	UNP P11021
A	455	GLY	SER	conflict	UNP P11021
A	?	-	ASP	deletion	UNP P11021
A	?	-	ASN	deletion	UNP P11021
A	?	-	GLN	deletion	UNP P11021
A	?	-	PRO	deletion	UNP P11021
B	24	SER	-	expression tag	UNP P11021
B	453	VAL	THR	conflict	UNP P11021
B	454	GLY	ALA	conflict	UNP P11021
B	455	GLY	SER	conflict	UNP P11021
B	?	-	ASP	deletion	UNP P11021
B	?	-	ASN	deletion	UNP P11021
B	?	-	GLN	deletion	UNP P11021
B	?	-	PRO	deletion	UNP P11021

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
3	A	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P) (labeled as "Ligand of Interest" by depositor).

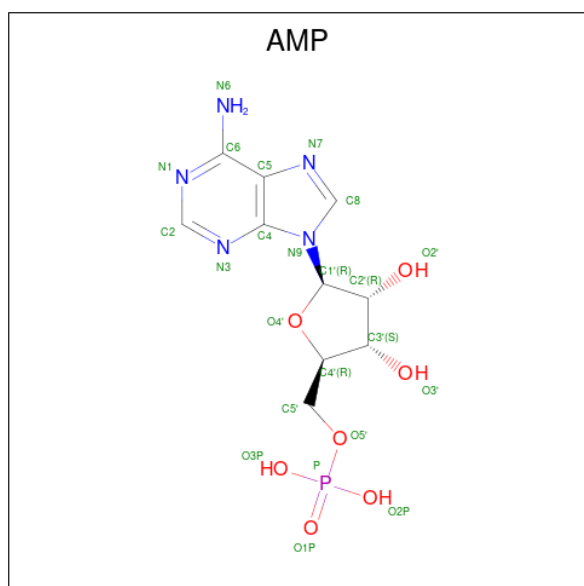


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0
4	B	1	Total O P 5 4 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 6 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O P 23 10 5 7 1	0	0
6	B	1	Total C N O P 23 10 5 7 1	0	0

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





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

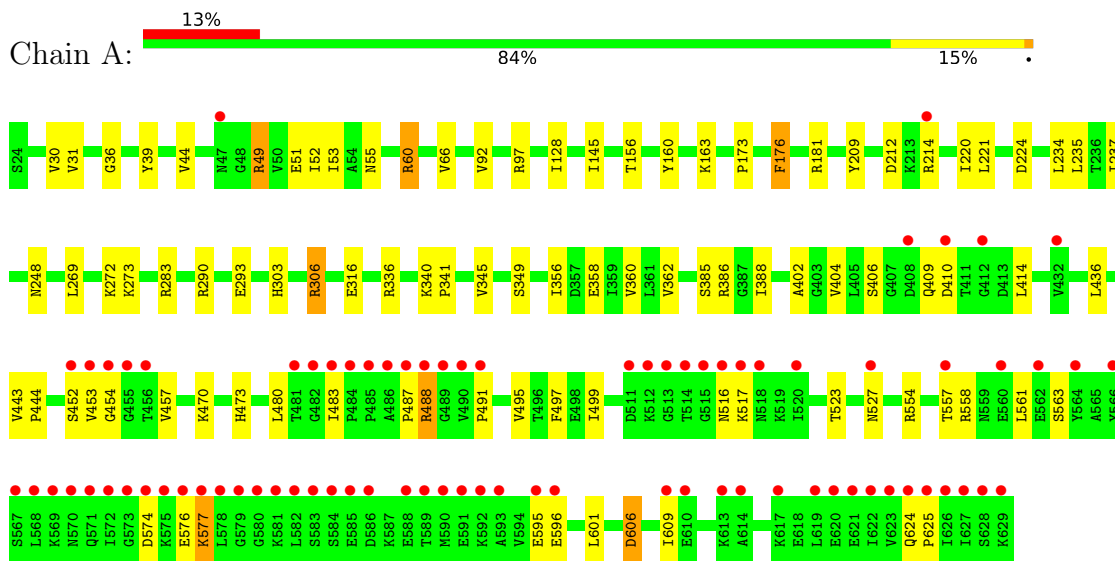
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	537	Total O 537 537	0	0
8	B	531	Total O 531 531	0	0

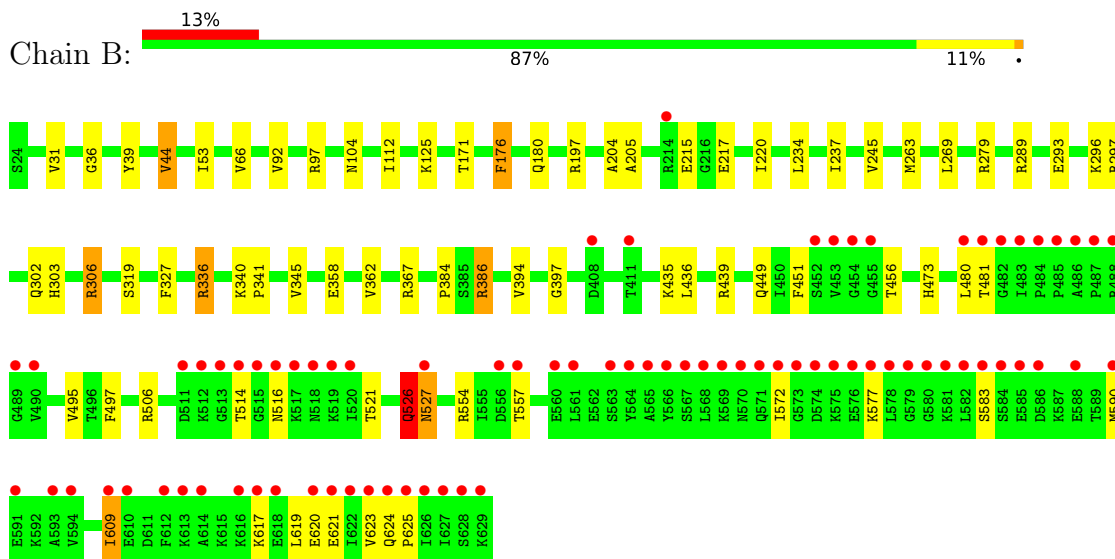
### 3 Residue-property plots [i](#)

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: Endoplasmic reticulum chaperone BiP



- Molecule 1: Endoplasmic reticulum chaperone BiP



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.99Å 76.39Å 79.92Å 84.88° 62.49° 63.14°	Depositor
Resolution (Å)	45.31 – 2.03 39.63 – 2.03	Depositor EDS
% Data completeness (in resolution range)	96.8 (45.31-2.03) 96.9 (39.63-2.03)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.51 (at 2.03Å)	Xtrriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.174 , 0.223 0.185 , 0.233	Depositor DCC
$R_{free}$ test set	4408 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.8	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.011 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10811	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% 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: PO4, GOL, PEG, MG, SO4, AMP

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	0.57	0/4839	0.71	1/6533 (0.0%)
1	B	0.58	0/4844	0.70	1/6539 (0.0%)
All	All	0.58	0/9683	0.71	2/13072 (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	6
1	B	0	4
All	All	0	10

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	181	ARG	CG-CD-NE	-5.47	100.31	111.80
1	B	367	ARG	NE-CZ-NH2	-5.34	117.63	120.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	212	ASP	Peptide
1	A	290	ARG	Sidechain
1	A	306	ARG	Sidechain
1	A	336	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	60	ARG	Sidechain
1	A	97	ARG	Sidechain
1	B	336	ARG	Sidechain
1	B	386	ARG	Sidechain
1	B	526	GLN	Peptide
1	B	527	ASN	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	4769	0	4796	57	0
1	B	4771	0	4797	61	0
2	A	24	0	32	2	0
2	B	24	0	32	5	0
3	A	10	0	0	0	0
3	B	20	0	0	2	0
4	A	40	0	0	4	0
4	B	30	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	23	0	12	0	0
6	B	23	0	12	0	0
7	A	7	0	10	1	0
8	A	537	0	0	14	1
8	B	531	0	0	15	1
All	All	10811	0	9691	122	1

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 6.

All (122) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ASP:HA	8:A:1070:HOH:O	1.56	1.05
4:A:709:PO4:O3	8:A:801:HOH:O	1.81	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:LYS:NZ	8:A:802:HOH:O	2.09	0.86
4:A:709:PO4:P	8:A:801:HOH:O	2.42	0.77
1:B:31:VAL:HG12	1:B:44[B]:VAL:HG22	1.69	0.74
1:A:306:ARG:HG2	1:A:306:ARG:HH11	1.54	0.72
1:B:220:ILE:HD12	1:B:358:GLU:HB2	1.72	0.72
1:B:439:ARG:HH22	2:B:704:GOL:H31	1.56	0.70
1:A:409:GLN:O	8:A:804:HOH:O	2.10	0.69
1:B:336:ARG:NH1	8:B:802:HOH:O	2.05	0.68
1:A:248:ASN:C	8:A:816:HOH:O	2.32	0.67
1:B:31:VAL:HG12	1:B:44[A]:VAL:HG13	1.76	0.66
1:B:514:THR:HG21	1:B:516:ASN:HD22	1.61	0.66
1:A:473:HIS:HE1	8:A:1243:HOH:O	1.78	0.65
1:A:557:THR:HG21	1:A:609:ILE:HD11	1.79	0.64
1:A:220:ILE:HD12	1:A:358:GLU:HB2	1.80	0.64
1:A:410:ASP:N	8:A:814:HOH:O	2.29	0.63
4:A:709:PO4:O2	8:A:805:HOH:O	2.16	0.61
1:B:384:PRO:HD3	8:B:885:HOH:O	2.00	0.60
1:B:557:THR:HG21	1:B:609:ILE:HD11	1.83	0.60
1:A:360:VAL:HG13	1:A:388:ILE:HD13	1.83	0.59
1:A:574:ASP:OD2	1:A:577:LYS:CB	2.50	0.59
1:A:234:LEU:HB2	1:A:345[A]:VAL:CG1	2.33	0.58
1:B:104[A]:ASN:ND2	8:B:815:HOH:O	2.36	0.58
1:A:283:ARG:NH1	8:A:823:HOH:O	2.36	0.57
1:A:454:GLY:HA2	1:A:483:ILE:HD13	1.84	0.57
1:B:269:LEU:HD23	1:B:269:LEU:O	2.05	0.57
1:A:293:GLU:OE2	8:A:806:HOH:O	2.17	0.57
1:B:234[A]:LEU:HD12	1:B:245:VAL:HB	1.86	0.57
1:B:340:LYS:HB2	1:B:341:PRO:HD3	1.86	0.57
1:A:49:ARG:NH2	7:A:717:PEG:O2	2.39	0.56
1:B:171:THR:HG21	1:B:394:VAL:HG12	1.85	0.56
1:B:44[A]:VAL:HG22	1:B:53:ILE:HD11	1.88	0.56
1:A:340:LYS:HB2	1:A:341:PRO:HD3	1.88	0.56
1:A:31:VAL:HG12	1:A:44[A]:VAL:CG1	2.36	0.56
1:B:340:LYS:NZ	8:B:821:HOH:O	2.39	0.55
1:A:487:PRO:O	1:A:488:ARG:CB	2.54	0.55
1:B:473:HIS:HE1	8:B:1223:HOH:O	1.88	0.55
1:B:44[B]:VAL:HG23	1:B:53:ILE:HD11	1.88	0.55
1:B:97:ARG:NH2	8:B:812:HOH:O	2.39	0.55
1:B:303:HIS:HD2	3:B:708:SO4:O3	1.90	0.54
1:B:234[A]:LEU:HB2	1:B:345[A]:VAL:CG1	2.38	0.54
1:B:205:ALA:HB1	1:B:362:VAL:HG11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:707:PO4:O1	8:A:807:HOH:O	2.19	0.53
2:B:705:GOL:H12	8:B:1232:HOH:O	2.08	0.53
1:A:234:LEU:HD21	1:A:356:ILE:CD1	2.38	0.53
1:A:44[B]:VAL:HG23	1:A:53:ILE:HD11	1.91	0.53
1:B:220:ILE:HG12	1:B:237:ILE:HD12	1.90	0.52
1:B:197:ARG:NH1	8:B:804:HOH:O	2.22	0.52
1:B:234[A]:LEU:C	1:B:234[A]:LEU:HD13	2.30	0.52
1:A:44[B]:VAL:CG2	1:A:53:ILE:HD11	2.40	0.52
1:B:554:ARG:HA	1:B:609:ILE:HD13	1.93	0.51
1:A:303:HIS:HD2	3:B:702:SO4:O4	1.96	0.49
1:B:279:ARG:NH1	8:B:823:HOH:O	2.41	0.49
1:A:214:ARG:HD2	1:B:215:GLU:HB3	1.93	0.49
1:B:204:ALA:O	1:B:397:GLY:HA3	2.12	0.49
1:B:31:VAL:HG12	1:B:44[A]:VAL:CG1	2.41	0.48
1:A:66:VAL:HG22	1:A:92:VAL:HB	1.95	0.48
1:A:36:GLY:HA3	1:A:39:TYR:O	2.14	0.48
2:B:705:GOL:H11	8:B:1104:HOH:O	2.13	0.47
1:A:173:PRO:HD2	1:A:176:PHE:CD2	2.49	0.47
1:B:293:GLU:OE2	1:B:297:ARG:NH2	2.48	0.47
1:A:316:GLU:HG3	8:A:1311:HOH:O	2.15	0.47
1:A:52:ILE:O	1:A:60:ARG:NH1	2.45	0.47
1:A:558:ARG:HH12	2:A:703:GOL:H32	1.80	0.47
1:A:30:VAL:HG12	1:A:402:ALA:HB1	1.97	0.46
1:A:480:LEU:HD11	1:A:495:VAL:HG21	1.98	0.46
1:A:209:TYR:O	1:B:386:ARG:NH1	2.48	0.46
1:B:220:ILE:CG1	1:B:237:ILE:HD12	2.45	0.46
1:A:452:SER:HA	1:A:491:PRO:O	2.15	0.46
1:A:606:ASP:OD1	1:A:606:ASP:C	2.54	0.45
1:B:436:LEU:HD21	1:B:497:PHE:CD1	2.51	0.45
1:B:624:GLN:HB3	1:B:625:PRO:HD3	1.98	0.45
1:A:386:ARG:HD3	2:A:702:GOL:O3	2.16	0.45
1:B:583:SER:OG	8:B:803:HOH:O	2.20	0.45
1:B:269:LEU:HD23	1:B:269:LEU:C	2.37	0.45
1:B:306:ARG:NH1	1:B:319:SER:OG	2.50	0.45
1:B:279:ARG:NH2	8:B:823:HOH:O	2.42	0.44
1:B:557:THR:OG1	1:B:609:ILE:CD1	2.65	0.44
1:A:453:VAL:CG1	1:A:457:VAL:HG22	2.47	0.44
1:B:449:GLN:HG2	1:B:451:PHE:CZ	2.53	0.44
1:A:345[B]:VAL:O	1:A:349[B]:SER:HB3	2.18	0.44
1:B:44[B]:VAL:CG2	1:B:53:ILE:HD11	2.47	0.43
1:B:125:LYS:CE	1:B:527:ASN:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:PRO:CD	8:B:885:HOH:O	2.63	0.43
1:B:480:LEU:HD11	1:B:495:VAL:HG21	1.99	0.43
1:A:269:LEU:HD21	1:A:273:LYS:HE3	1.99	0.43
1:B:36:GLY:HA3	1:B:39:TYR:O	2.17	0.43
1:B:296:LYS:HG3	1:B:327:PHE:CZ	2.53	0.43
1:B:572:ILE:HD11	1:B:590:MET:HB3	1.99	0.43
1:A:220:ILE:HG13	1:A:237:ILE:HD12	1.99	0.43
1:A:561:LEU:HG	1:A:601:LEU:HD11	2.01	0.43
1:B:435:LYS:HZ3	2:B:705:GOL:H11	1.84	0.43
1:A:409:GLN:HA	8:A:814:HOH:O	2.19	0.43
1:B:176:PHE:CD2	1:B:180:GLN:HB3	2.53	0.43
1:A:234:LEU:HD13	1:A:235:LEU:N	2.34	0.43
1:A:269:LEU:HD23	1:A:269:LEU:O	2.19	0.42
1:B:439:ARG:NH2	2:B:704:GOL:H31	2.30	0.42
1:B:66:VAL:HG22	1:B:92:VAL:HB	2.02	0.42
1:B:171:THR:HG21	1:B:394:VAL:CG1	2.49	0.42
1:B:514:THR:CG2	1:B:516:ASN:HD22	2.29	0.42
1:B:97:ARG:CZ	8:B:812:HOH:O	2.68	0.42
1:B:217[A]:GLU:OE1	1:B:217[A]:GLU:C	2.58	0.42
1:A:128:ILE:HD13	1:A:145:ILE:HG13	2.02	0.42
1:A:55:ASN:HA	1:A:156:THR:HG23	2.02	0.42
1:B:617:LYS:HA	1:B:620:GLU:HB2	2.02	0.42
1:A:444:PRO:HA	1:A:499:ILE:O	2.20	0.42
1:A:624:GLN:HB3	1:A:625:PRO:HD3	2.02	0.42
1:A:51:GLU:HG2	1:A:160:TYR:CZ	2.55	0.41
1:B:263[A]:MET:SD	1:B:289:ARG:HA	2.60	0.41
1:A:224:ASP:HA	1:A:362:VAL:O	2.21	0.41
1:A:234:LEU:HD13	1:A:234:LEU:C	2.41	0.41
1:A:443:VAL:HA	1:A:444:PRO:C	2.40	0.41
1:B:619:LEU:O	1:B:623:VAL:HG23	2.21	0.41
1:A:269:LEU:HD23	1:A:269:LEU:C	2.40	0.41
1:A:66:VAL:CG2	1:A:92:VAL:HB	2.50	0.41
1:A:436:LEU:HD21	1:A:497:PHE:CD1	2.56	0.41
1:B:302:GLN:NE2	8:B:858:HOH:O	2.54	0.41
1:B:506:ARG:NH1	1:B:521:THR:OG1	2.53	0.41
1:A:554:ARG:HH12	1:A:606:ASP:HA	1.86	0.40
1:A:404:VAL:HG21	1:A:414:LEU:HD23	2.04	0.40
1:B:112:ILE:HD13	1:B:112:ILE:HG21	1.88	0.40

All (1) 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)
8:A:830:HOH:O	8:B:820:HOH:O[1_565]	1.95	0.25

### 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	613/606 (101%)	587 (96%)	23 (4%)	3 (0%)	29	22
1	B	613/606 (101%)	594 (97%)	17 (3%)	2 (0%)	41	36
All	All	1226/1212 (101%)	1181 (96%)	40 (3%)	5 (0%)	34	28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	488	ARG
1	A	527	ASN
1	A	577	LYS
1	B	526	GLN
1	B	577	LYS

#### 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	525/519 (101%)	509 (97%)	16 (3%)	41	40
1	B	525/519 (101%)	516 (98%)	9 (2%)	60	63
All	All	1050/1038 (101%)	1025 (98%)	25 (2%)	52	49

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ARG
1	A	176	PHE
1	A	221	LEU
1	A	272	LYS
1	A	385	SER
1	A	406	SER
1	A	470	LYS
1	A	516	ASN
1	A	517	LYS
1	A	523[A]	THR
1	A	523[B]	THR
1	A	563	SER
1	A	576	GLU
1	A	595	GLU
1	A	596	GLU
1	A	606	ASP
1	B	44[A]	VAL
1	B	44[B]	VAL
1	B	176	PHE
1	B	306	ARG
1	B	456	THR
1	B	481	THR
1	B	526	GLN
1	B	609	ILE
1	B	621	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	GLN
1	A	302	GLN
1	A	303	HIS
1	A	473	HIS
1	A	527	ASN
1	A	571	GLN
1	B	302	GLN
1	B	303	HIS
1	B	516	ASN
1	B	526	GLN
1	B	624	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 2 are monoatomic - leaving 31 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	GOL	B	705	-	5,5,5	0.66	0	5,5,5	0.79	0
2	GOL	A	702	-	5,5,5	0.44	0	5,5,5	0.83	0
4	PO4	A	712	-	4,4,4	1.19	0	6,6,6	0.66	0
4	PO4	A	713	-	4,4,4	0.71	0	6,6,6	0.85	0
4	PO4	B	716	5	4,4,4	2.09	2 (50%)	6,6,6	0.71	0
3	SO4	B	707	-	4,4,4	0.46	0	6,6,6	0.23	0
7	PEG	A	717	-	6,6,6	0.53	0	5,5,5	0.58	0
3	SO4	B	708	-	4,4,4	0.36	0	6,6,6	0.69	0
3	SO4	A	705	-	4,4,4	0.47	0	6,6,6	0.32	0
4	PO4	B	712	-	4,4,4	0.68	0	6,6,6	0.59	0
4	PO4	A	708	-	4,4,4	0.80	0	6,6,6	0.97	0
3	SO4	B	702	-	4,4,4	0.47	0	6,6,6	0.88	0
4	PO4	A	710	-	4,4,4	0.85	0	6,6,6	0.31	0
4	PO4	B	711	-	4,4,4	0.47	0	6,6,6	0.59	0
2	GOL	B	704	-	5,5,5	0.41	0	5,5,5	0.69	0
2	GOL	A	703	-	5,5,5	0.50	0	5,5,5	0.34	0
4	PO4	B	710	-	4,4,4	0.73	0	6,6,6	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	B	706	-	5,5,5	0.53	0	5,5,5	0.40	0
2	GOL	A	701	-	5,5,5	0.38	0	5,5,5	0.62	0
2	GOL	B	701	-	5,5,5	0.43	0	5,5,5	0.88	0
4	PO4	A	707	-	4,4,4	0.65	0	6,6,6	0.57	0
3	SO4	B	709	-	4,4,4	0.36	0	6,6,6	0.61	0
6	AMP	B	715	5	22,25,25	1.15	2 (9%)	25,38,38	2.10	9 (36%)
6	AMP	A	715	5	22,25,25	1.45	4 (18%)	25,38,38	1.26	5 (20%)
4	PO4	B	713	-	4,4,4	0.88	0	6,6,6	0.61	0
4	PO4	A	711	-	4,4,4	0.97	0	6,6,6	0.64	0
2	GOL	A	704	-	5,5,5	0.57	0	5,5,5	0.33	0
4	PO4	A	716	5	4,4,4	2.34	2 (50%)	6,6,6	1.13	0
3	SO4	A	706	-	4,4,4	0.44	0	6,6,6	0.53	0
4	PO4	A	709	-	4,4,4	0.85	0	6,6,6	0.73	0
4	PO4	B	714	-	4,4,4	0.79	0	6,6,6	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	B	706	-	-	4/4/4/4	-
2	GOL	A	701	-	-	4/4/4/4	-
2	GOL	B	701	-	-	2/4/4/4	-
2	GOL	B	705	-	-	2/4/4/4	-
2	GOL	A	702	-	-	2/4/4/4	-
2	GOL	A	704	-	-	4/4/4/4	-
7	PEG	A	717	-	-	2/4/4/4	-
2	GOL	B	704	-	-	4/4/4/4	-
2	GOL	A	703	-	-	2/4/4/4	-
6	AMP	B	715	5	-	0/6/26/26	0/3/3/3
6	AMP	A	715	5	-	0/6/26/26	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	715	AMP	C2-N3	3.88	1.38	1.32
4	B	716	PO4	P-O3	-3.11	1.45	1.54
6	A	715	AMP	C2'-C1'	-3.11	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	716	PO4	P-O3	-2.90	1.45	1.54
6	A	715	AMP	C2-N1	2.90	1.39	1.33
4	A	716	PO4	P-O2	-2.87	1.46	1.54
6	B	715	AMP	C2-N1	2.61	1.38	1.33
6	A	715	AMP	C5-C4	2.29	1.47	1.40
4	B	716	PO4	P-O2	-2.20	1.48	1.54
6	B	715	AMP	C2-N3	2.03	1.35	1.32

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	715	AMP	O3P-P-O2P	4.85	126.17	107.64
6	B	715	AMP	C5-C6-N6	-4.30	113.82	120.35
6	B	715	AMP	N3-C2-N1	-3.90	122.58	128.68
6	B	715	AMP	C1'-N9-C4	-3.46	120.57	126.64
6	B	715	AMP	N6-C6-N1	3.45	125.73	118.57
6	A	715	AMP	N3-C2-N1	-3.12	123.81	128.68
6	A	715	AMP	C1'-N9-C4	-2.60	122.07	126.64
6	B	715	AMP	O2'-C2'-C3'	2.50	119.91	111.82
6	A	715	AMP	O3P-P-O1P	2.19	119.24	110.68
6	B	715	AMP	O2P-P-O5'	-2.17	100.95	106.73
6	B	715	AMP	O4'-C1'-C2'	-2.14	103.80	106.93
6	B	715	AMP	O3P-P-O5'	-2.12	101.10	106.73
6	A	715	AMP	N6-C6-N1	2.08	122.90	118.57
6	A	715	AMP	C5-C6-N6	-2.01	117.29	120.35

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	GOL	O1-C1-C2-C3
2	A	701	GOL	C1-C2-C3-O3
2	A	704	GOL	O1-C1-C2-C3
2	A	704	GOL	C1-C2-C3-O3
2	B	704	GOL	O1-C1-C2-C3
2	B	705	GOL	C1-C2-C3-O3
2	B	706	GOL	O1-C1-C2-C3
2	B	706	GOL	C1-C2-C3-O3
2	A	704	GOL	O2-C2-C3-O3
2	B	704	GOL	O1-C1-C2-O2
2	B	705	GOL	O2-C2-C3-O3
2	B	706	GOL	O2-C2-C3-O3

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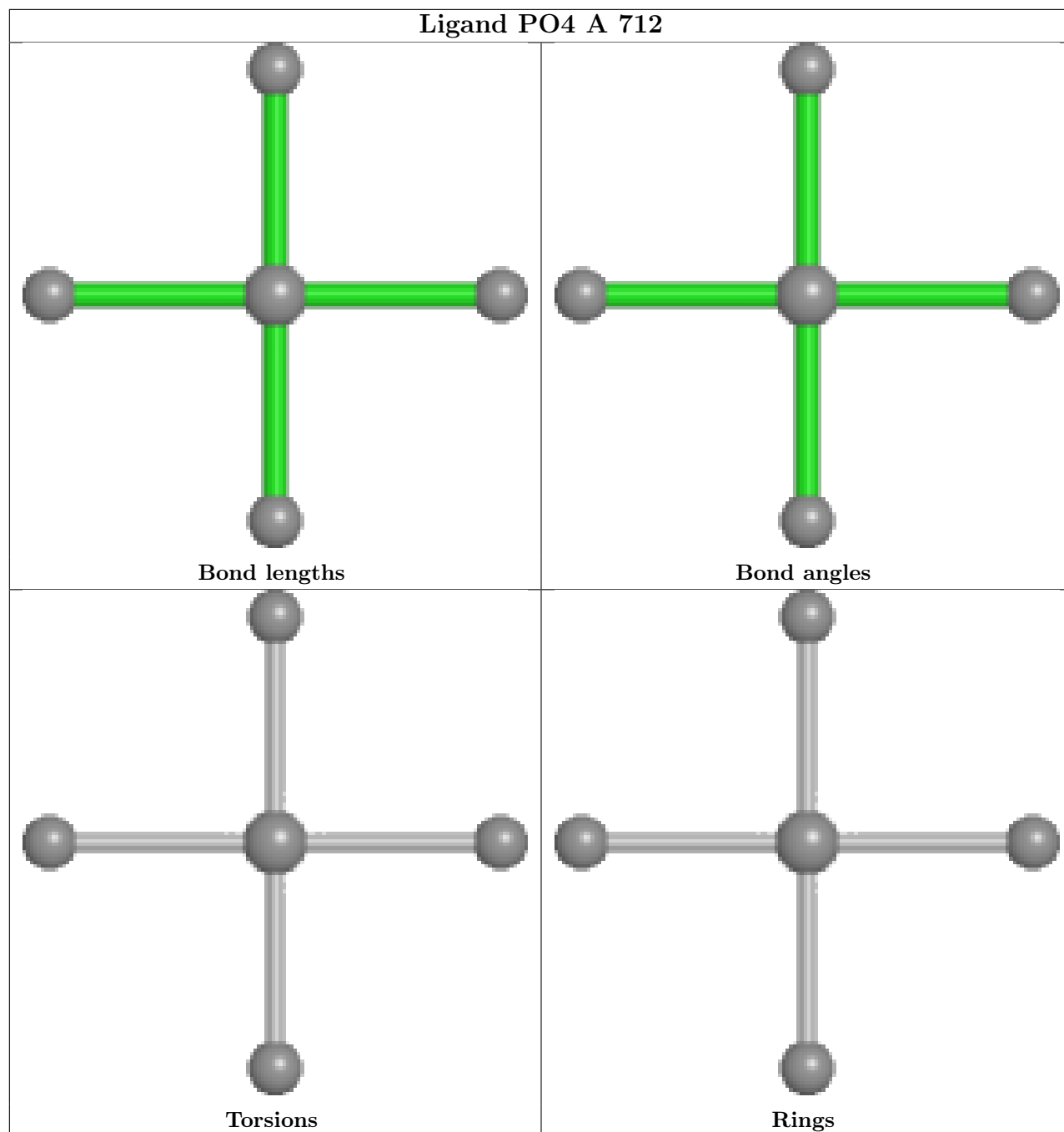
Mol	Chain	Res	Type	Atoms
2	A	702	GOL	C1-C2-C3-O3
2	B	701	GOL	O1-C1-C2-C3
2	B	704	GOL	C1-C2-C3-O3
2	A	701	GOL	O2-C2-C3-O3
2	A	702	GOL	O2-C2-C3-O3
2	A	704	GOL	O1-C1-C2-O2
2	B	706	GOL	O1-C1-C2-O2
7	A	717	PEG	O1-C1-C2-O2
2	B	701	GOL	O1-C1-C2-O2
2	A	701	GOL	O1-C1-C2-O2
7	A	717	PEG	O2-C3-C4-O4
2	A	703	GOL	C1-C2-C3-O3
2	B	704	GOL	O2-C2-C3-O3
2	A	703	GOL	O1-C1-C2-C3

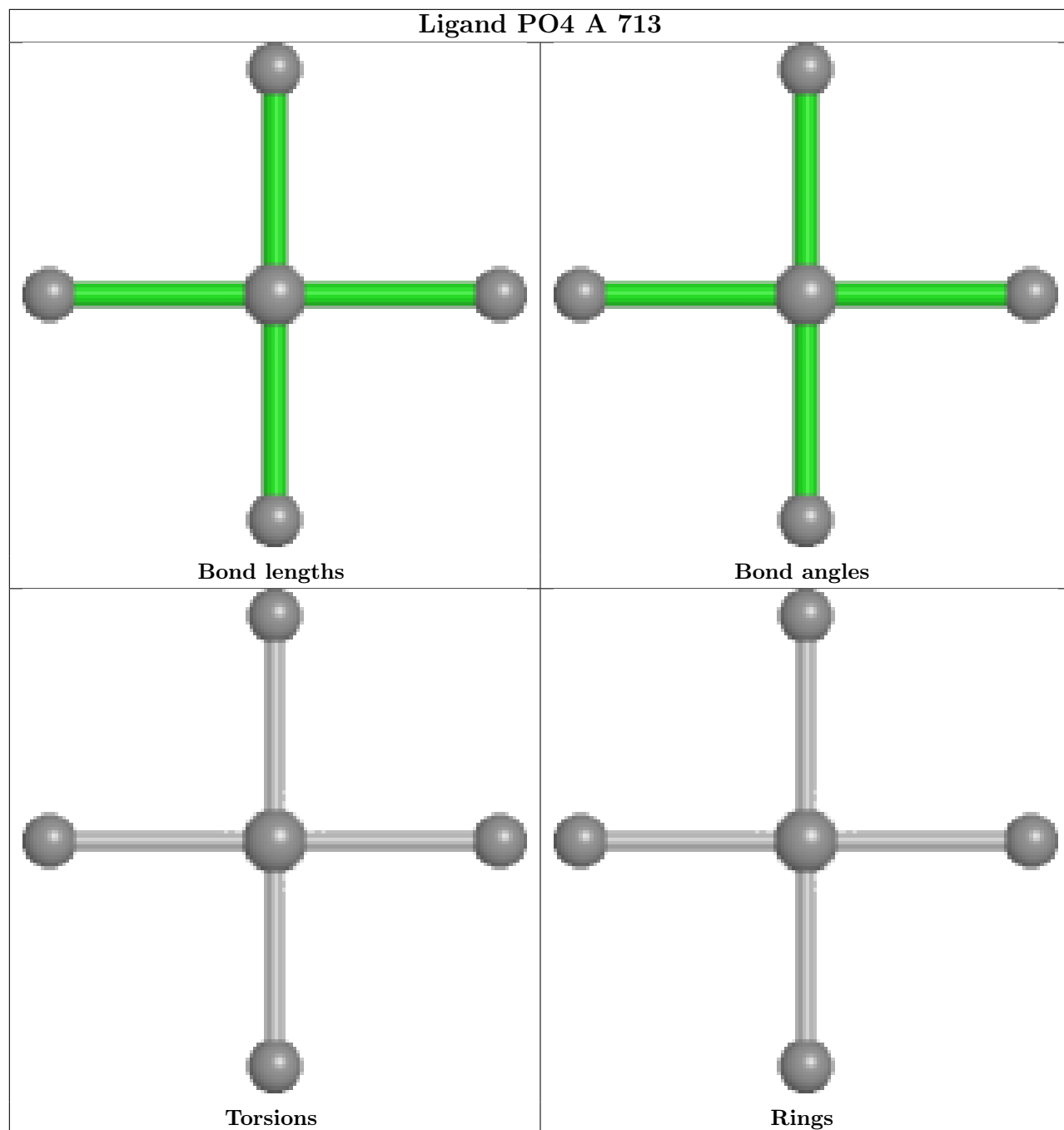
There are no ring outliers.

9 monomers are involved in 14 short contacts:

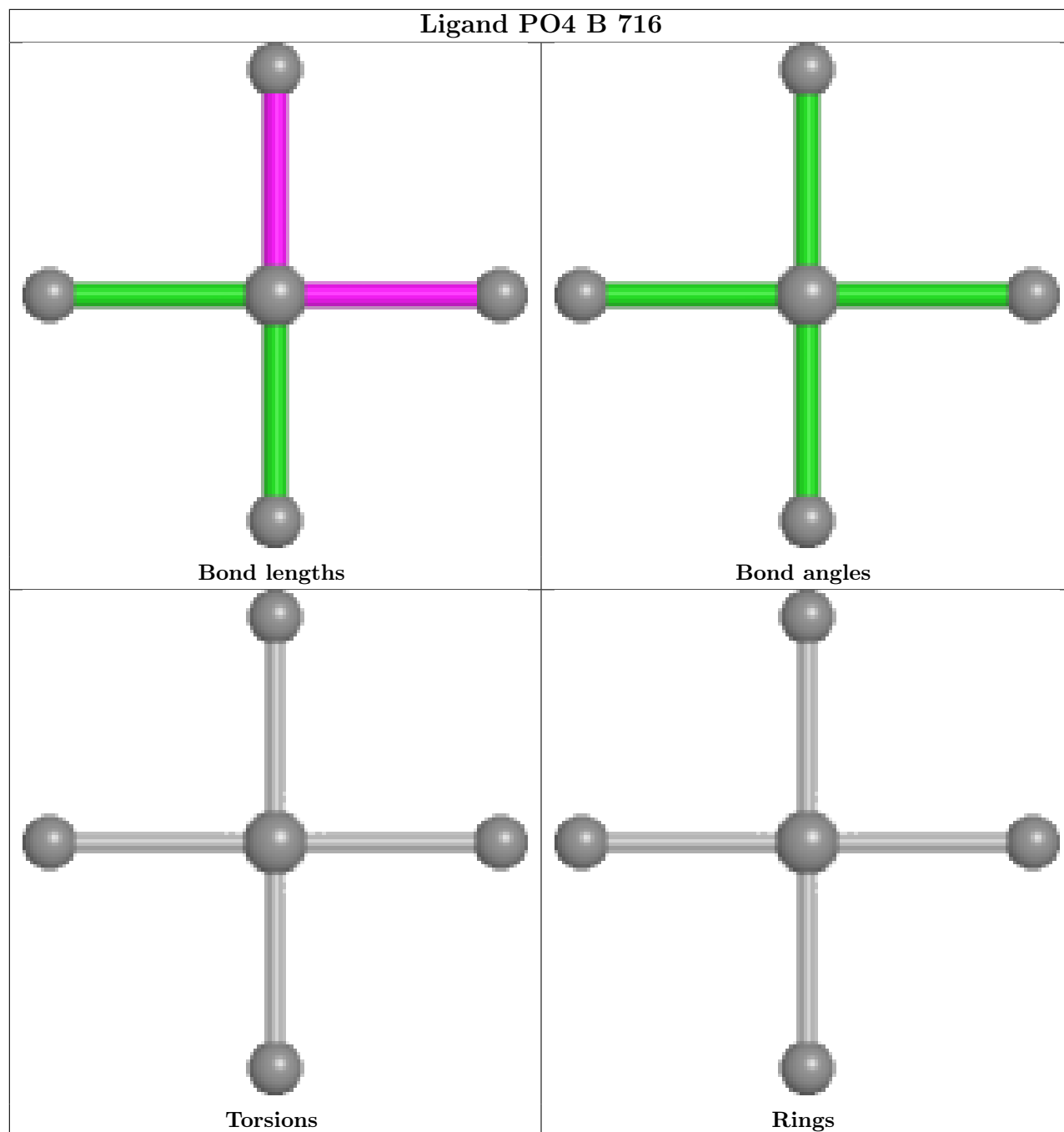
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	705	GOL	3	0
2	A	702	GOL	1	0
7	A	717	PEG	1	0
3	B	708	SO4	1	0
3	B	702	SO4	1	0
2	B	704	GOL	2	0
2	A	703	GOL	1	0
4	A	707	PO4	1	0
4	A	709	PO4	3	0

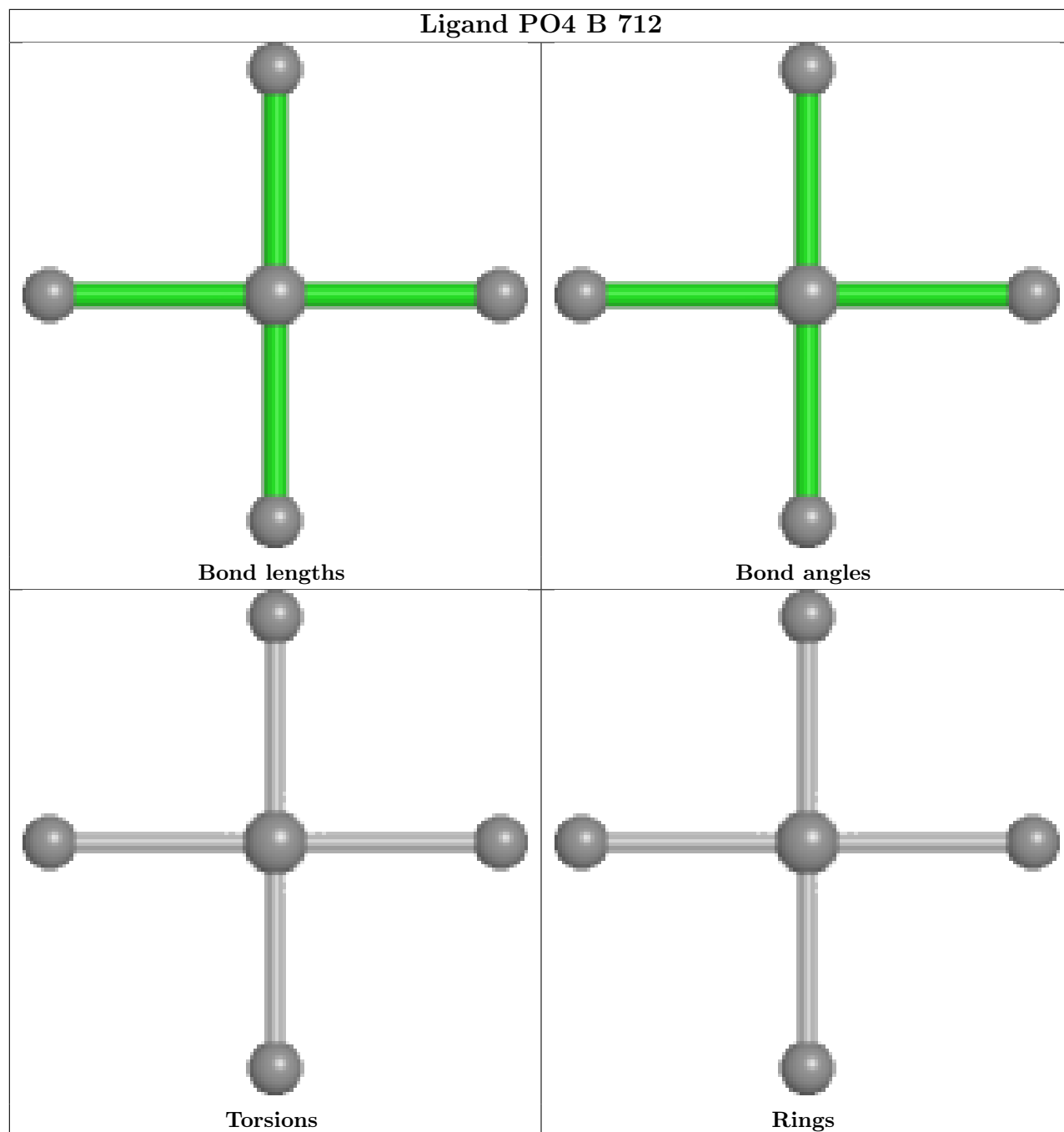
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

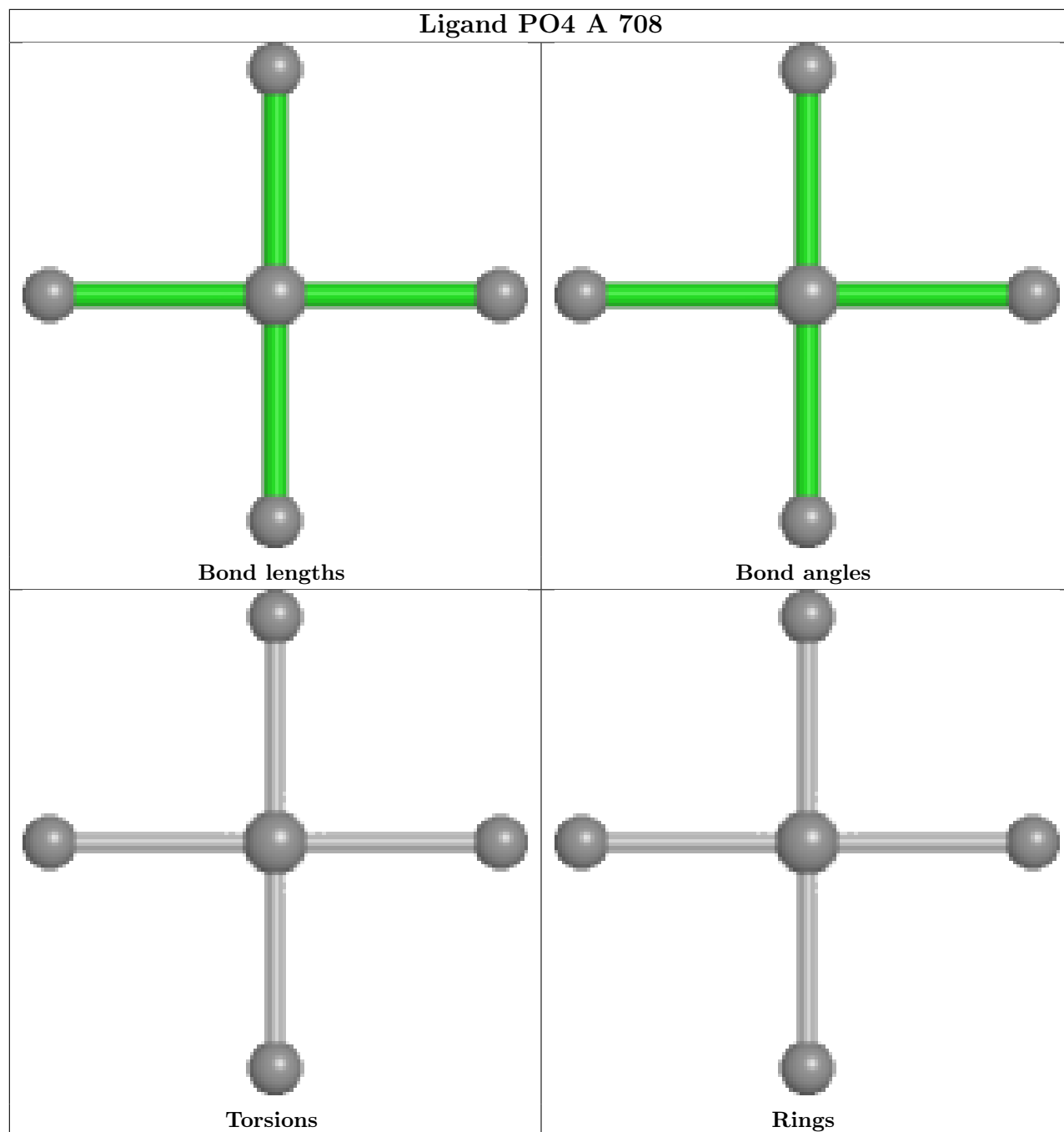


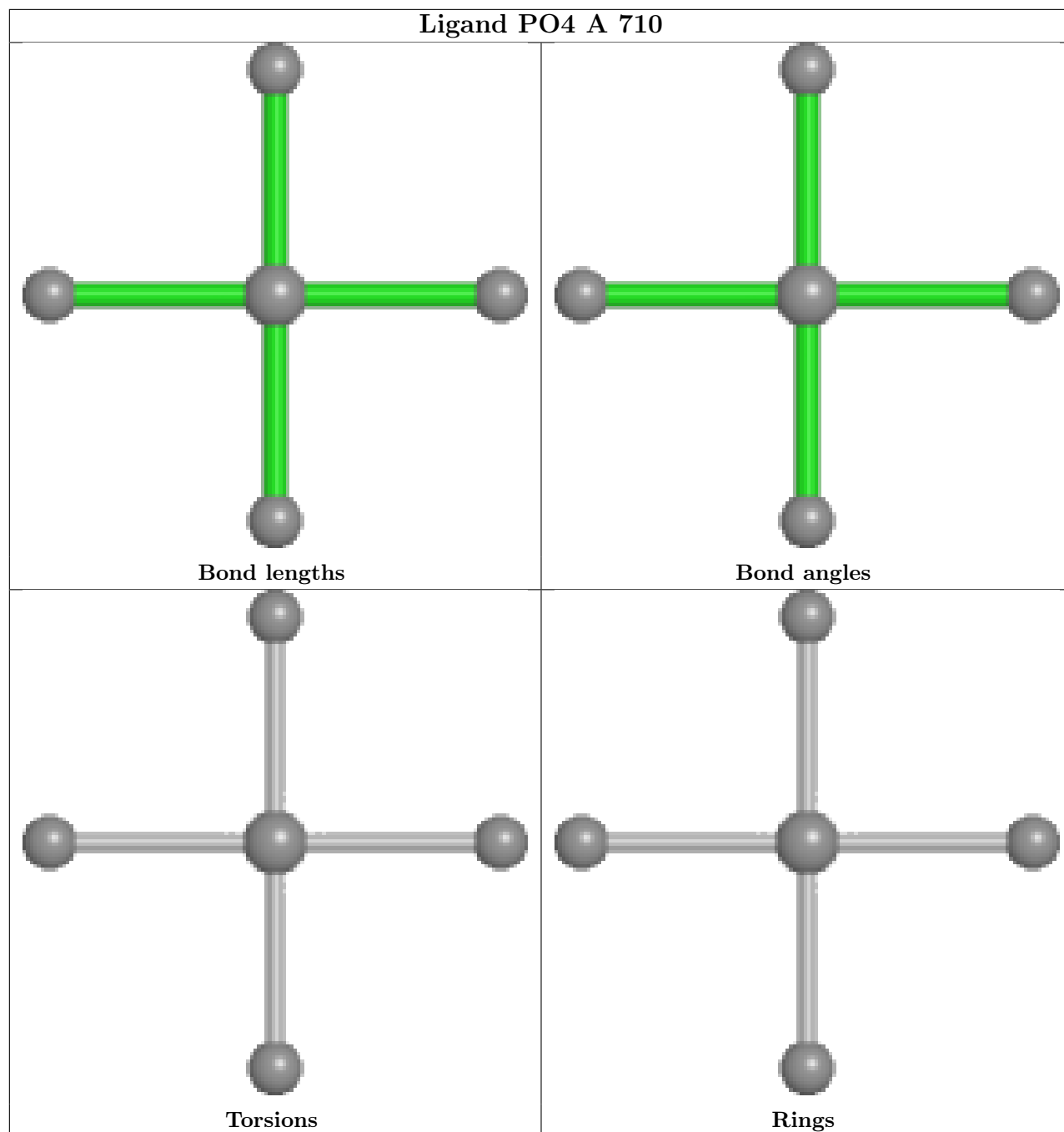


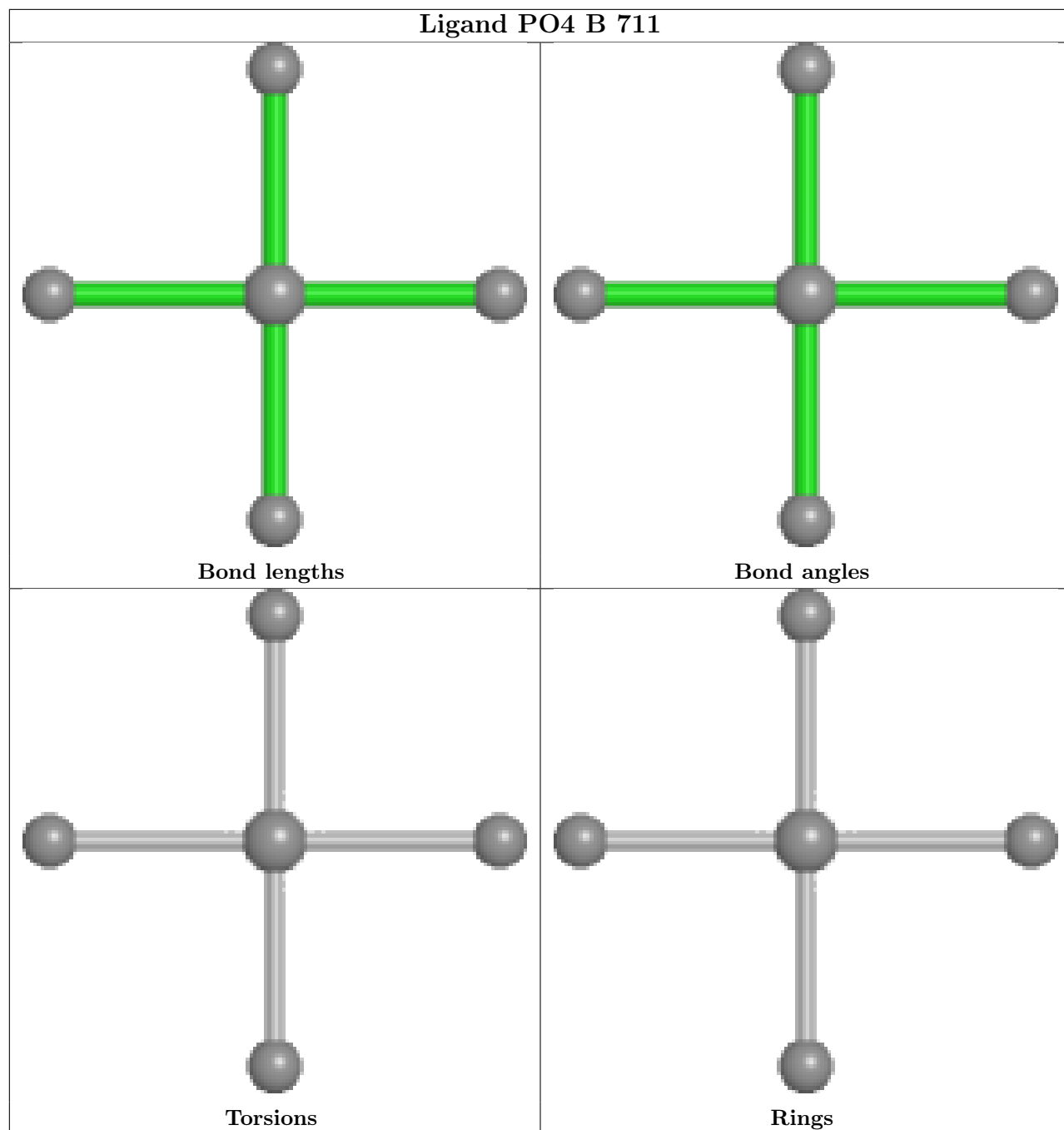


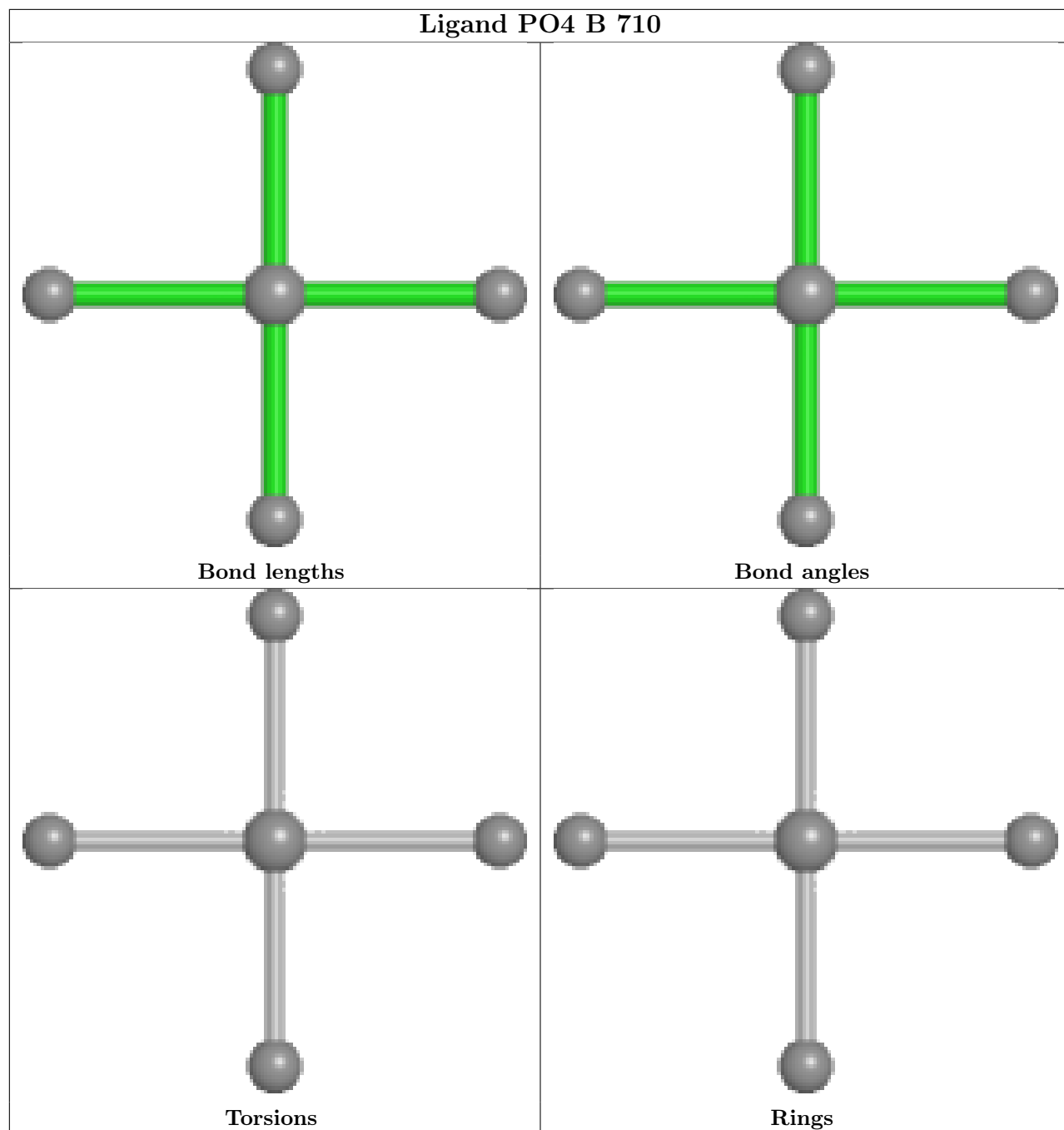


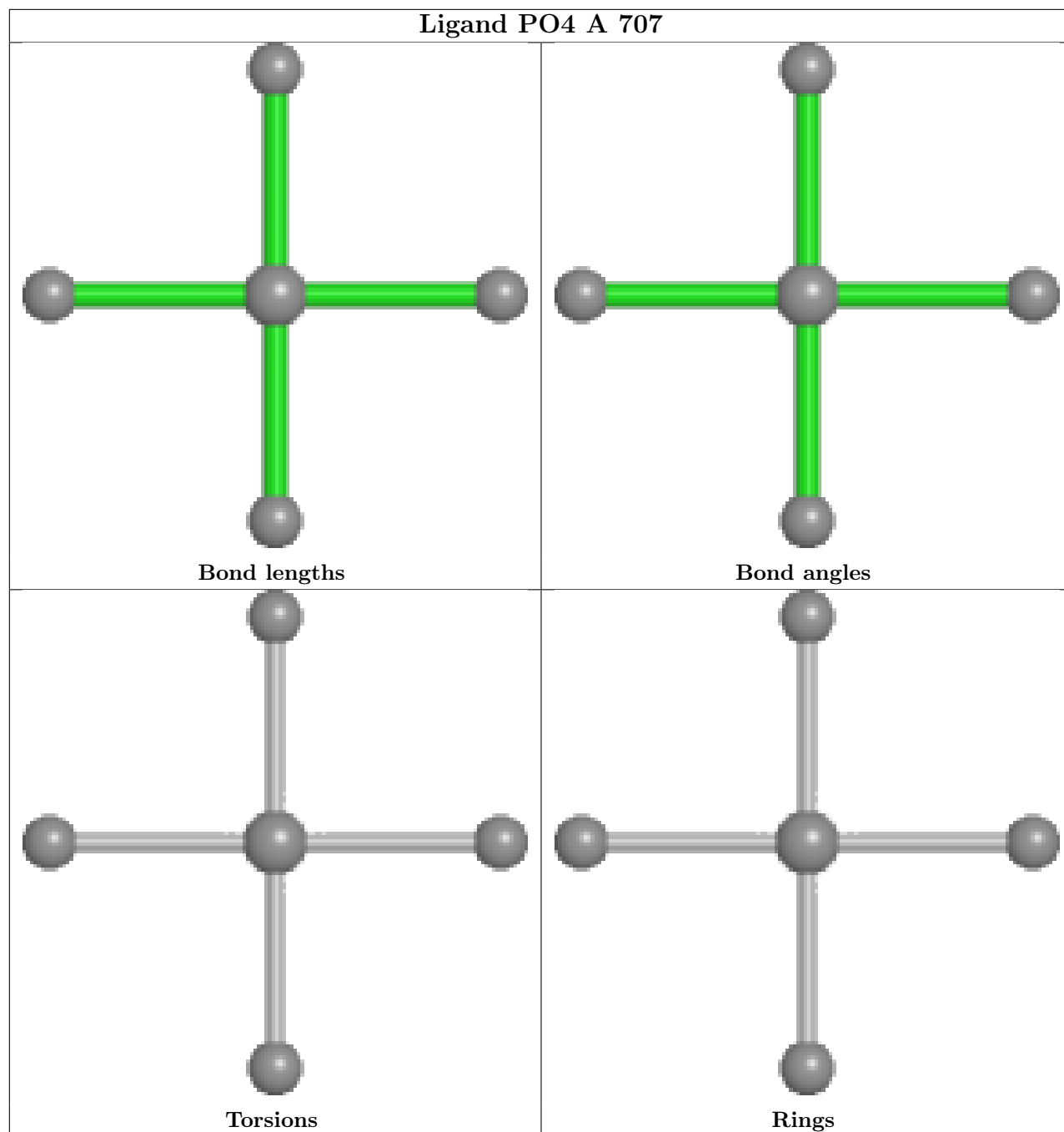


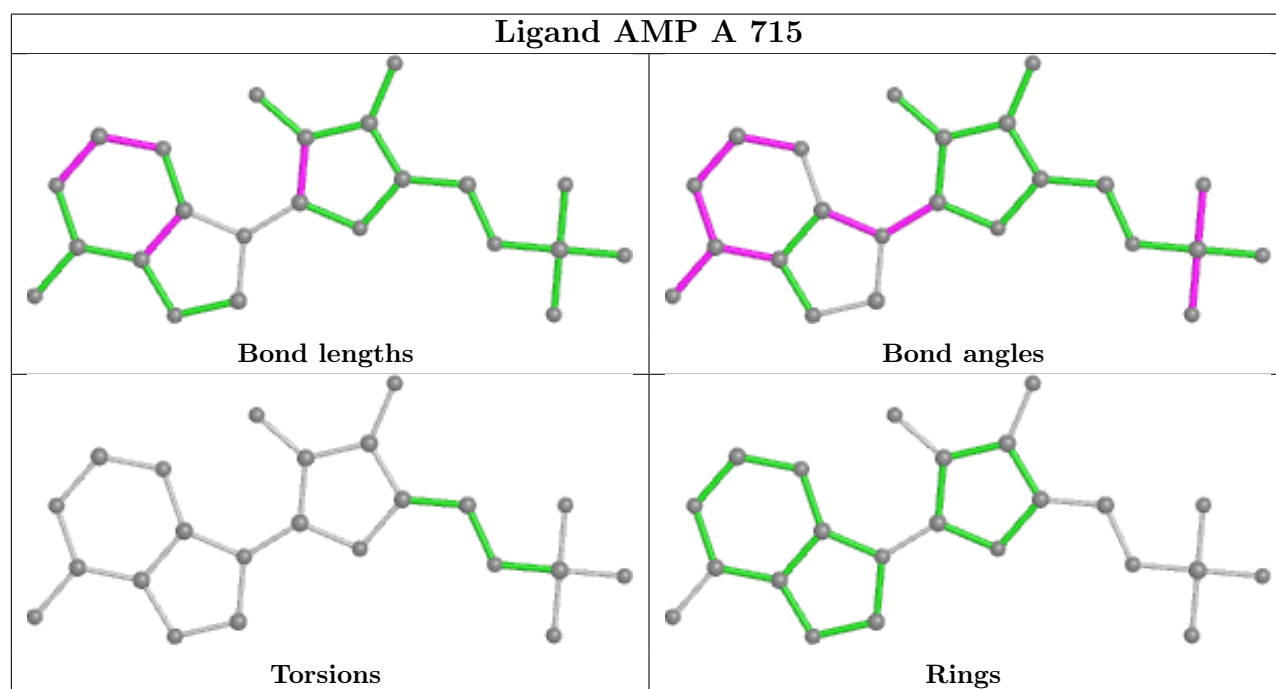
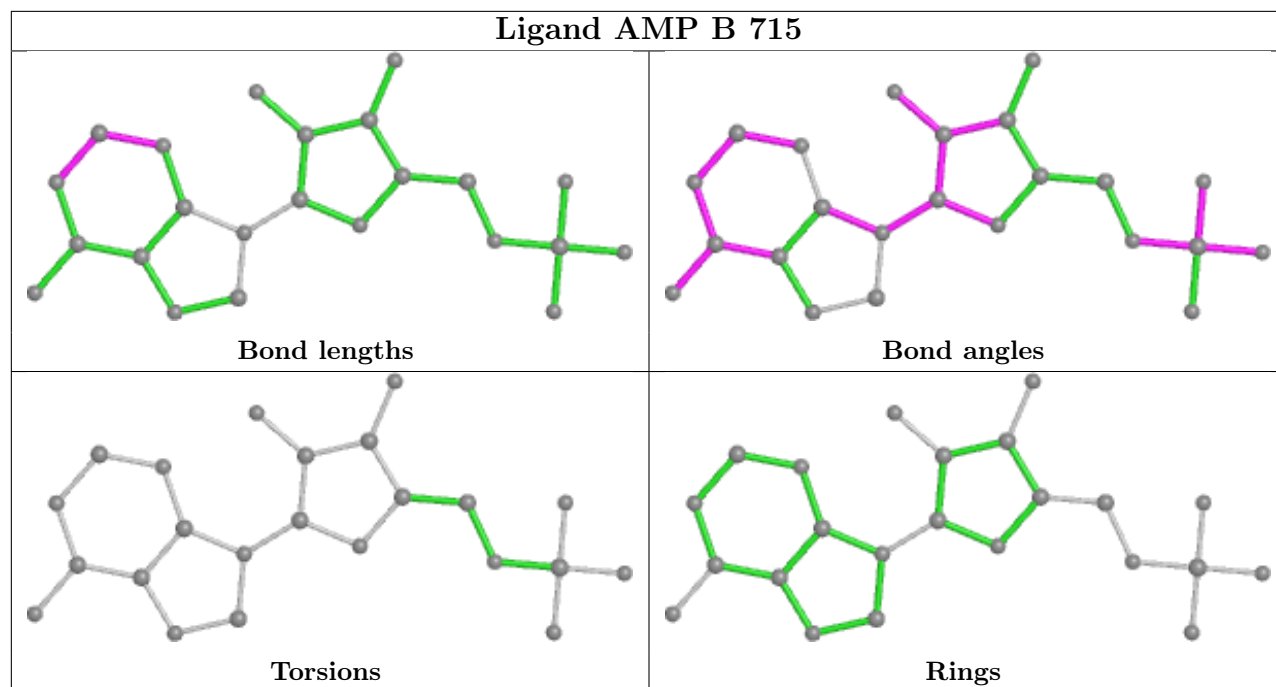




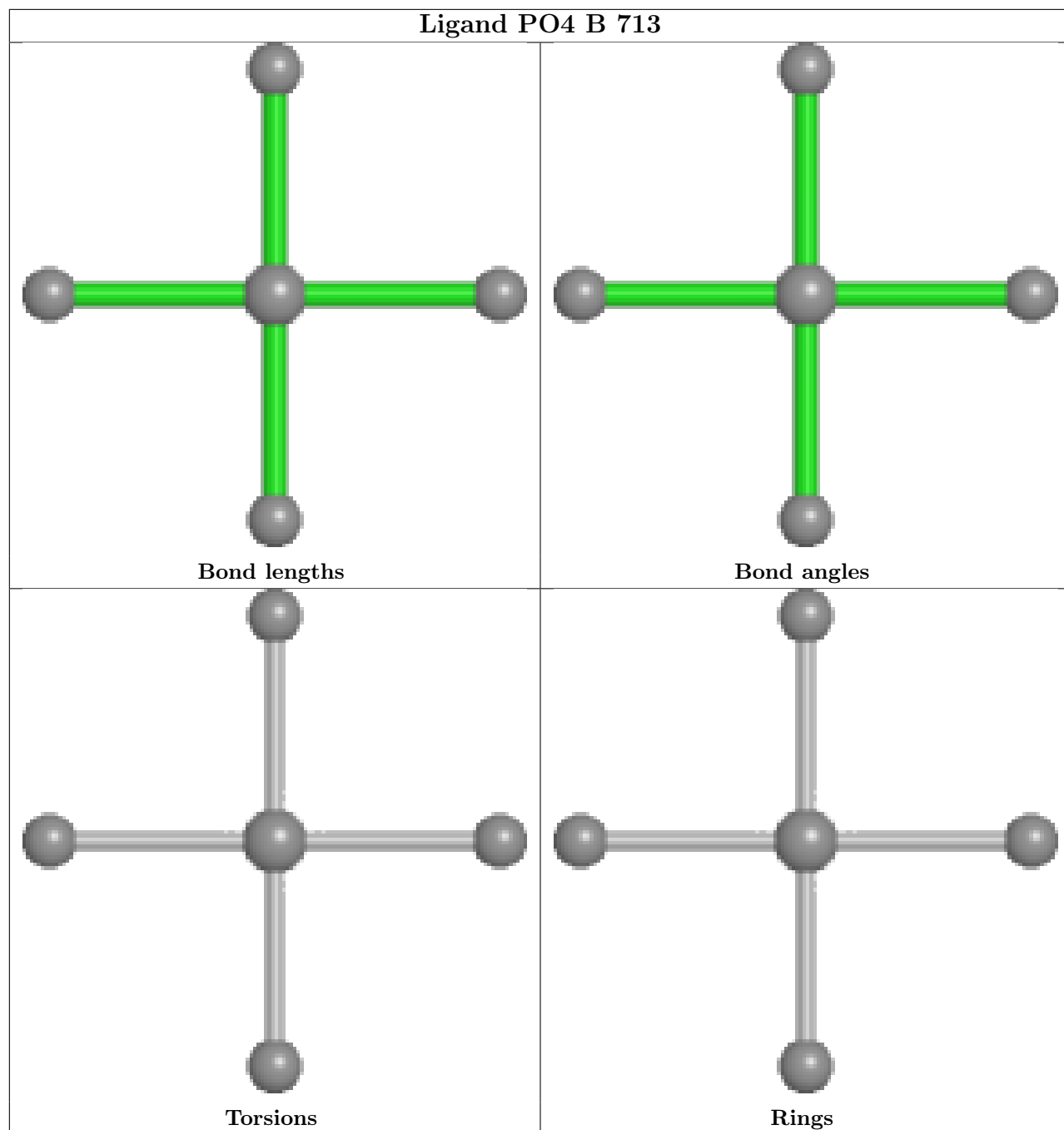


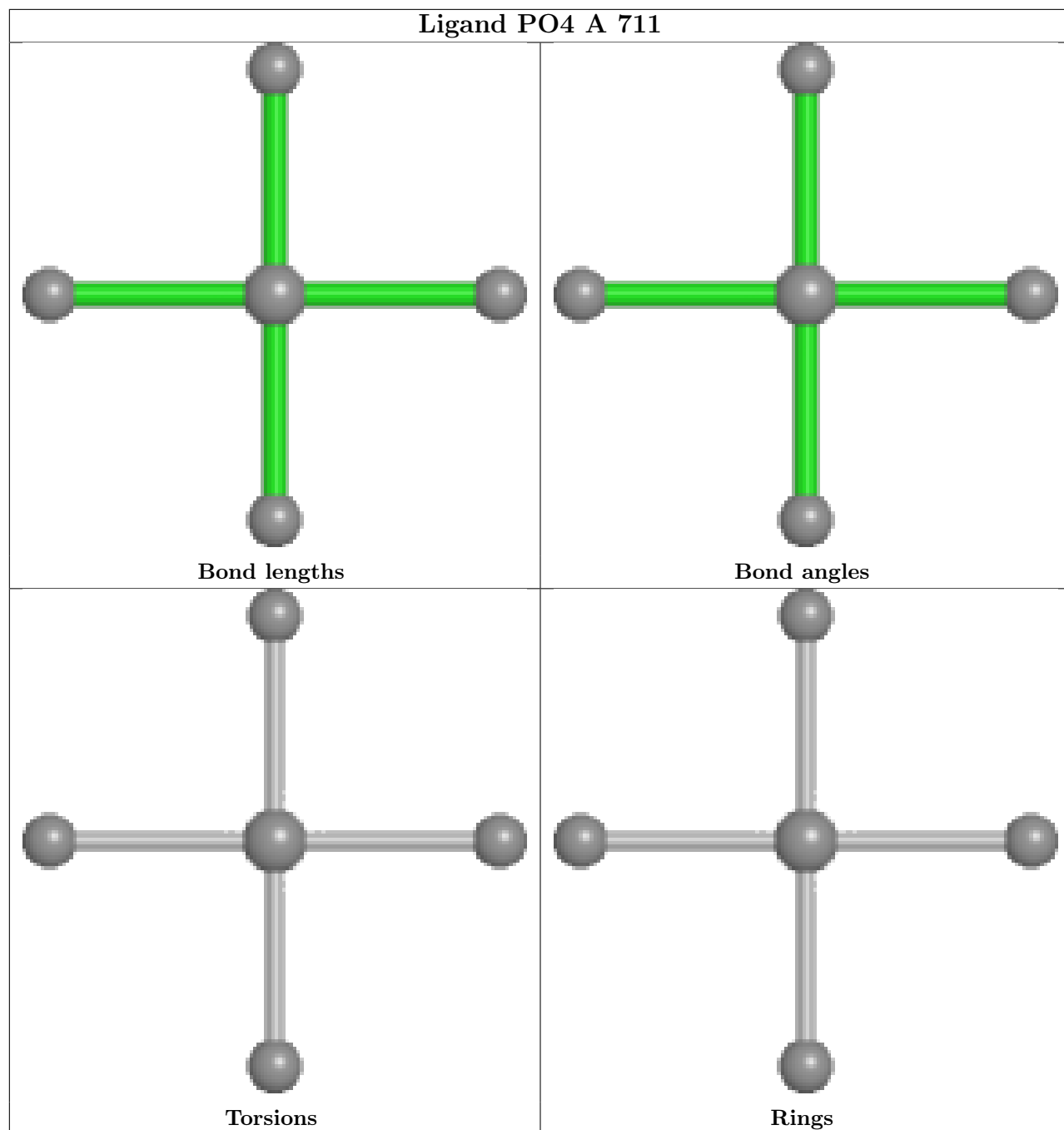


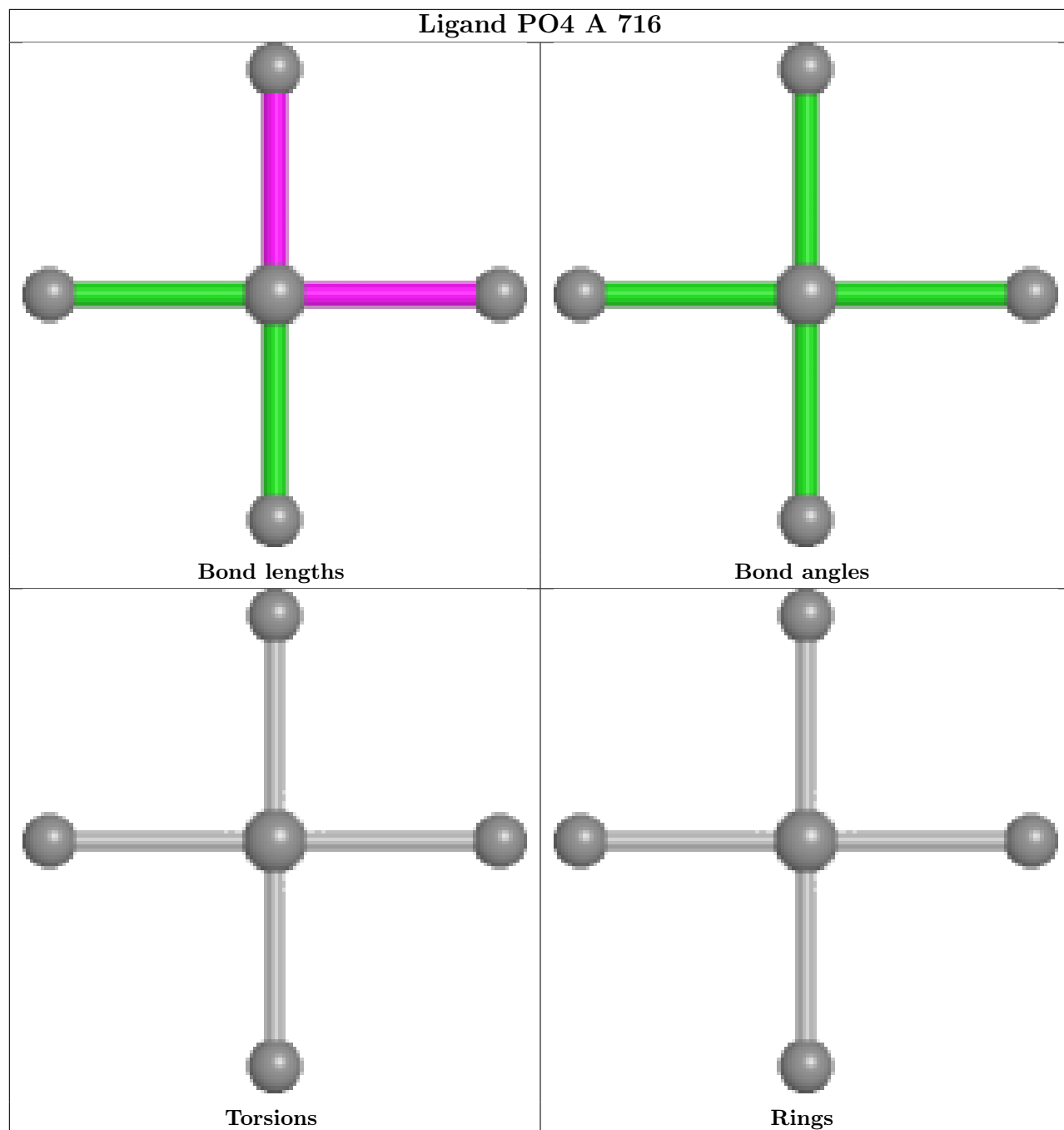


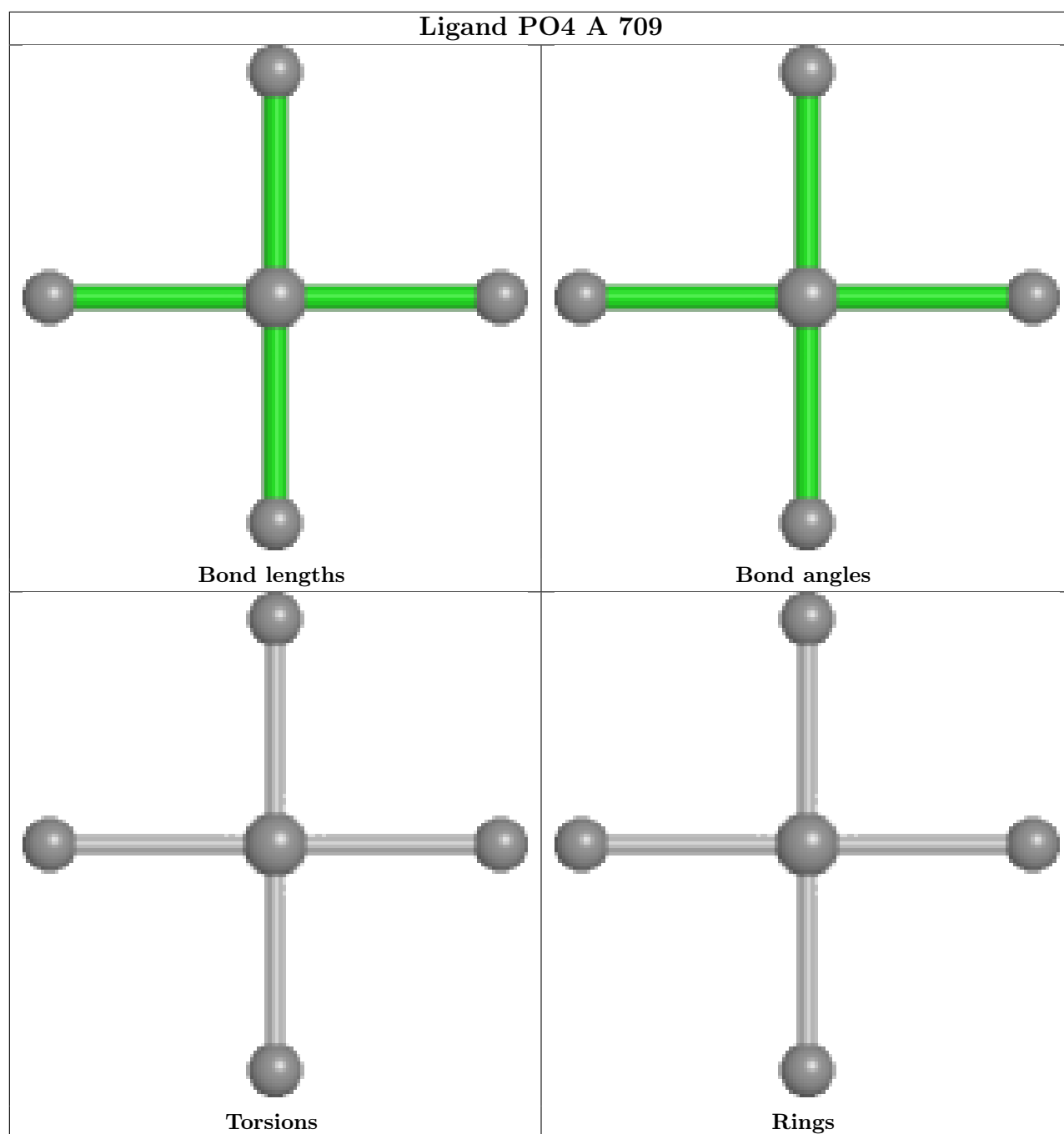


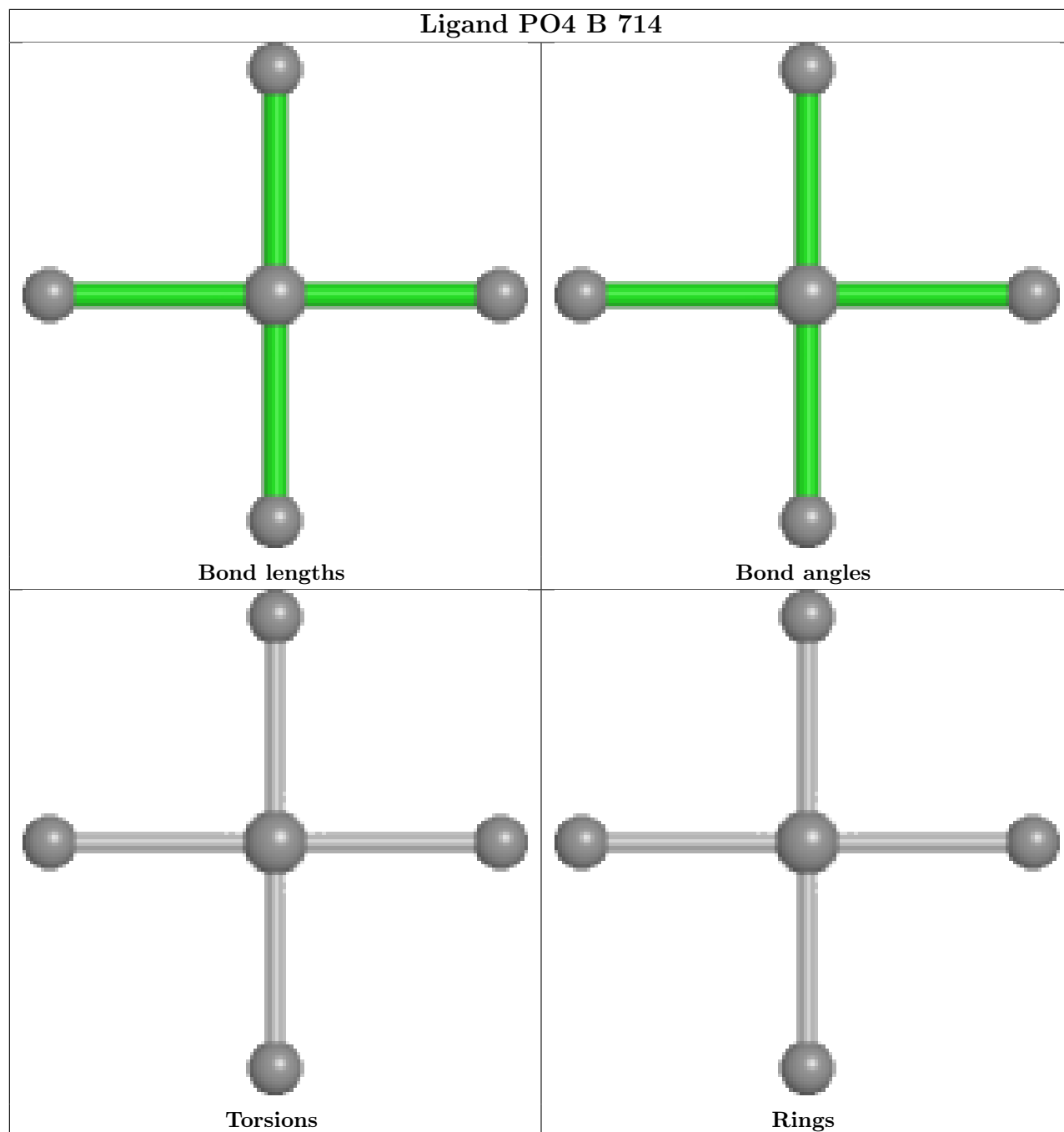












## 5.7 Other polymers [i](#)

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	606/606 (100%)	0.48	81 (13%) 3 2	8, 20, 114, 188	0
1	B	606/606 (100%)	0.43	80 (13%) 3 2	8, 21, 105, 182	0
All	All	1212/1212 (100%)	0.46	161 (13%) 3 2	8, 21, 112, 188	0

All (161) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	579	GLY	18.9
1	B	487	PRO	18.9
1	A	578	LEU	17.5
1	B	515	GLY	15.4
1	A	485	PRO	14.6
1	B	580	GLY	14.4
1	A	487	PRO	13.8
1	A	488	ARG	13.8
1	B	490	VAL	13.1
1	A	490	VAL	11.7
1	A	626	ILE	11.3
1	B	488	ARG	11.3
1	A	584	SER	10.3
1	A	575	LYS	9.8
1	A	513	GLY	9.4
1	B	579	GLY	9.4
1	B	514	THR	9.3
1	A	582	LEU	9.2
1	A	453	VAL	9.1
1	A	489	GLY	9.0
1	B	453	VAL	9.0
1	B	572	ILE	8.8
1	B	485	PRO	8.6
1	A	486	ALA	8.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	484	PRO	8.4
1	B	483	ILE	8.2
1	A	483	ILE	8.2
1	B	486	ALA	8.1
1	B	489	GLY	7.9
1	B	578	LEU	7.6
1	A	580	GLY	7.5
1	A	629	LYS	7.5
1	A	515	GLY	7.4
1	B	573	GLY	7.2
1	B	627	ILE	7.1
1	B	582	LEU	7.0
1	A	627	ILE	6.9
1	B	626	ILE	6.9
1	A	624	GLN	6.9
1	B	484	PRO	6.8
1	A	571	GLN	6.7
1	A	581	LYS	6.6
1	A	514	THR	6.6
1	A	589	THR	6.4
1	A	628	SER	6.4
1	B	482	GLY	6.4
1	B	567	SER	6.4
1	B	571	GLN	6.3
1	A	623	VAL	6.3
1	A	518	ASN	6.2
1	B	577	LYS	6.2
1	B	624	GLN	6.2
1	A	625	PRO	6.2
1	B	623	VAL	6.1
1	A	574	ASP	6.1
1	A	590	MET	5.9
1	A	573	GLY	5.9
1	A	572	ILE	5.9
1	A	622	ILE	5.9
1	B	513	GLY	5.8
1	A	482	GLY	5.7
1	A	564	TYR	5.3
1	B	568	LEU	5.3
1	A	567	SER	5.2
1	B	617	LYS	5.1
1	A	517	LYS	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	574	ASP	5.0
1	B	591	GLU	5.0
1	B	570	ASN	5.0
1	A	591	GLU	4.9
1	A	619	LEU	4.8
1	A	568	LEU	4.8
1	A	617	LYS	4.8
1	B	569	LYS	4.8
1	B	628	SER	4.7
1	A	516	ASN	4.6
1	B	629	LYS	4.6
1	B	576	GLU	4.6
1	B	566	TYR	4.5
1	B	564	TYR	4.4
1	A	588	GLU	4.4
1	A	621	GLU	4.3
1	B	575	LYS	4.3
1	B	622	ILE	4.3
1	B	625	PRO	4.3
1	B	584	SER	4.3
1	A	577	LYS	4.2
1	B	621	GLU	4.2
1	B	516	ASN	4.1
1	A	569	LYS	4.0
1	A	614	ALA	3.9
1	A	613	LYS	3.9
1	B	610	GLU	3.8
1	A	452	SER	3.8
1	A	412	GLY	3.8
1	B	565	ALA	3.8
1	B	614	ALA	3.8
1	B	583	SER	3.7
1	B	481	THR	3.6
1	B	581	LYS	3.5
1	A	491	PRO	3.5
1	B	560	GLU	3.5
1	A	481	THR	3.5
1	A	576	GLU	3.5
1	B	620	GLU	3.5
1	A	566	TYR	3.5
1	B	518	ASN	3.4
1	B	613	LYS	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	527	ASN	3.3
1	A	620	GLU	3.2
1	B	452	SER	3.2
1	B	519	LYS	3.2
1	A	557	THR	3.1
1	A	570	ASN	3.1
1	A	586	ASP	3.1
1	A	512	LYS	2.9
1	B	590	MET	2.9
1	B	585	GLU	2.9
1	A	527	ASN	2.9
1	A	595	GLU	2.9
1	B	408	ASP	2.8
1	A	583	SER	2.8
1	A	455	GLY	2.8
1	B	557	THR	2.7
1	A	609	ILE	2.7
1	A	511	ASP	2.6
1	A	520	ILE	2.6
1	A	214	ARG	2.6
1	B	517	LYS	2.6
1	B	455	GLY	2.5
1	B	520	ILE	2.5
1	A	592	LYS	2.5
1	A	408	ASP	2.5
1	A	454	GLY	2.5
1	A	610	GLU	2.4
1	B	594	VAL	2.4
1	B	588	GLU	2.4
1	A	47	ASN	2.4
1	A	560	GLU	2.4
1	B	511	ASP	2.4
1	B	556	ASP	2.4
1	B	609	ILE	2.3
1	A	585	GLU	2.3
1	B	593	ALA	2.3
1	B	214	ARG	2.3
1	B	586	ASP	2.2
1	A	410	ASP	2.2
1	B	563	SER	2.2
1	B	618	GLU	2.2
1	B	616	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	562	GLU	2.2
1	A	432[A]	VAL	2.1
1	B	612	PHE	2.1
1	B	454	GLY	2.1
1	B	411	THR	2.1
1	B	561	LEU	2.1
1	A	593	ALA	2.1
1	B	480	LEU	2.1
1	A	456	THR	2.1
1	A	596	GLU	2.0
1	B	512	LYS	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no 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(Å <sup>2</sup> )	Q<0.9
4	PO4	A	712	5/5	0.65	0.27	57,67,76,79	0
2	GOL	A	701	6/6	0.71	0.22	57,60,63,69	0
2	GOL	A	703	6/6	0.72	0.21	53,54,57,58	0
2	GOL	A	702	6/6	0.73	0.20	38,40,45,47	0
2	GOL	A	704	6/6	0.75	0.21	48,52,53,55	0
2	GOL	B	706	6/6	0.79	0.24	50,56,66,73	0
7	PEG	A	717	7/7	0.82	0.15	43,49,52,53	0
4	PO4	B	713	5/5	0.86	0.26	75,75,84,84	0
2	GOL	B	701	6/6	0.87	0.18	30,40,43,45	0
2	GOL	B	704	6/6	0.89	0.14	34,34,39,44	0
2	GOL	B	705	6/6	0.90	0.16	28,32,33,42	0
3	SO4	B	707	5/5	0.91	0.16	66,70,77,81	0

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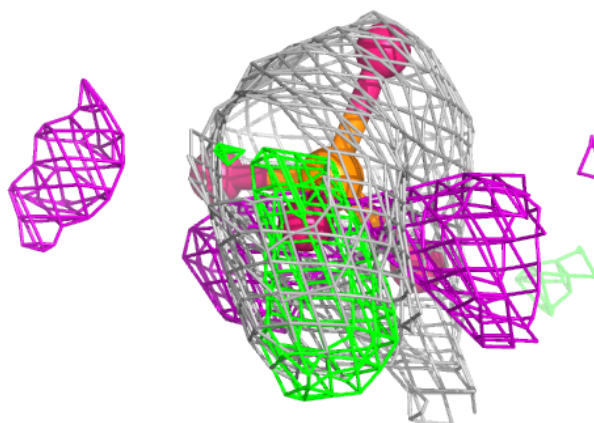
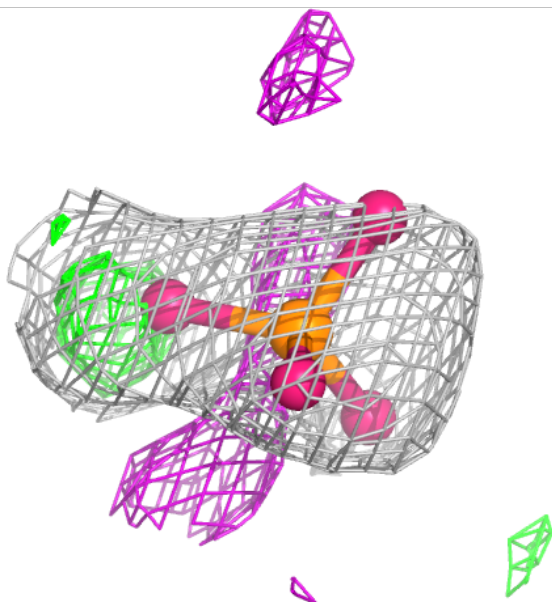
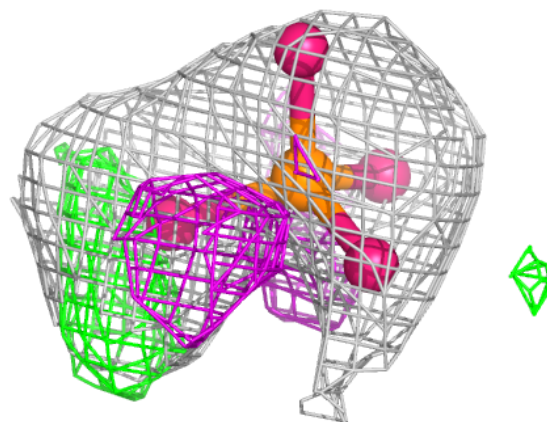
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	PO4	B	714	5/5	0.91	0.17	75,77,81,81	0
4	PO4	B	710	5/5	0.91	0.10	42,44,51,59	0
4	PO4	B	712	5/5	0.92	0.14	50,54,60,63	0
4	PO4	A	707	5/5	0.92	0.10	41,45,48,59	0
3	SO4	A	705	5/5	0.93	0.23	47,51,57,64	0
3	SO4	A	706	5/5	0.93	0.18	62,62,68,75	0
4	PO4	A	713	5/5	0.94	0.15	42,42,46,53	0
4	PO4	A	708	5/5	0.95	0.09	41,41,46,49	0
4	PO4	A	709	5/5	0.95	0.15	54,55,58,60	0
3	SO4	B	709	5/5	0.95	0.18	35,46,50,56	0
4	PO4	A	710	5/5	0.96	0.15	52,56,59,66	0
4	PO4	A	711	5/5	0.97	0.13	33,37,40,41	0
4	PO4	B	711	5/5	0.97	0.13	41,43,51,54	0
6	AMP	B	715	23/23	0.98	0.10	11,12,14,16	0
3	SO4	B	708	5/5	0.98	0.06	40,43,47,47	0
4	PO4	B	716	5/5	0.99	0.10	13,13,16,17	0
5	MG	A	714	1/1	0.99	0.06	23,23,23,23	0
5	MG	B	703	1/1	0.99	0.05	22,22,22,22	0
6	AMP	A	715	23/23	0.99	0.09	11,13,13,14	0
4	PO4	A	716	5/5	0.99	0.11	13,15,17,19	0
3	SO4	B	702	5/5	0.99	0.08	36,37,38,39	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.

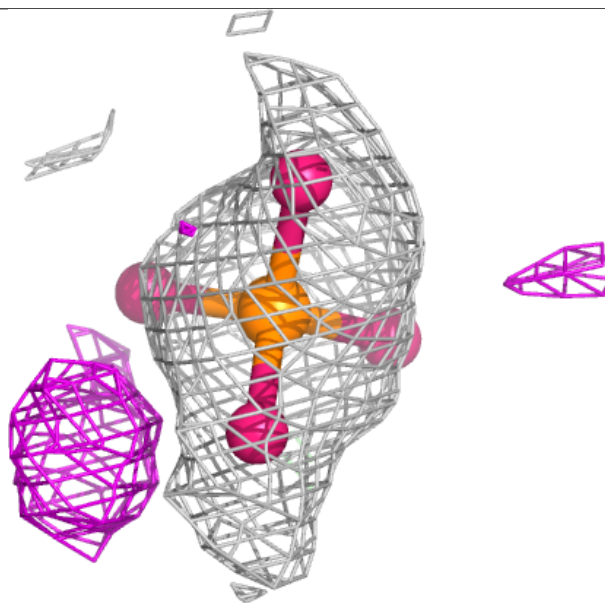
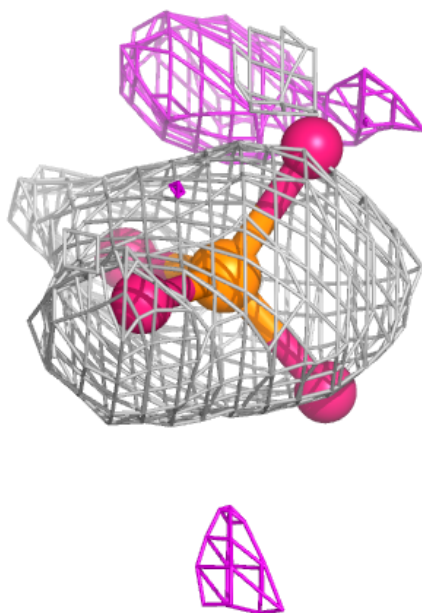
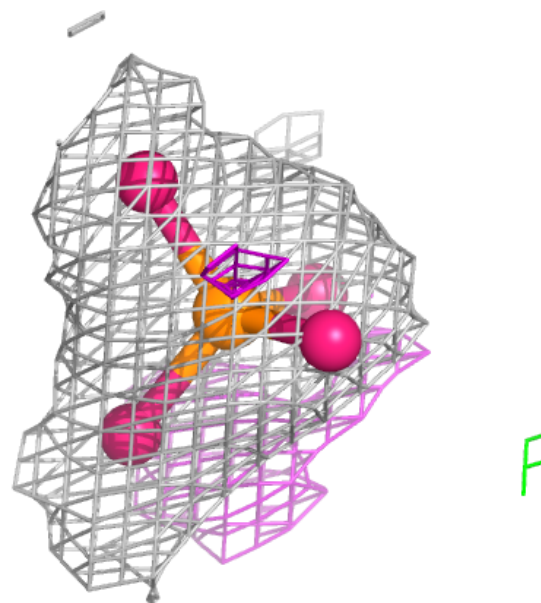
**Electron density around PO4 A 712:**

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



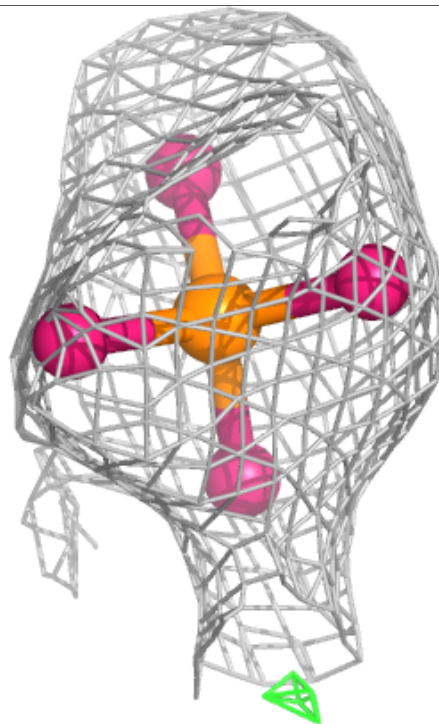
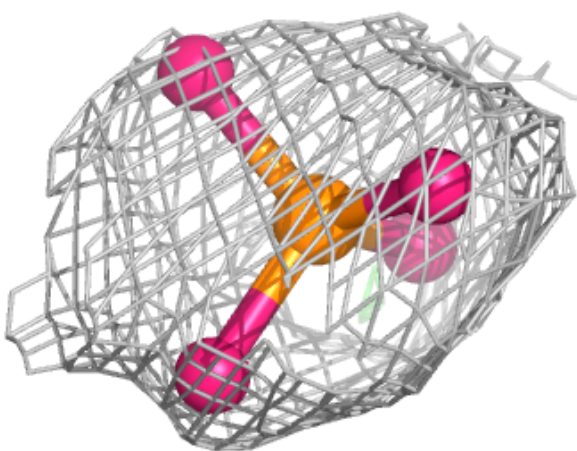
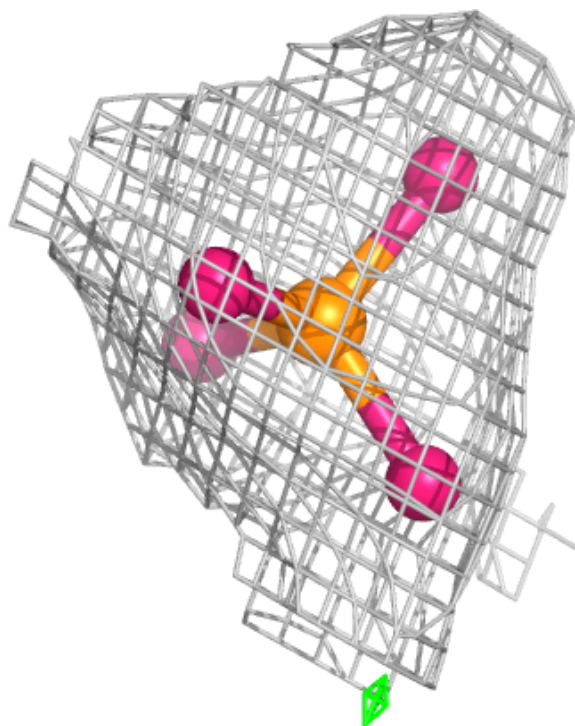
**Electron density around PO4 B 713:**

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



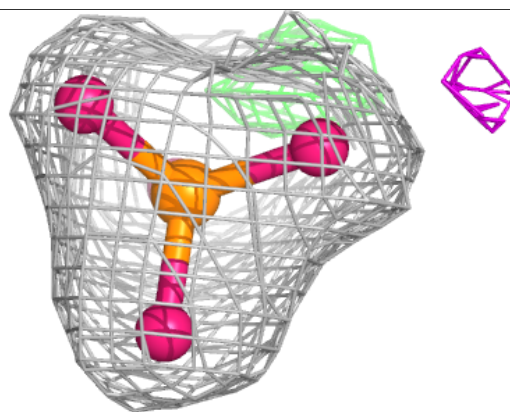
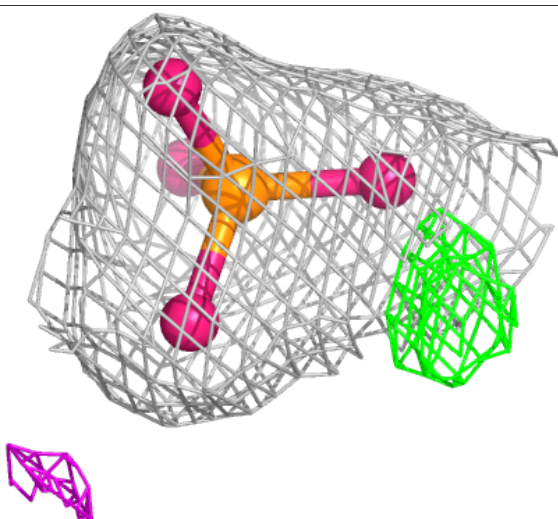
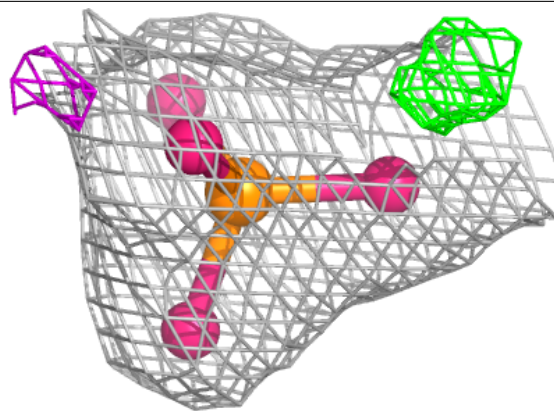
**Electron density around PO4 B 714:**

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



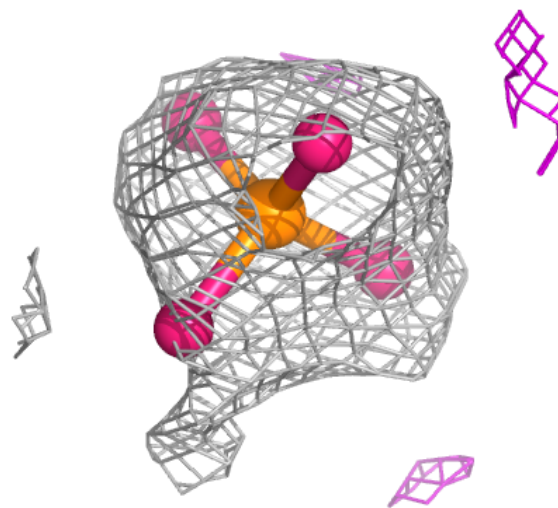
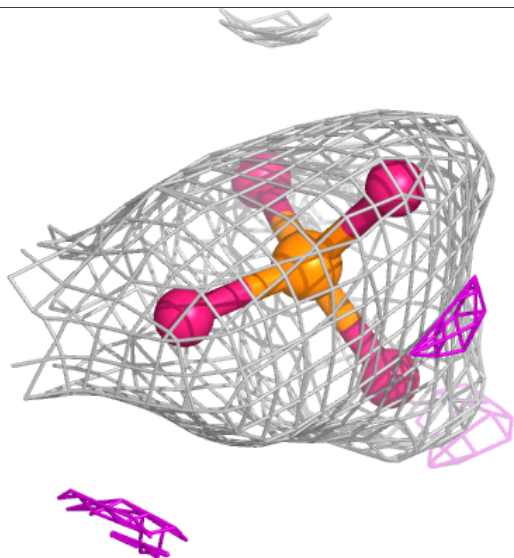
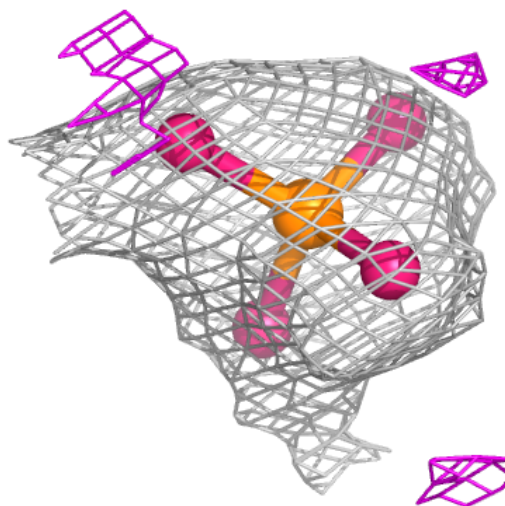
**Electron density around PO4 B 710:**

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



**Electron density around PO4 B 712:**

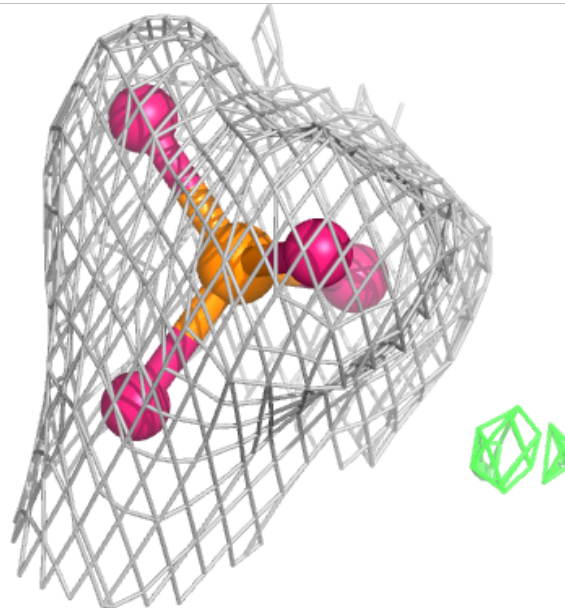
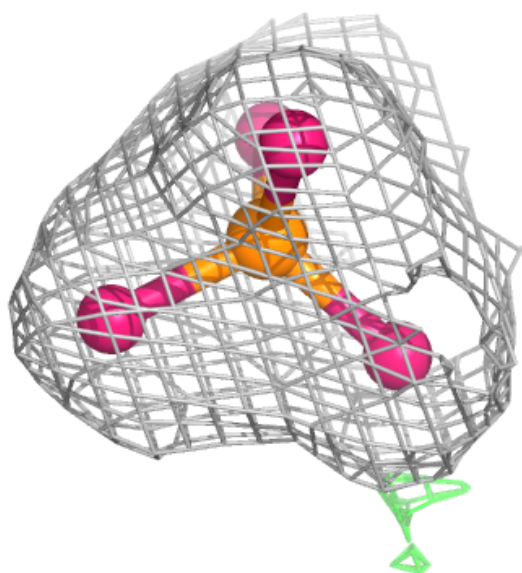
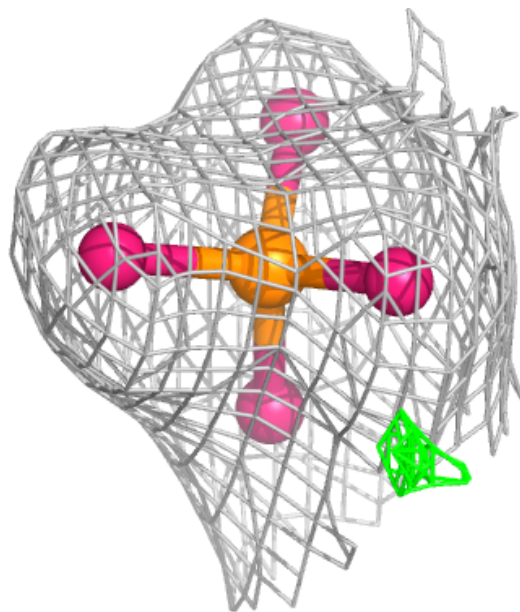
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





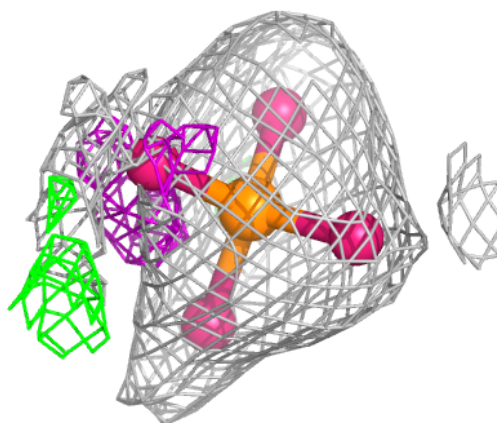
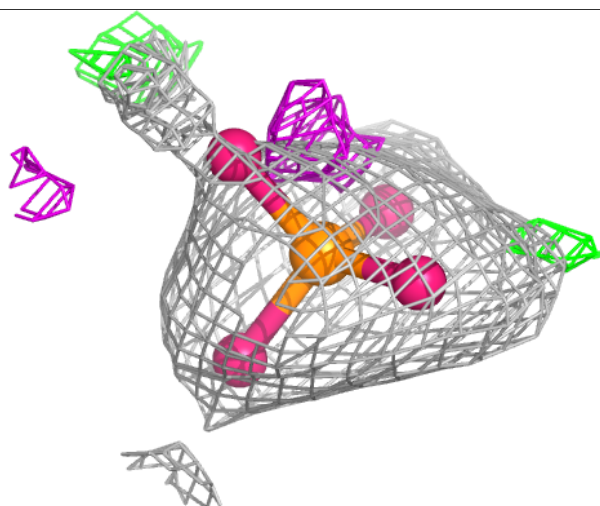
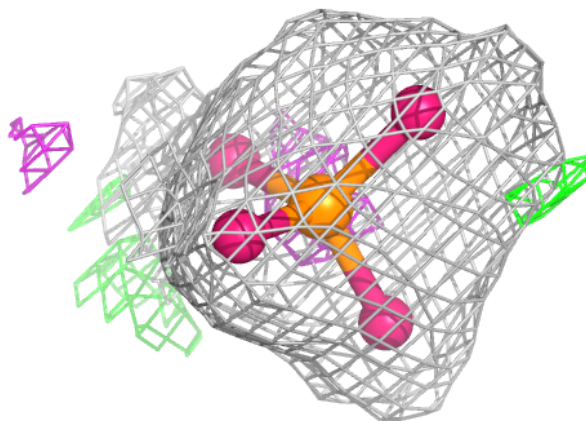
**Electron density around PO4 A 707:**

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



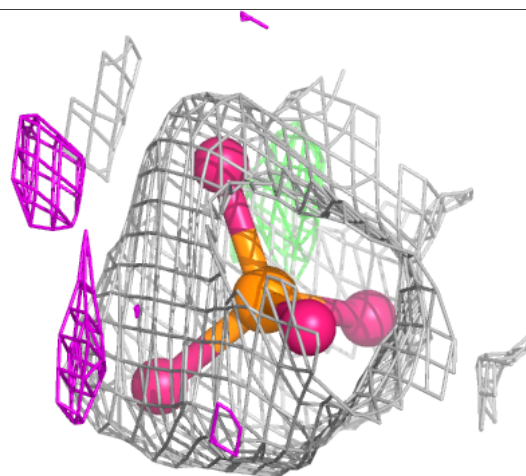
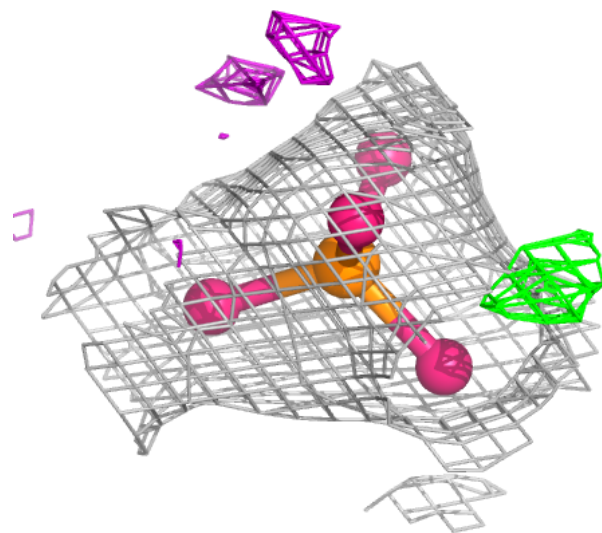
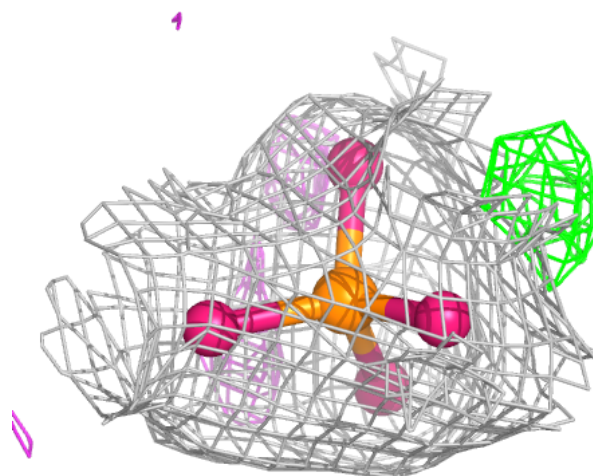
**Electron density around PO4 A 713:**

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



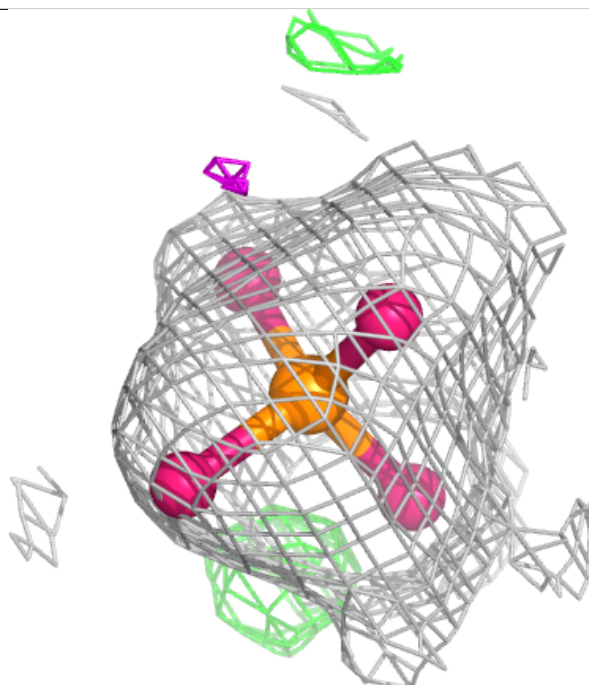
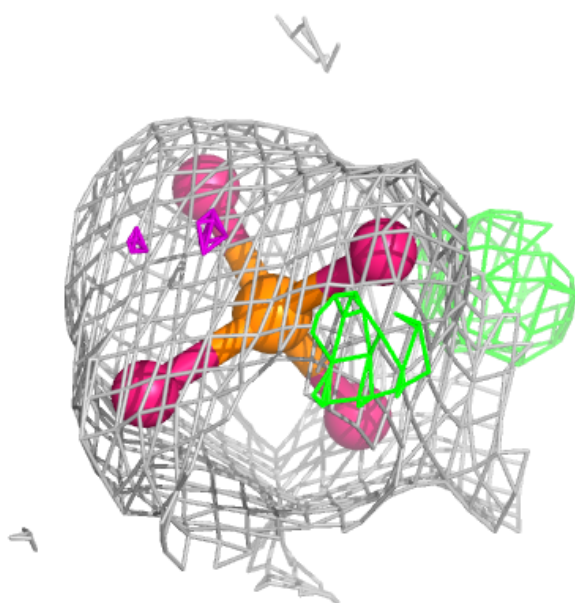
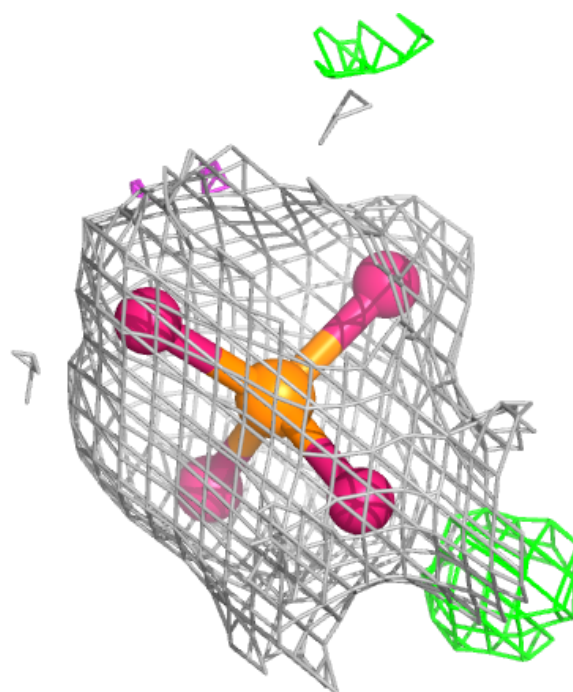
**Electron density around PO4 A 708:**

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



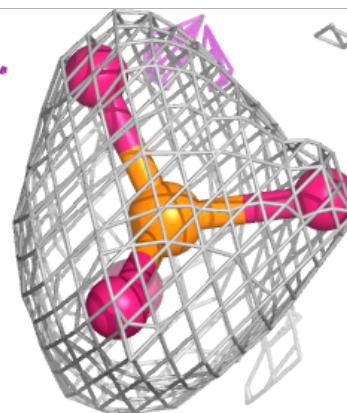
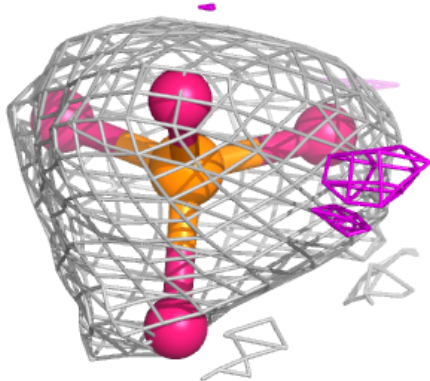
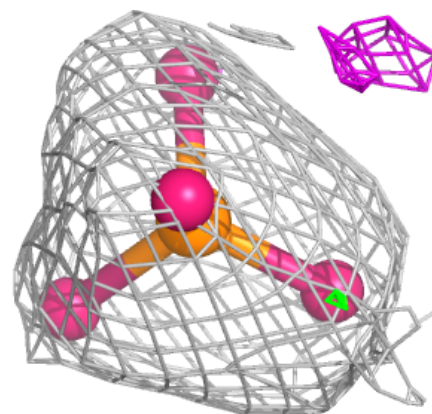
**Electron density around PO4 A 709:**

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



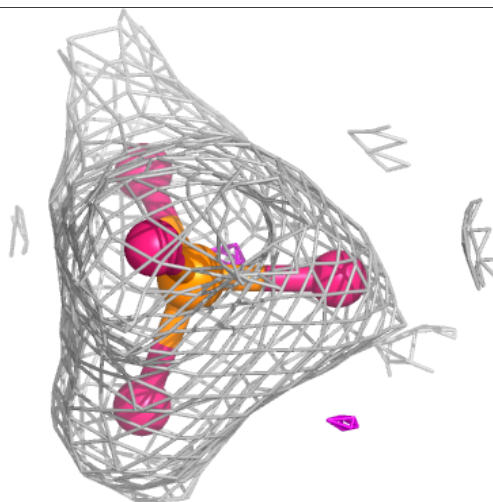
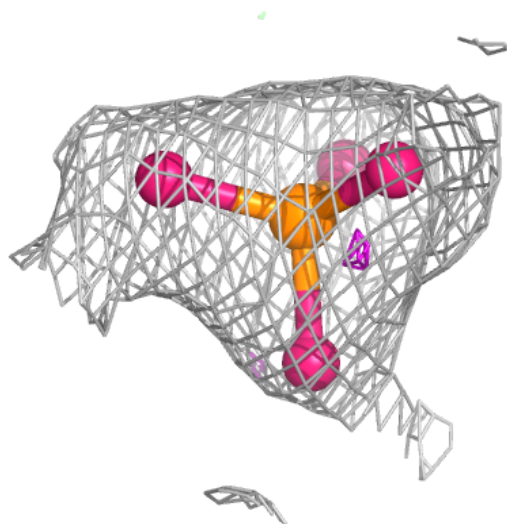
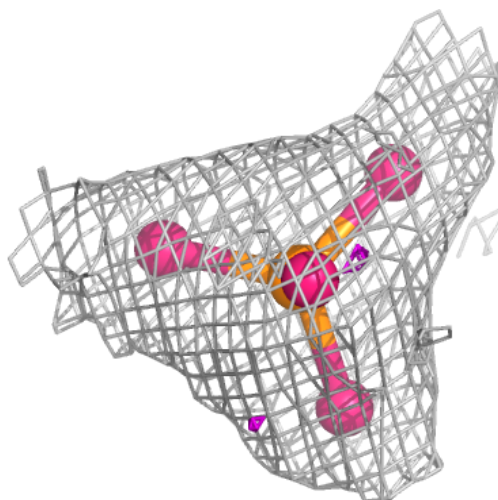
**Electron density around PO4 A 710:**

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



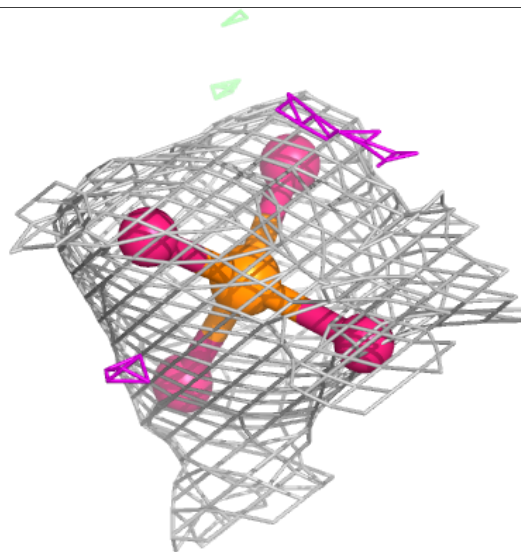
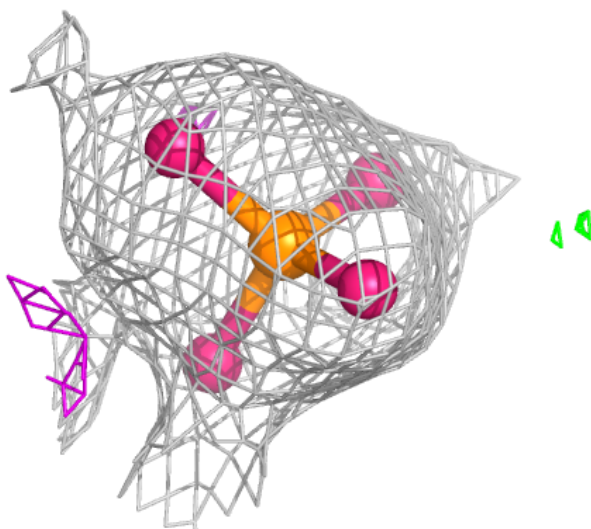
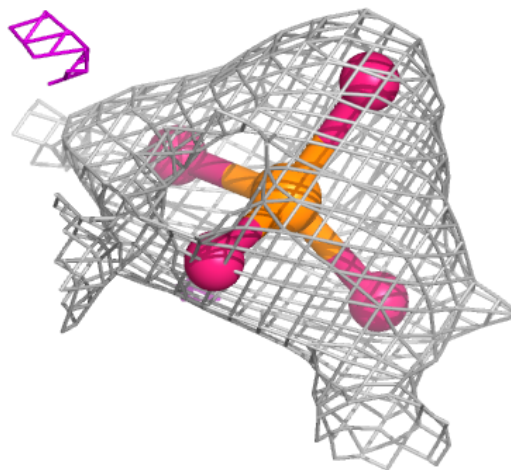
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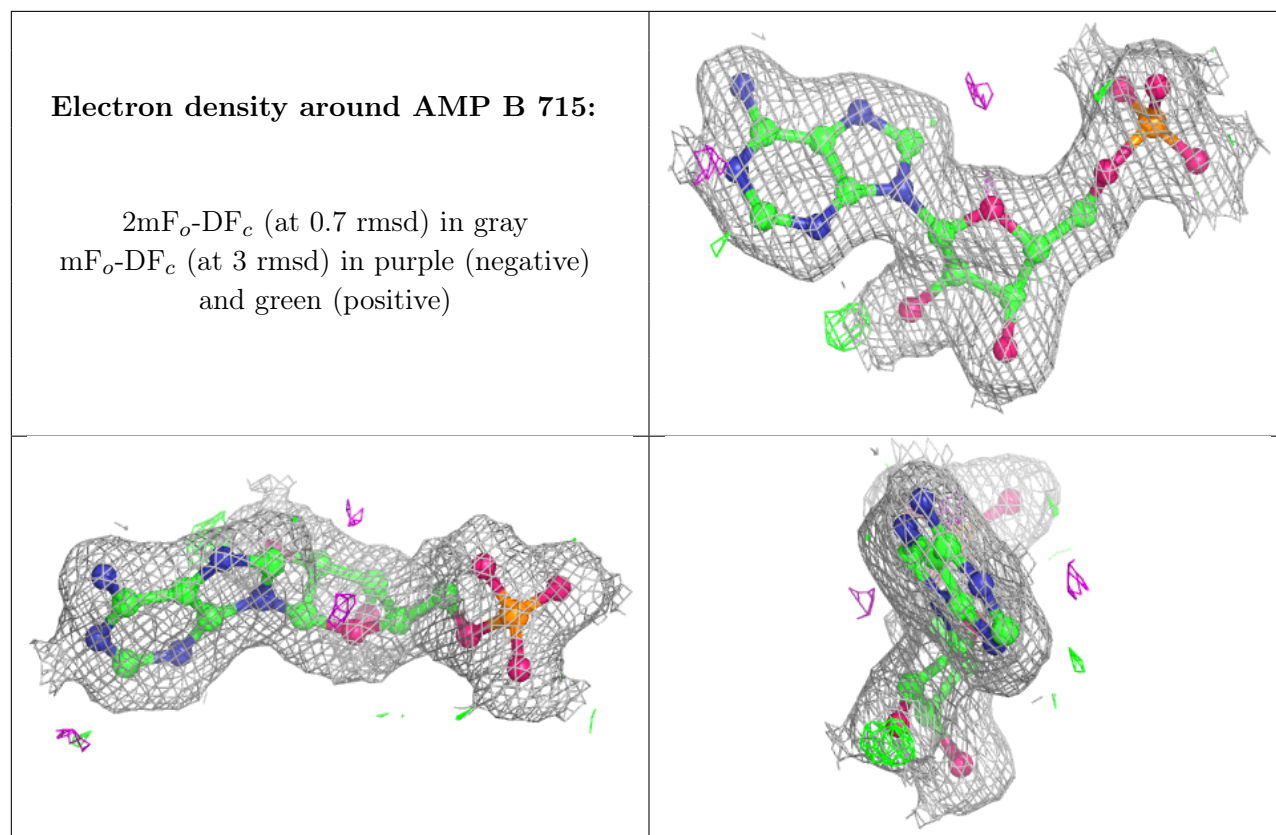
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around PO4 B 711:**

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

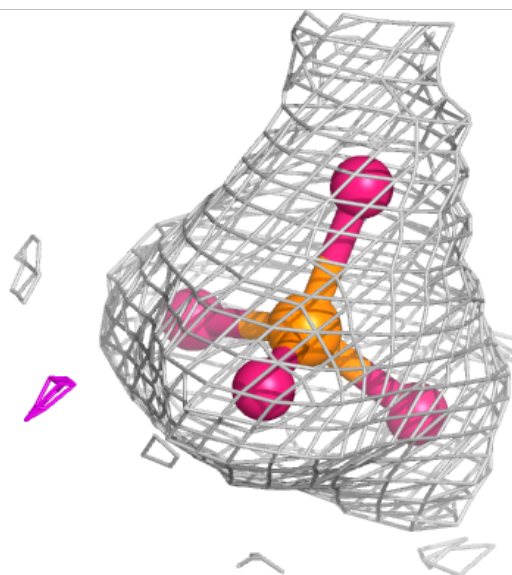
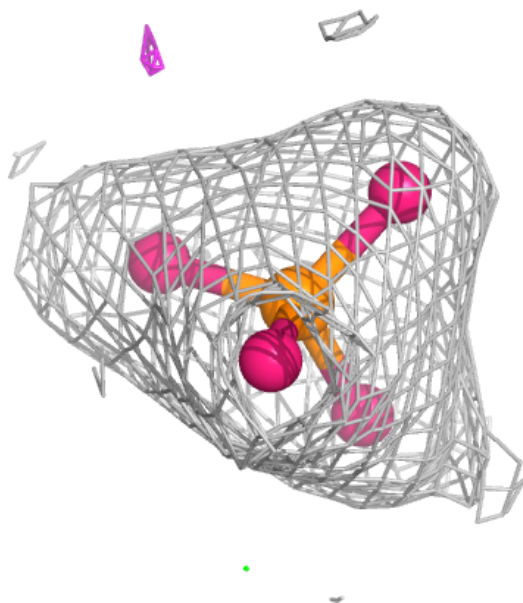
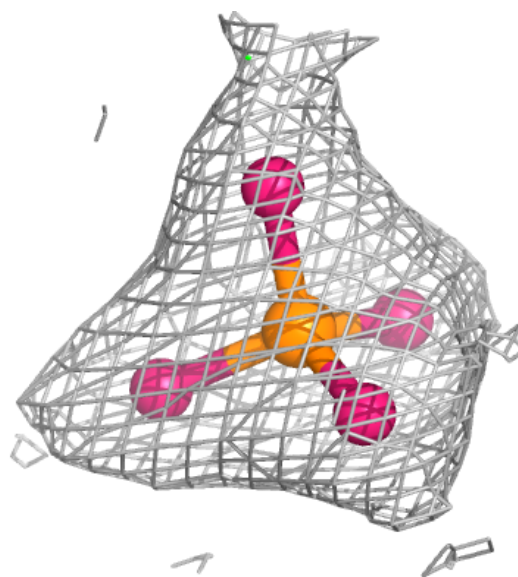






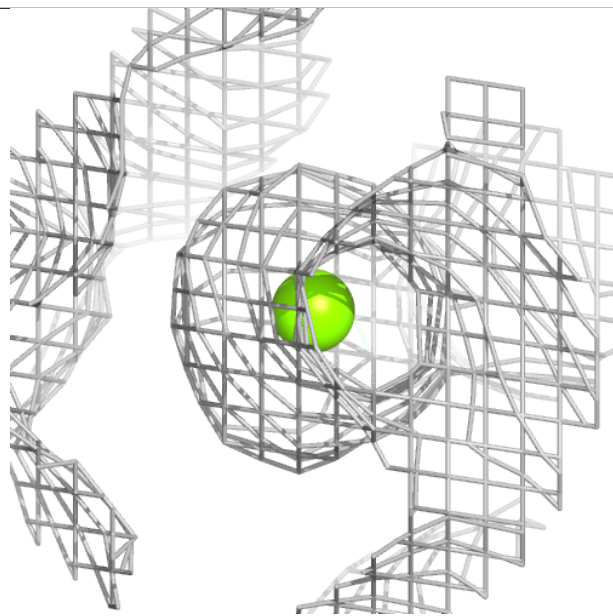
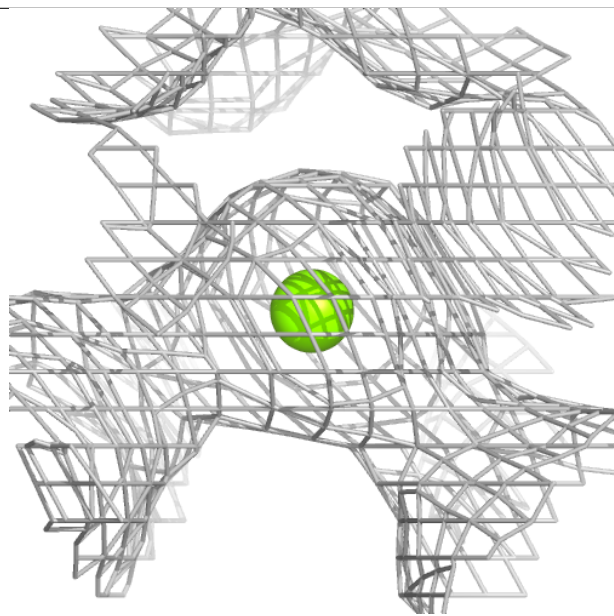
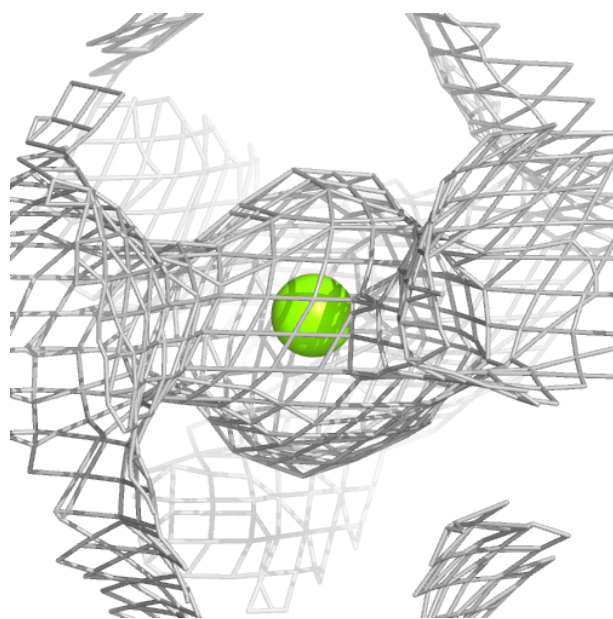
**Electron density around PO4 B 716:**

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



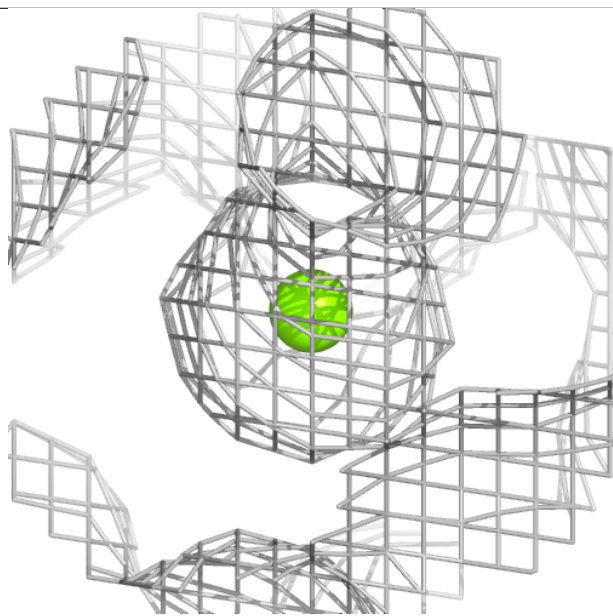
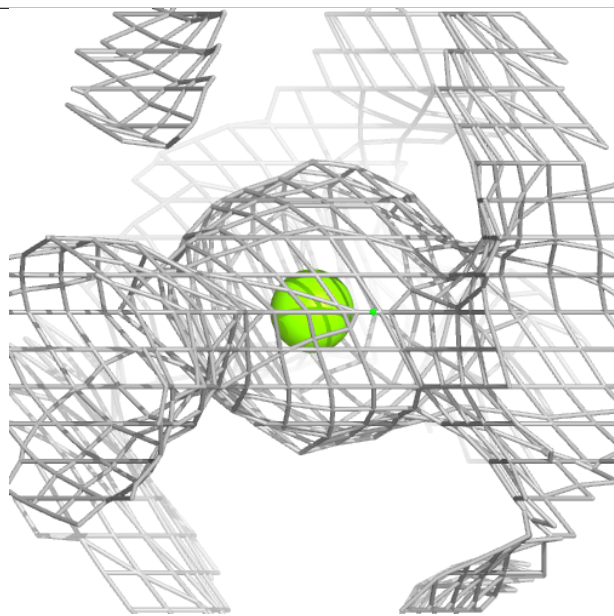
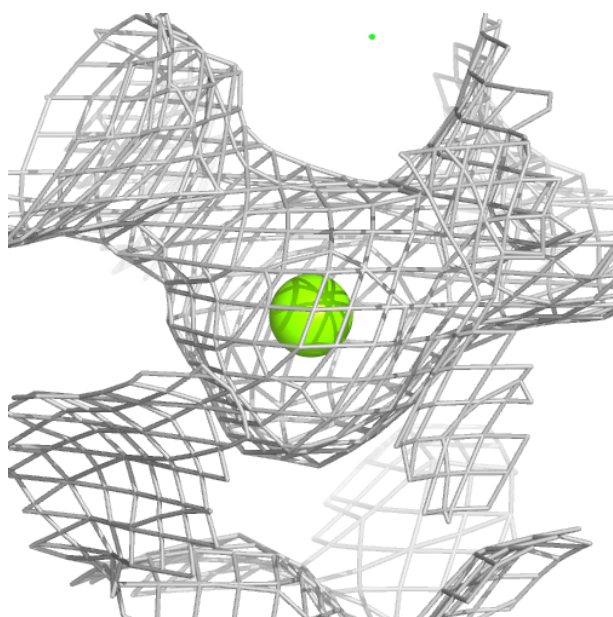
**Electron density around MG A 714:**

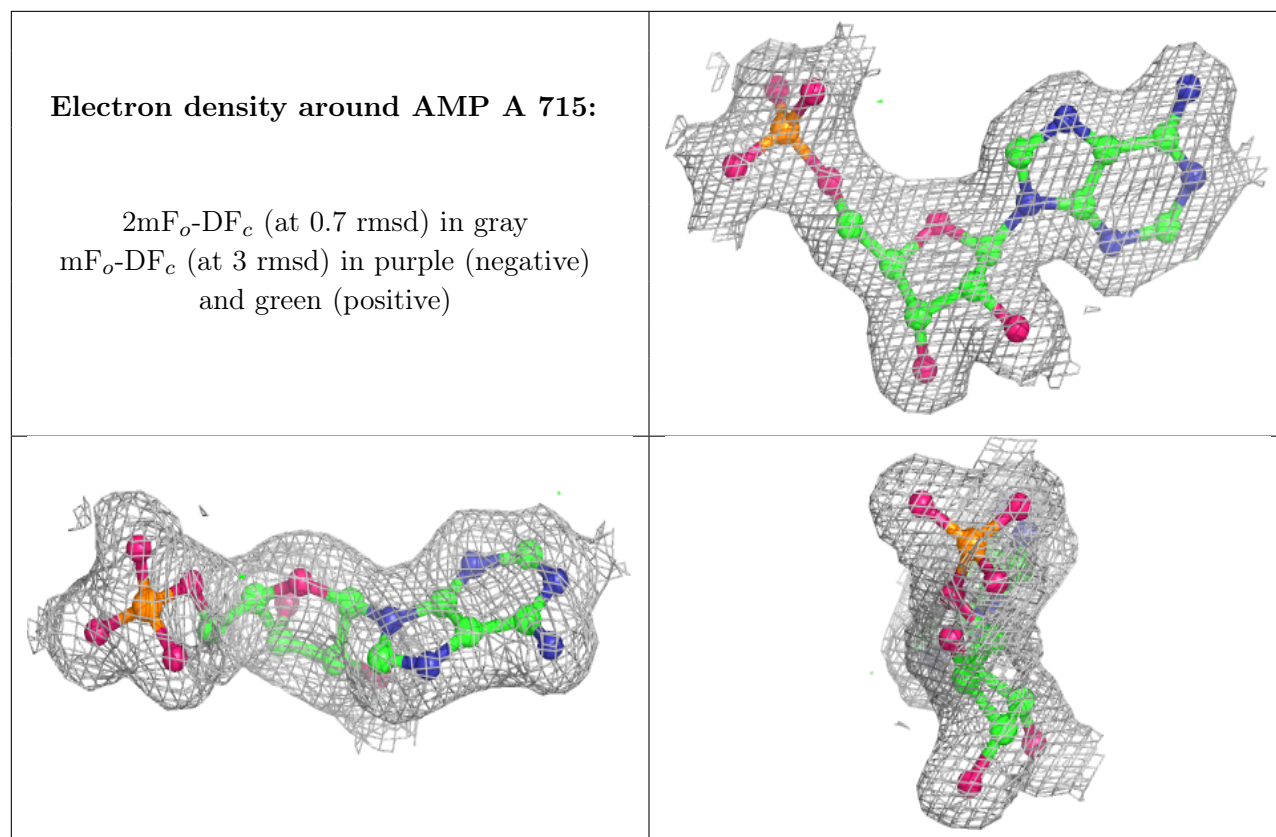
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

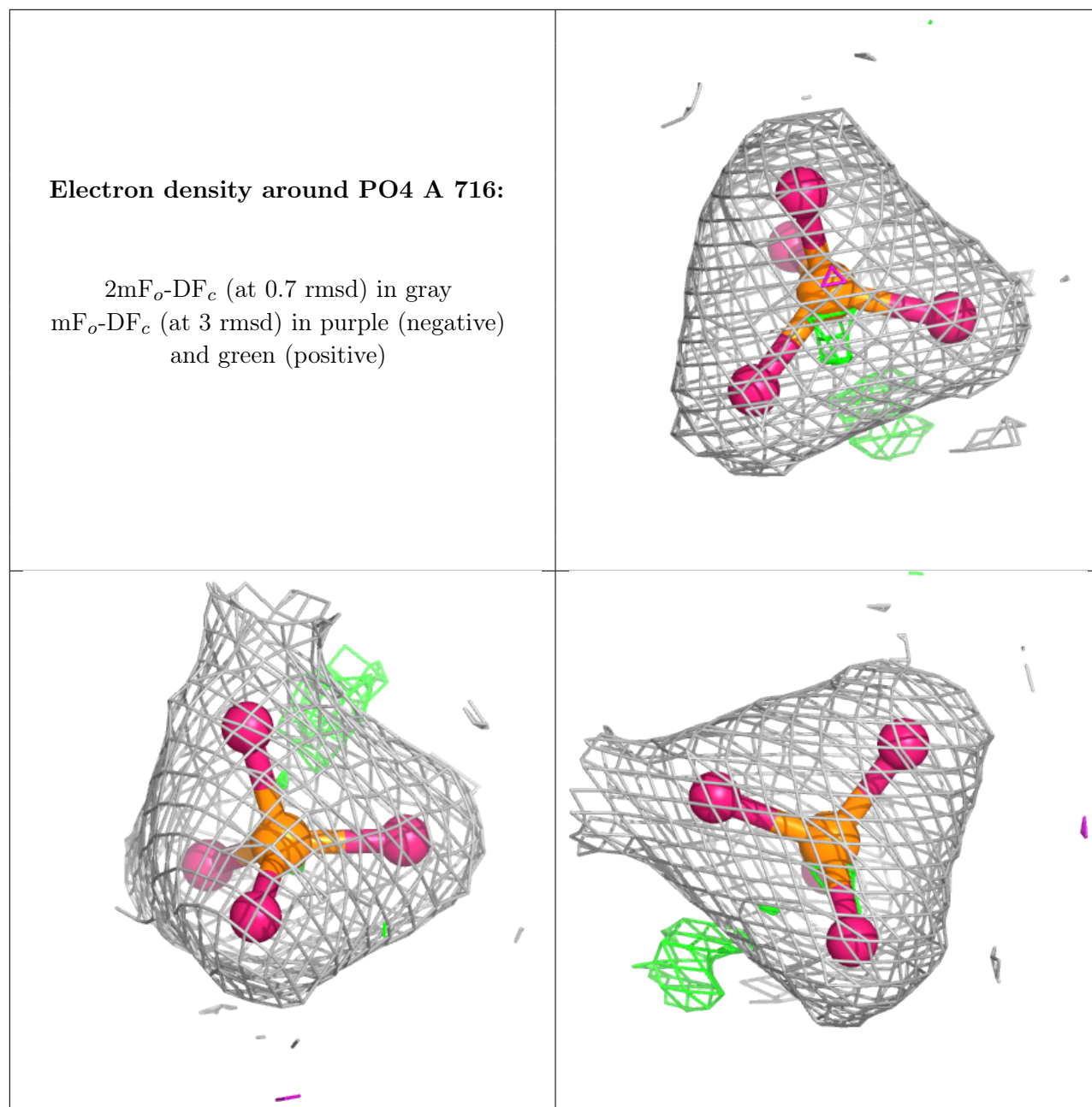


**Electron density around MG B 703:**

$2mF_o-DF_c$  (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.