



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 22, 2025 – 07:06 pm BST

PDB ID : 9S2T / pdb\_00009s2t  
Title : Carbamoyl transferase NovN involved in Novobiocin biosynthesis  
Authors : Gomez Garcia, I.; Lawson, D.M.  
Deposited on : 2025-07-22  
Resolution : 2.24 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 : 4-5-2 with Phenix2.0rc1  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

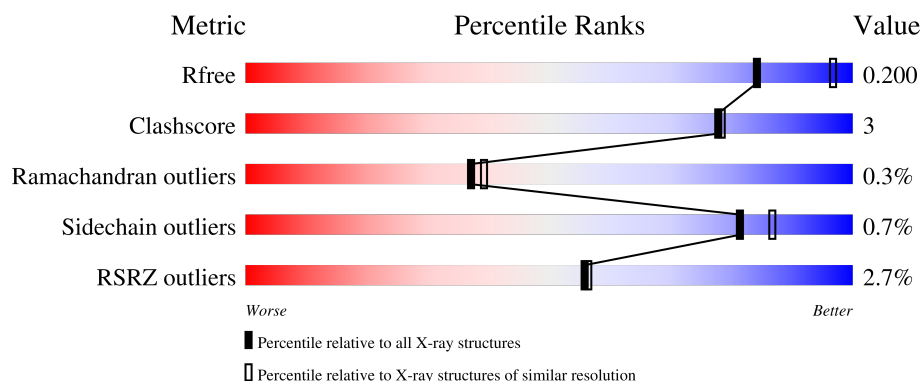
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

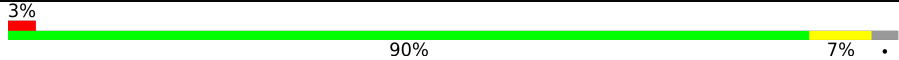
The reported resolution of this entry is 2.24 Å.

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	3139 (2.26-2.22)
Clashscore	180529	3381 (2.26-2.22)
Ramachandran outliers	177936	3334 (2.26-2.22)
Sidechain outliers	177891	3335 (2.26-2.22)
RSRZ outliers	164620	3138 (2.26-2.22)

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	687	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5747 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 Decarbamoylnovobiocin carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	669	5275	3337	940	982	16	0	11	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	678	LEU	-	expression tag	UNP Q9L9F4
A	679	GLU	-	expression tag	UNP Q9L9F4
A	680	HIS	-	expression tag	UNP Q9L9F4
A	681	HIS	-	expression tag	UNP Q9L9F4
A	682	HIS	-	expression tag	UNP Q9L9F4
A	683	HIS	-	expression tag	UNP Q9L9F4
A	684	HIS	-	expression tag	UNP Q9L9F4
A	685	HIS	-	expression tag	UNP Q9L9F4
A	686	HIS	-	expression tag	UNP Q9L9F4
A	687	HIS	-	expression tag	UNP Q9L9F4

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		

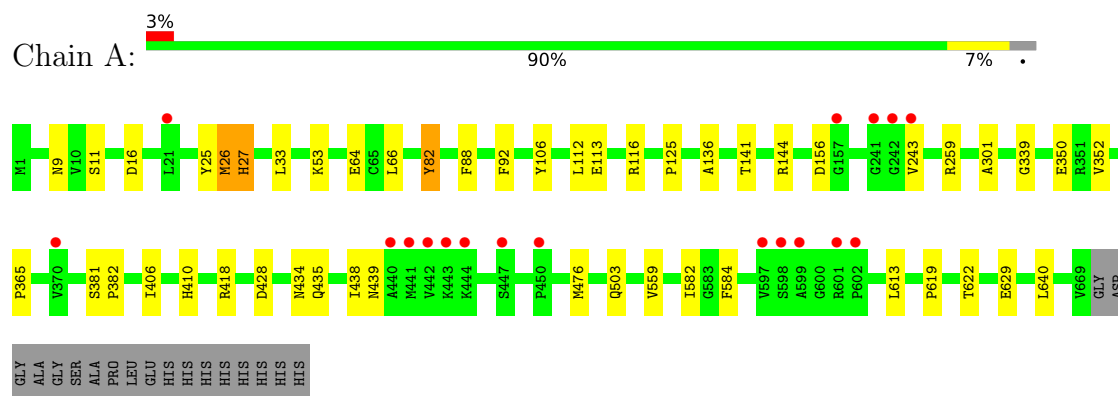
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	434	Total	O	0	7
			441	441		

### 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: Decarbamoylnovobiocin carbamoyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.50Å 113.26Å 166.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.17 – 2.24 39.17 – 2.24	Depositor EDS
% Data completeness (in resolution range)	94.0 (39.17-2.24) 94.0 (39.17-2.24)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.09 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.105)	Depositor
R, $R_{free}$	0.160 , 0.200 0.160 , 0.200	Depositor DCC
$R_{free}$ test set	2364 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.5	Xtriage
Anisotropy	0.410	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 41.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5747	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, PO4

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	0.54	0/5432	1.10	8/7392 (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

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	435	GLN	N-CA-CB	6.68	119.69	110.01
1	A	106	TYR	CB-CA-C	6.56	124.73	111.60
1	A	428	ASP	CA-CB-CG	6.47	119.08	112.60
1	A	27	HIS	CA-CB-CG	-5.72	108.08	113.80
1	A	156	ASP	CA-CB-CG	5.44	118.04	112.60
1	A	622	THR	CA-CB-OG1	-5.36	101.57	109.60
1	A	584	PHE	CA-CB-CG	5.16	118.96	113.80
1	A	92	PHE	N-CA-CB	5.04	117.53	110.12

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	ARG	Sidechain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5275	0	5206	28	0
2	A	30	0	0	0	0
3	A	1	0	0	0	0
4	A	441	0	0	1	0
All	All	5747	0	5206	28	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 3.

All (28) 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:26:MET:HG3	1:A:82:TYR:OH	1.69	0.92
1:A:112:LEU:HD11	1:A:125:PRO:HA	1.66	0.77
1:A:25:TYR:O	1:A:26:MET:HB2	1.87	0.74
1:A:26:MET:HG3	1:A:82:TYR:HH	1.56	0.68
1:A:9:ASN:ND2	1:A:26:MET:HE2	2.09	0.68
1:A:33:LEU:HD11	1:A:66:LEU:HD23	1.78	0.64
1:A:27:HIS:CD2	1:A:27:HIS:H	2.18	0.61
1:A:476:MET:HG3	1:A:503:GLN:HB2	1.83	0.60
1:A:141:THR:HG22	1:A:301:ALA:HB1	1.85	0.58
1:A:9:ASN:HD22	1:A:26:MET:HE2	1.70	0.55
1:A:9:ASN:ND2	1:A:26:MET:CE	2.69	0.55
1:A:582:ILE:HD12	1:A:640:LEU:HD21	1.89	0.55
1:A:582:ILE:CD1	1:A:640:LEU:HD21	2.38	0.54
1:A:53:LYS:HD3	4:A:939:HOH:O	2.12	0.48
1:A:434:ASN:O	1:A:438:ILE:HG12	2.15	0.47
1:A:11:SER:HB3	1:A:16:ASP:HA	1.98	0.46
1:A:418[B]:ARG:HD3	1:A:418[B]:ARG:HA	1.73	0.45
1:A:136:ALA:O	1:A:339:GLY:HA3	2.17	0.44
1:A:64:GLU:HB3	1:A:365:PRO:HG3	1.99	0.44
1:A:26:MET:HE3	1:A:88:PHE:HE2	1.84	0.43
1:A:381:SER:N	1:A:382:PRO:CD	2.82	0.43
1:A:406:ILE:HG22	1:A:559:VAL:CG1	2.49	0.43
1:A:113:GLU:HG3	1:A:116[B]:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:GLU:HG2	1:A:352:VAL:HG13	2.02	0.42
1:A:26:MET:HE3	1:A:88:PHE:CE2	2.55	0.41
1:A:613:LEU:HD12	1:A:619:PRO:HG2	2.02	0.41
1:A:476:MET:HE3	1:A:503:GLN:HB2	2.03	0.40
1:A:144:ARG:HD3	1:A:144:ARG:HA	1.89	0.40

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	678/687 (99%)	662 (98%)	14 (2%)	2 (0%)	37 39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	439	ASN
1	A	26	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	558/562 (99%)	553 (99%)	5 (1%)	75 82

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	TYR
1	A	243	VAL
1	A	410	HIS
1	A	629[A]	GLU
1	A	629[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
1	A	313	ASN

### 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 7 ligands modelled in this entry, 1 is 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	PO4	A	703	-	4,4,4	1.23	1 (25%)	6,6,6	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	A	704	-	4,4,4	0.59	0	6,6,6	0.66	0
2	PO4	A	701	-	4,4,4	0.71	0	6,6,6	0.45	0
2	PO4	A	702	-	4,4,4	0.84	0	6,6,6	0.48	0
2	PO4	A	707	-	4,4,4	0.69	0	6,6,6	0.47	0
2	PO4	A	705	-	4,4,4	0.72	0	6,6,6	0.43	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	703	PO4	P-O1	2.41	1.56	1.50

There are no bond angle outliers.

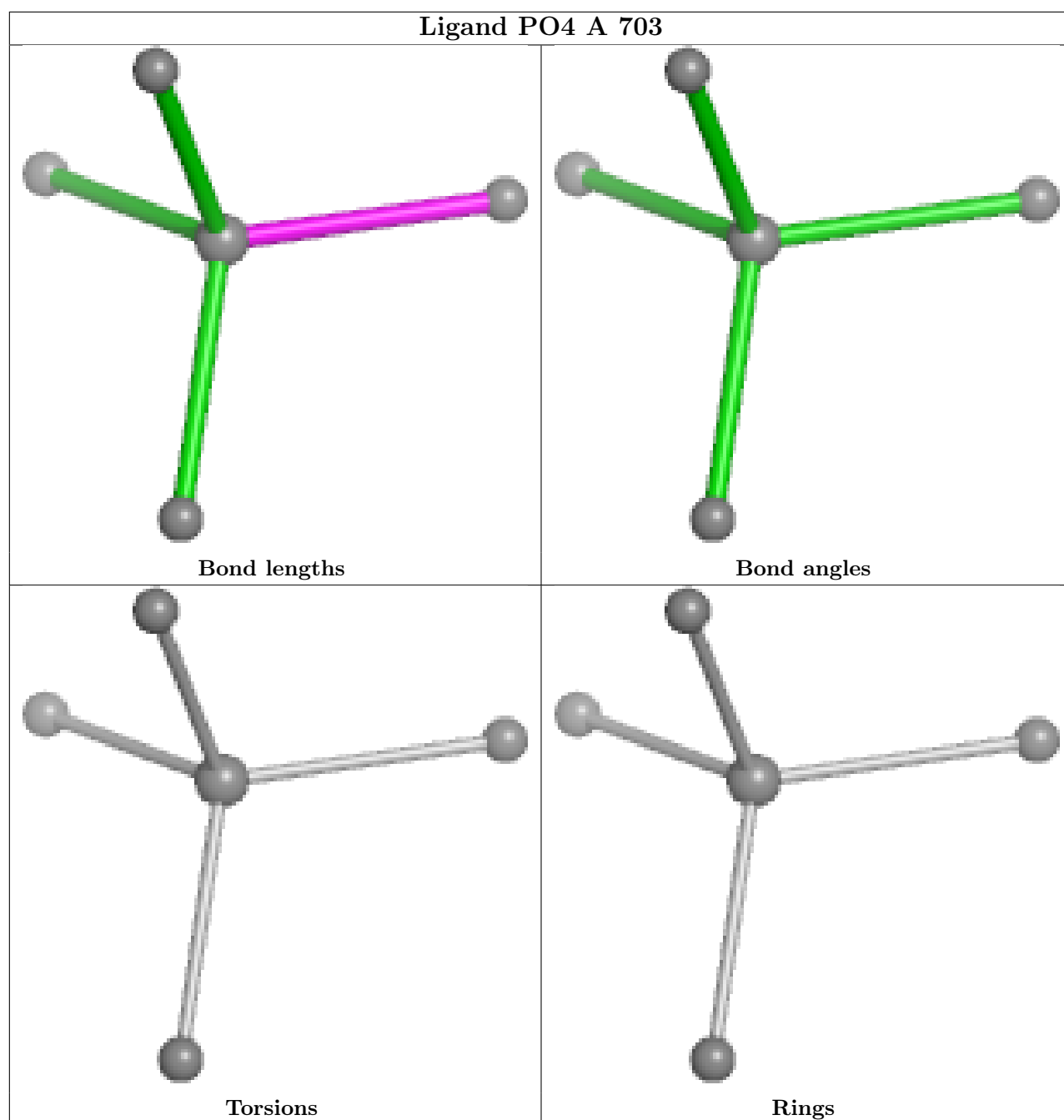
There are no chirality outliers.

There are no torsion outliers.

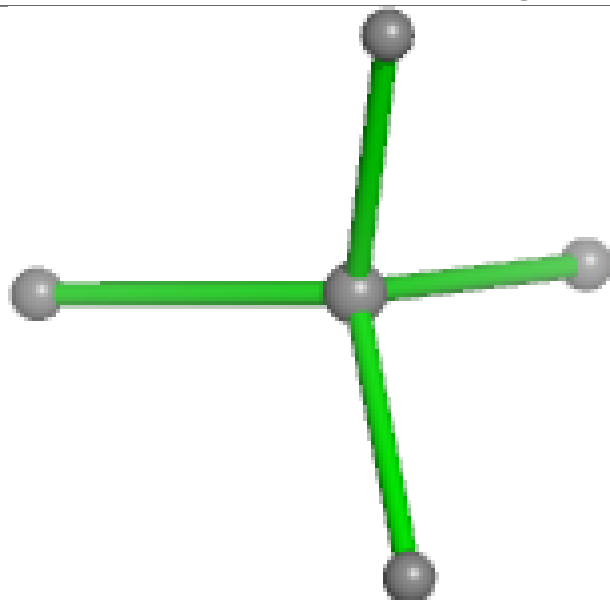
There are no ring outliers.

No monomer is involved in short contacts.

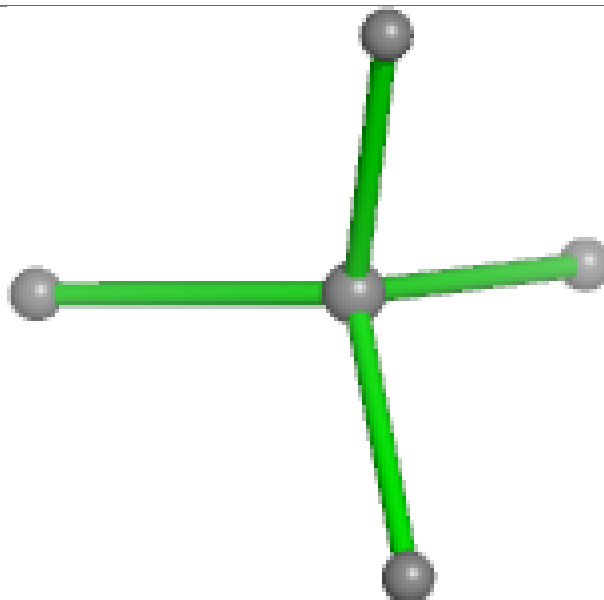
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



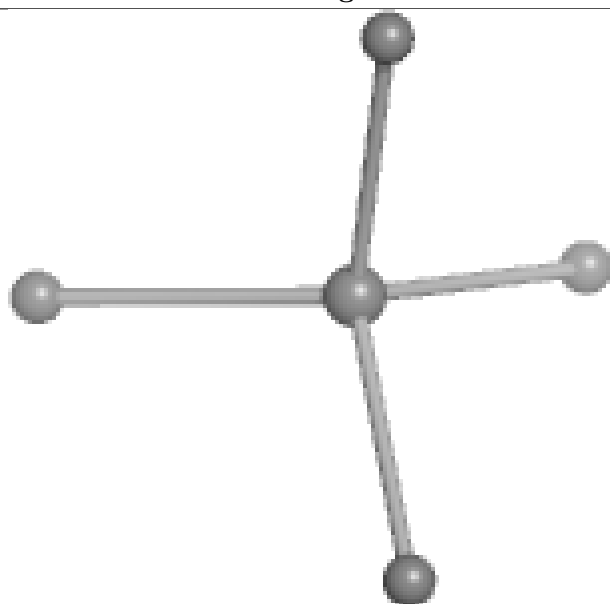
## Ligand PO4 A 704



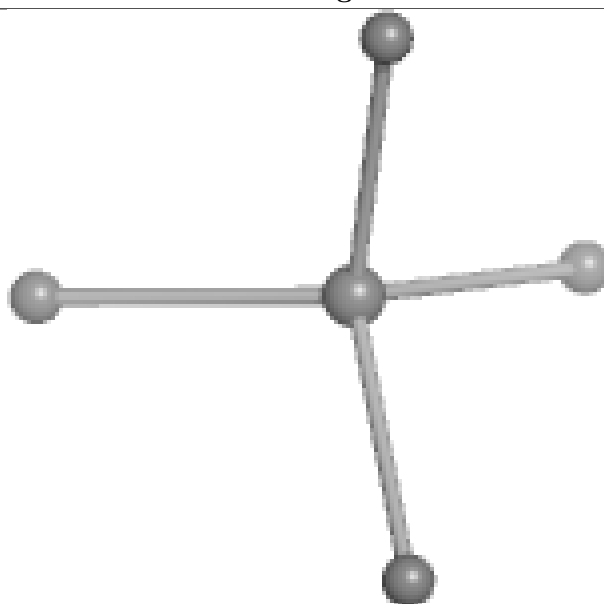
Bond lengths



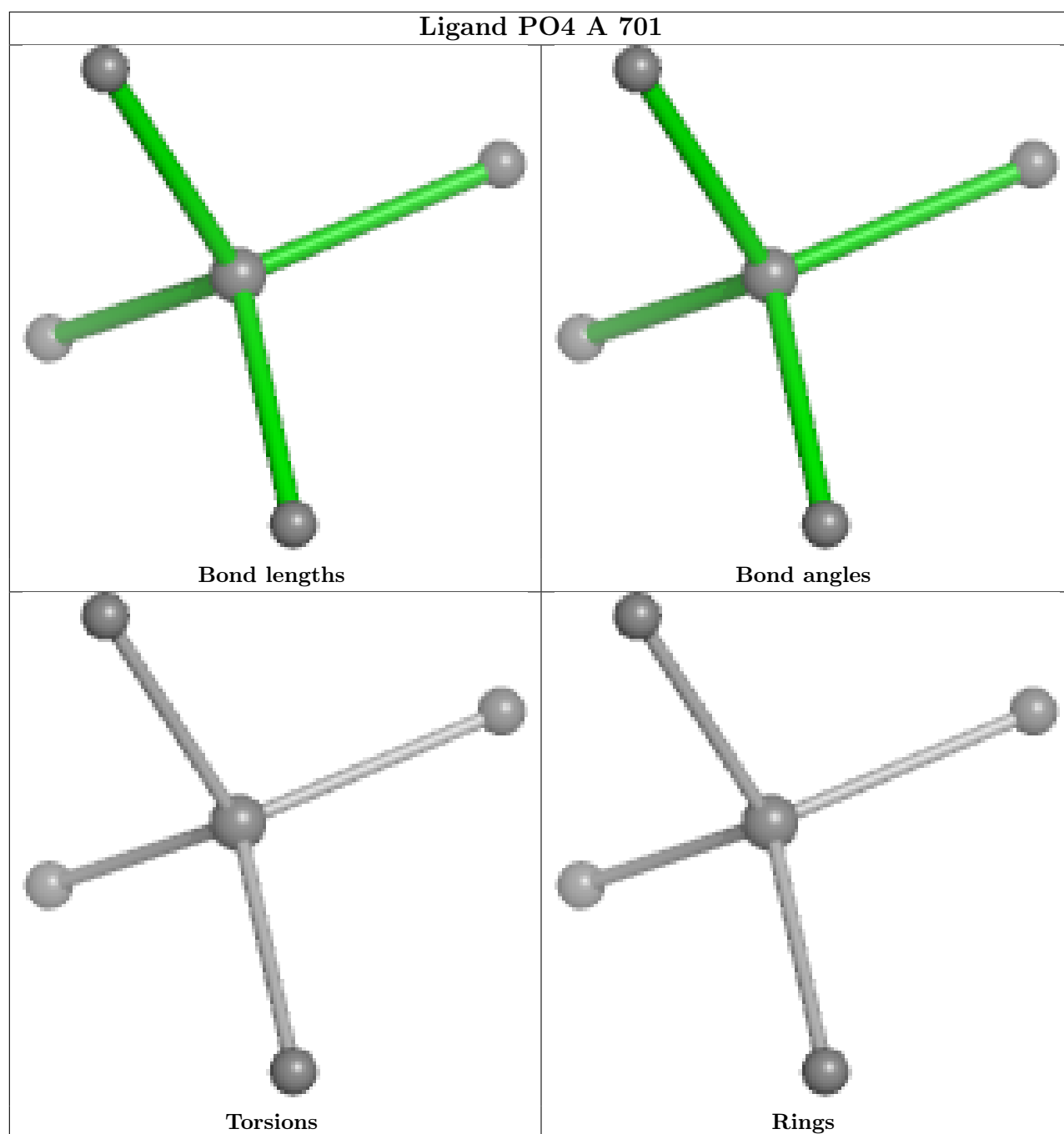
Bond angles



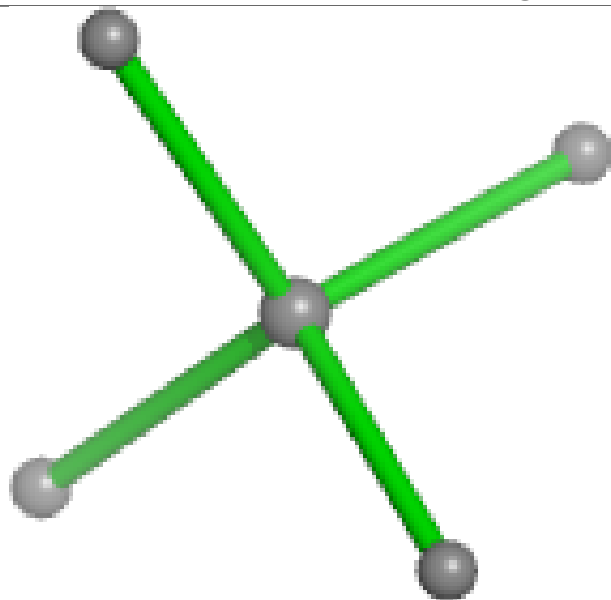
Torsions



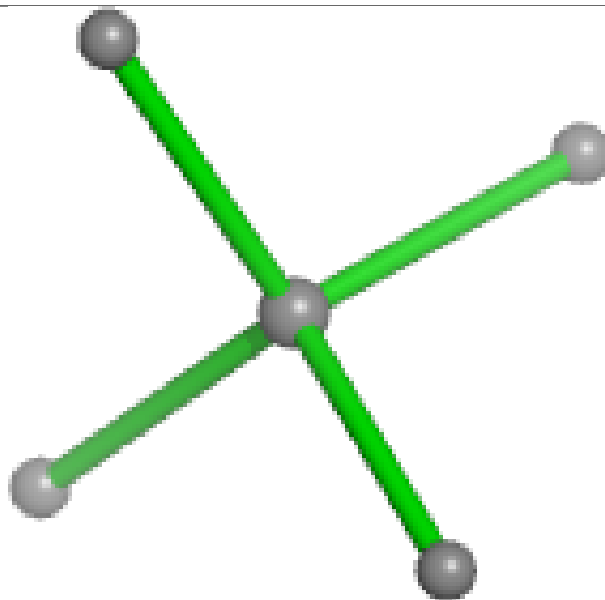
Rings



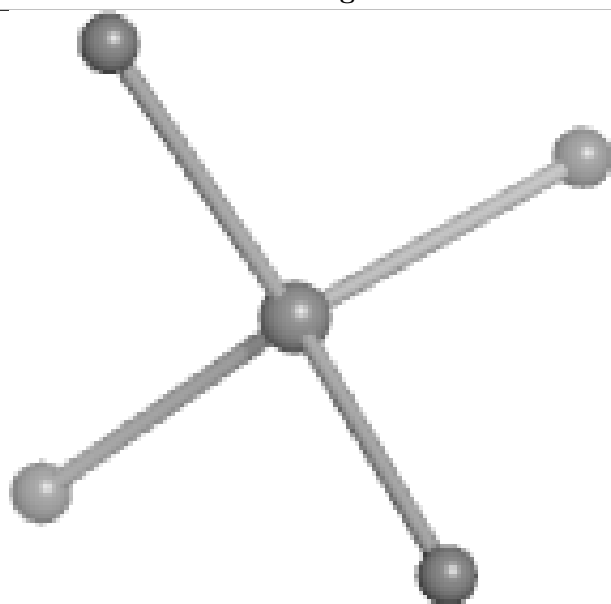
## Ligand PO4 A 702



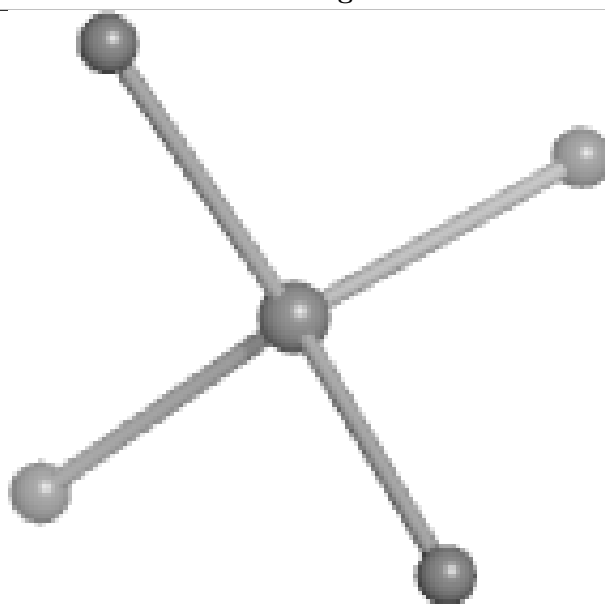
Bond lengths



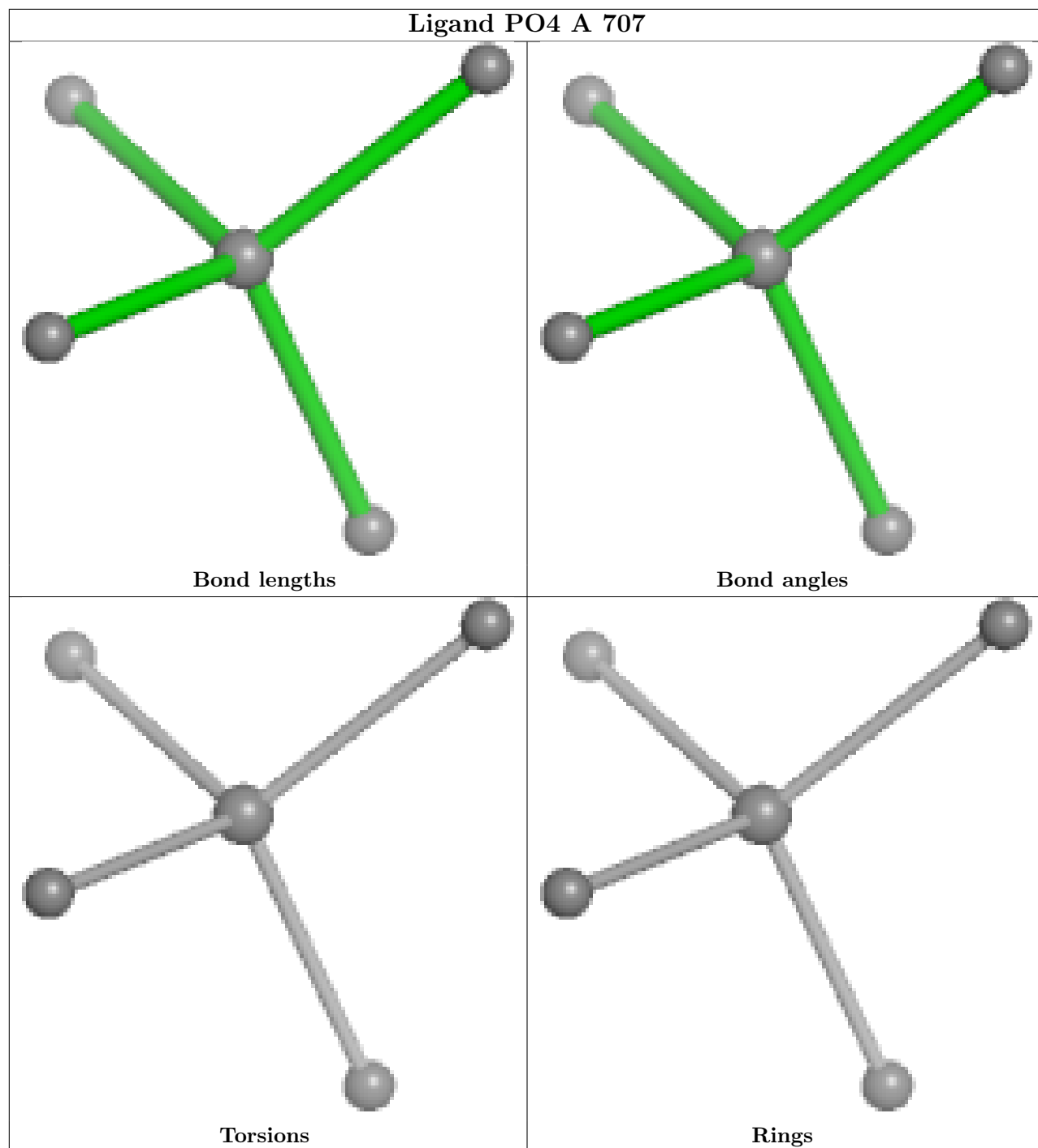
Bond angles



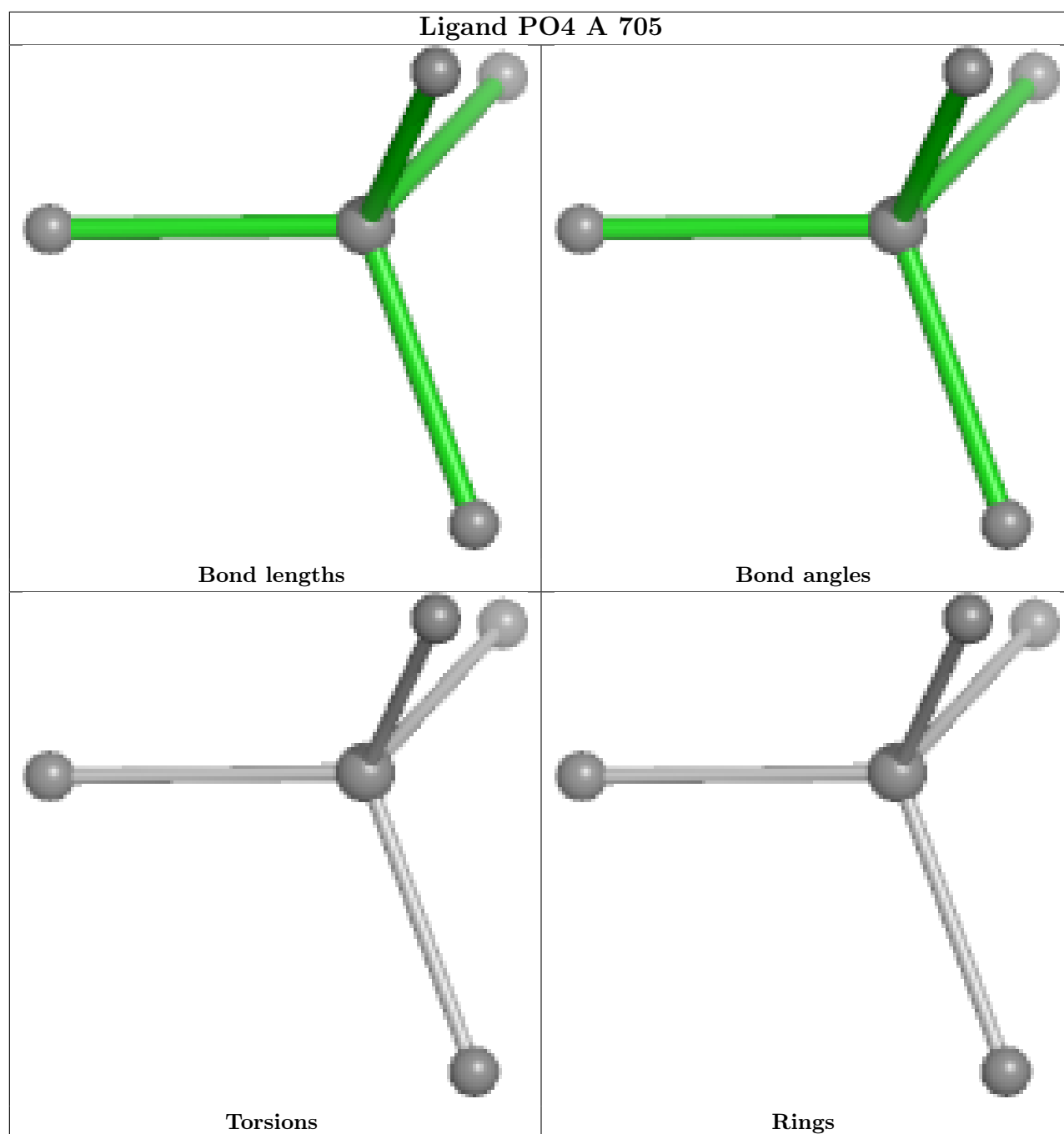
Torsions



Rings







## 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	669/687 (97%)	-0.57	18 (2%) 56 56	14, 31, 63, 112	11 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	599	ALA	5.4
1	A	243	VAL	4.6
1	A	441	MET	4.3
1	A	440	ALA	4.2
1	A	157	GLY	4.2
1	A	242	GLY	3.9
1	A	598	SER	3.7
1	A	444	LYS	3.3
1	A	602	PRO	2.9
1	A	450	PRO	2.8
1	A	597	VAL	2.6
1	A	601	ARG	2.5
1	A	241	GLY	2.5
1	A	443	LYS	2.3
1	A	442	VAL	2.2
1	A	21	LEU	2.2
1	A	447	SER	2.1
1	A	370	VAL	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

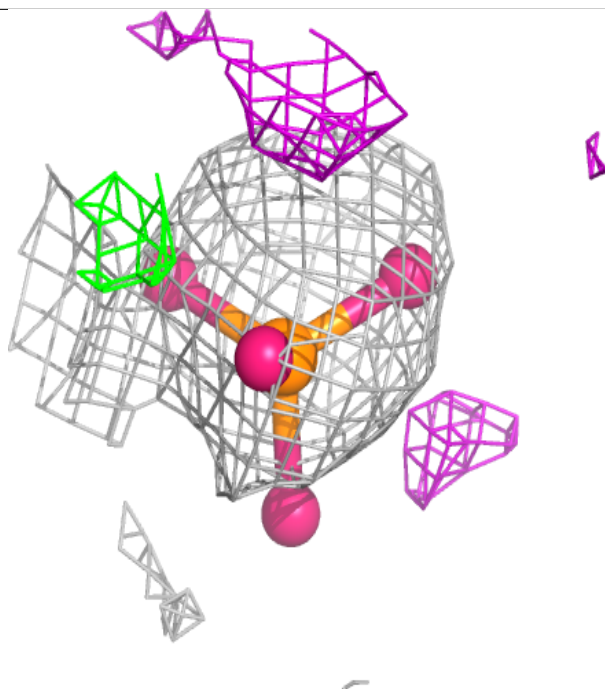
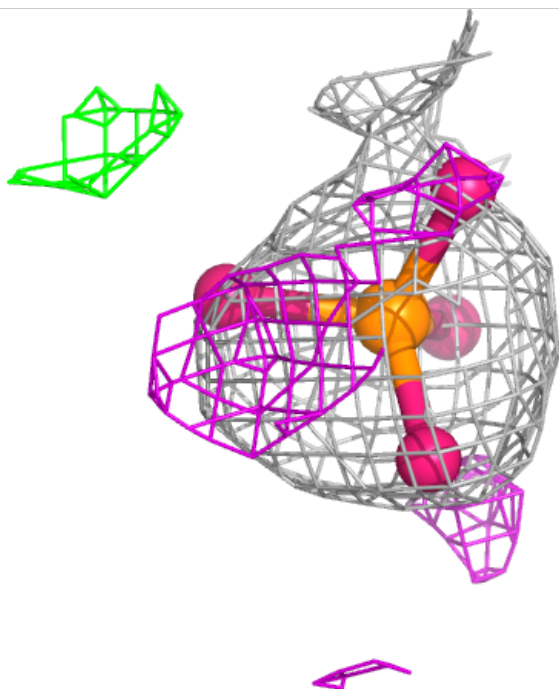
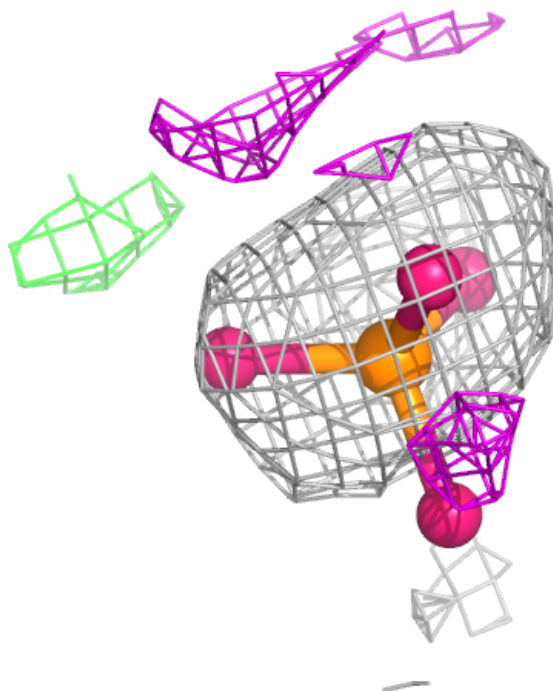
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	PO4	A	705	5/5	0.73	0.22	116,123,125,134	0
2	PO4	A	707	5/5	0.80	0.16	89,90,97,104	0
2	PO4	A	704	5/5	0.87	0.14	55,57,62,67	0
2	PO4	A	703	5/5	0.91	0.16	46,46,62,62	0
2	PO4	A	702	5/5	0.93	0.09	51,56,60,64	0
2	PO4	A	701	5/5	0.95	0.08	44,45,48,56	0
3	FE	A	706	1/1	0.98	0.06	27,27,27,27	1

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.

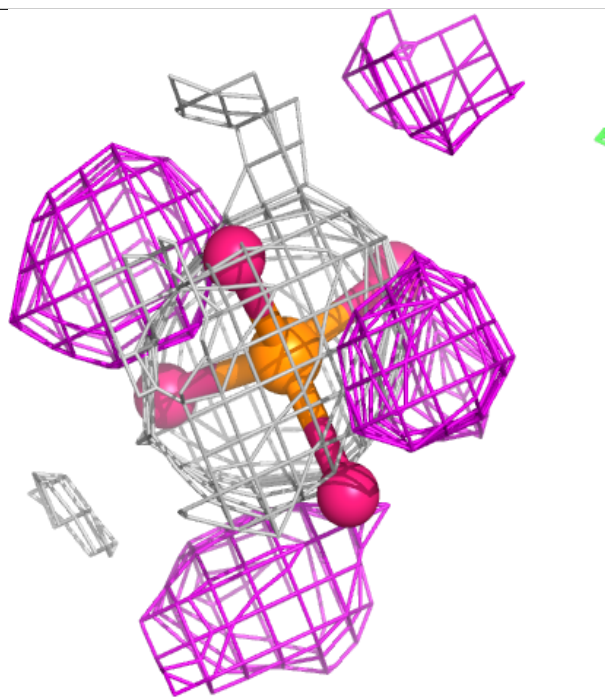
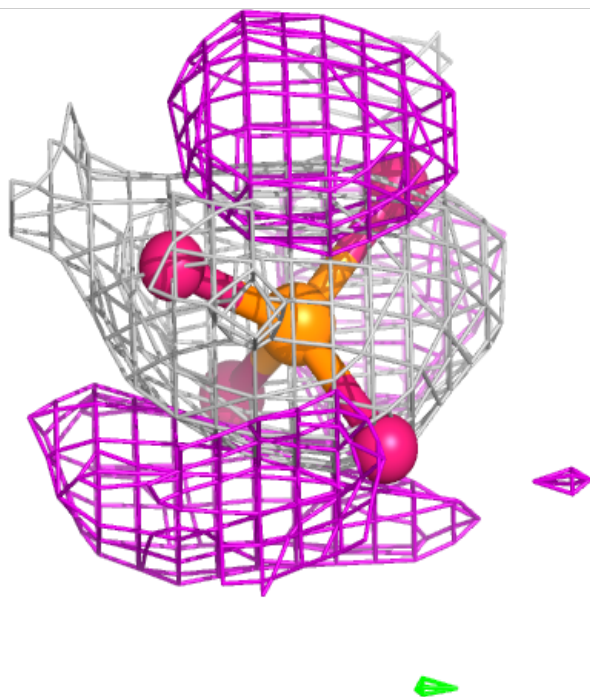
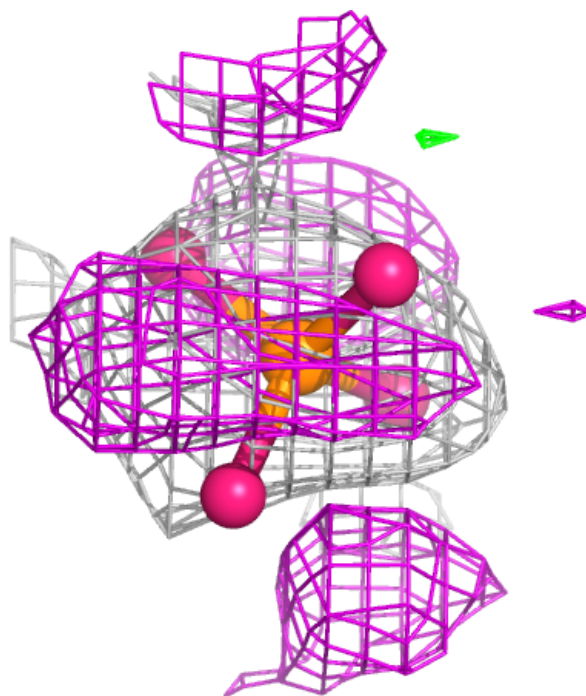
**Electron density around PO4 A 705:**

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



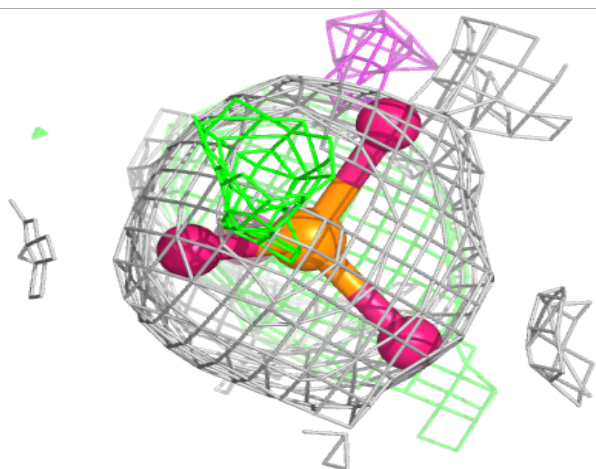
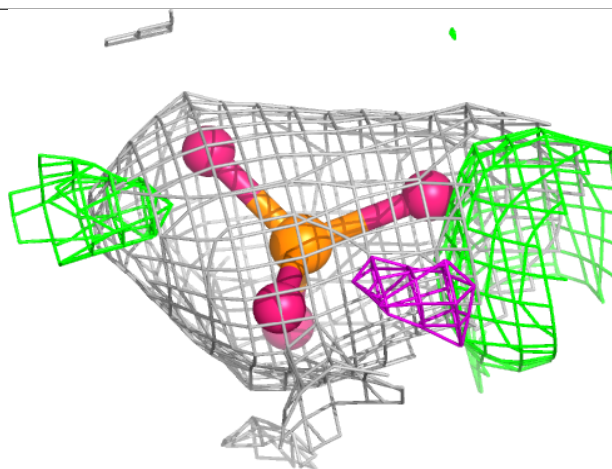
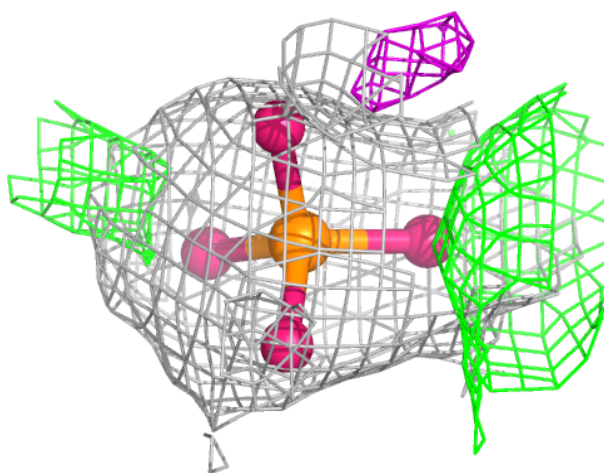
**Electron density around PO4 A 707:**

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



**Electron density around PO4 A 704:**

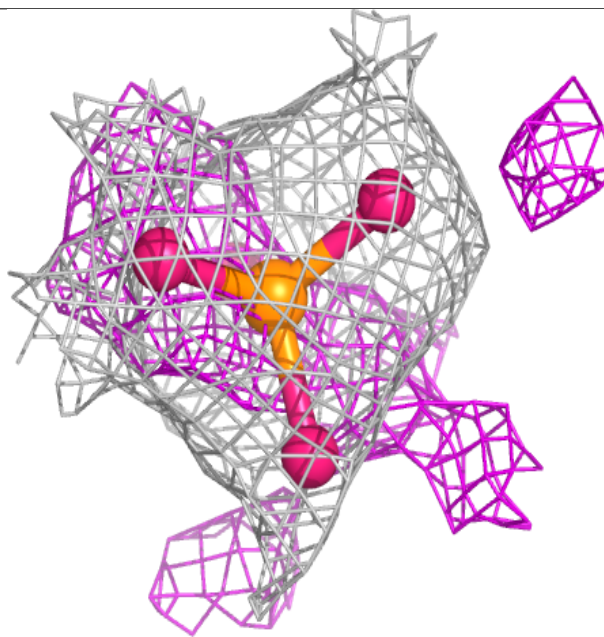
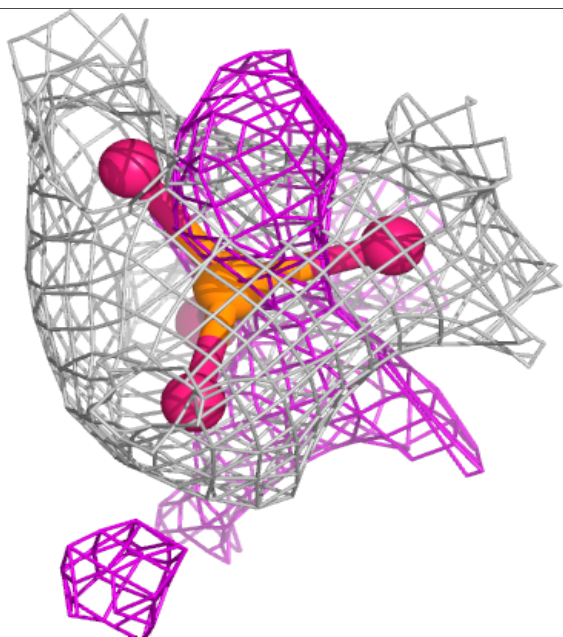
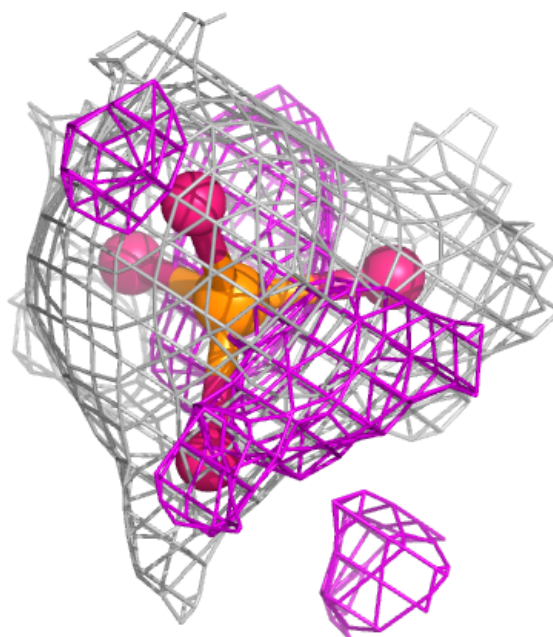
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





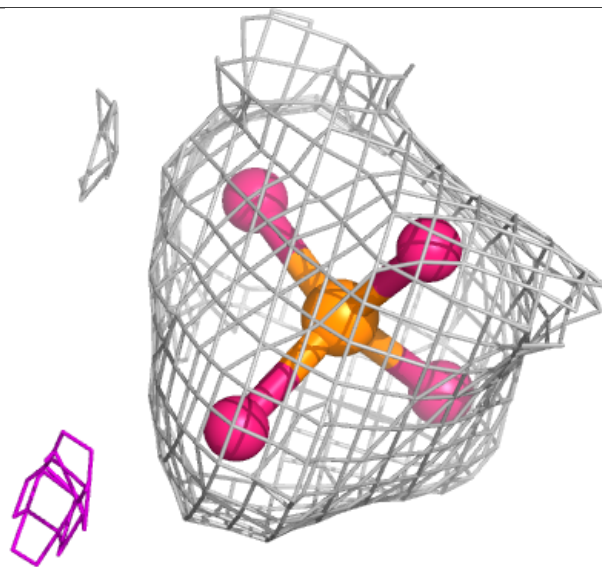
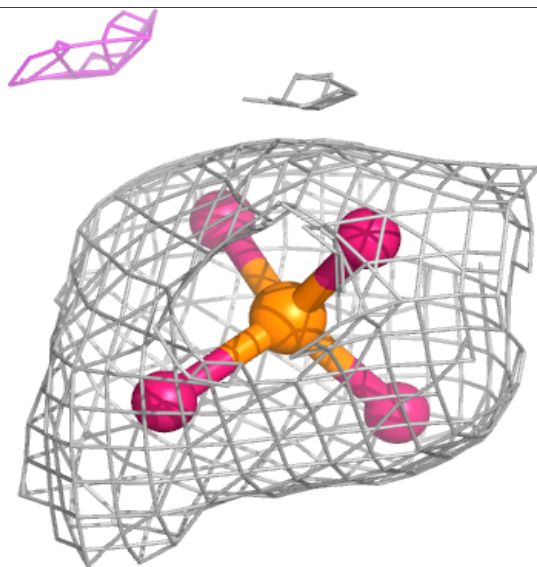
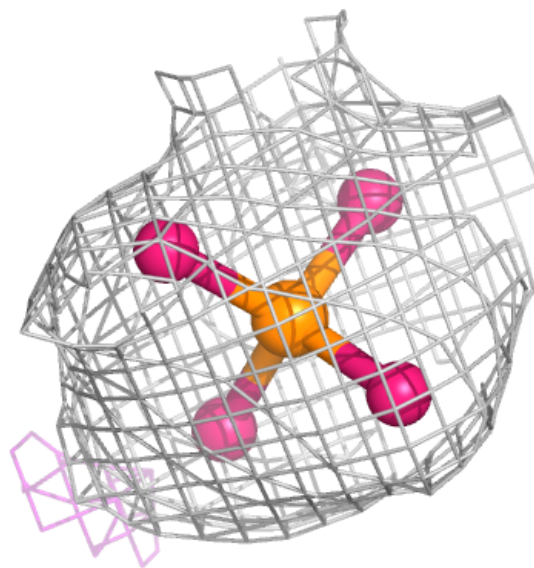
**Electron density around PO4 A 703:**

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



**Electron density around PO4 A 702:**

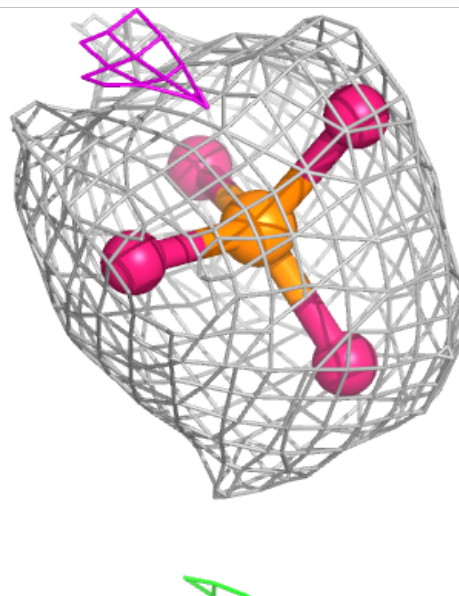
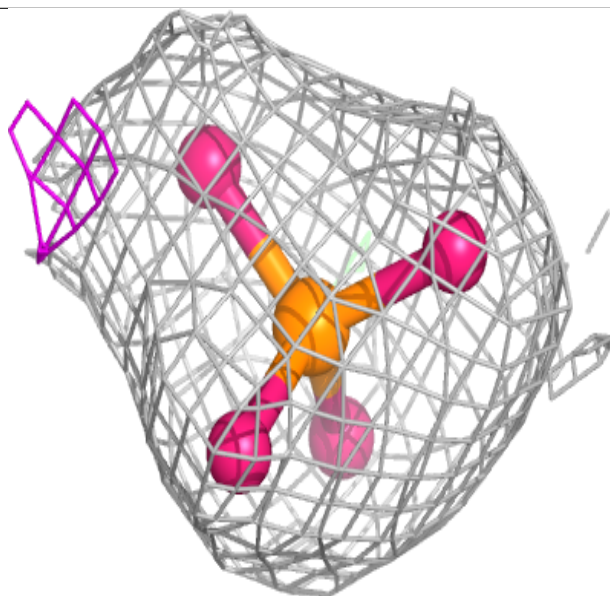
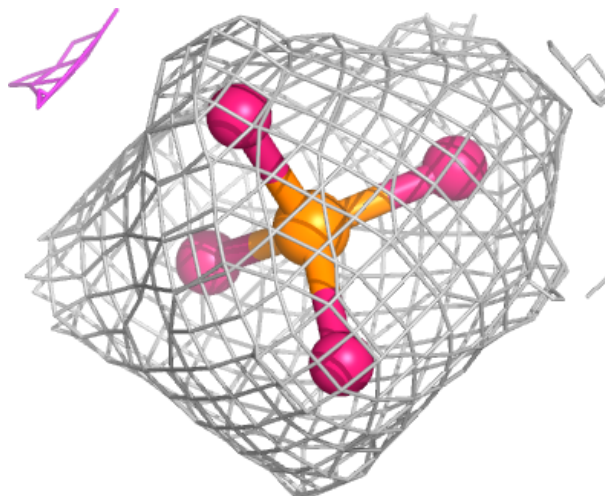
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

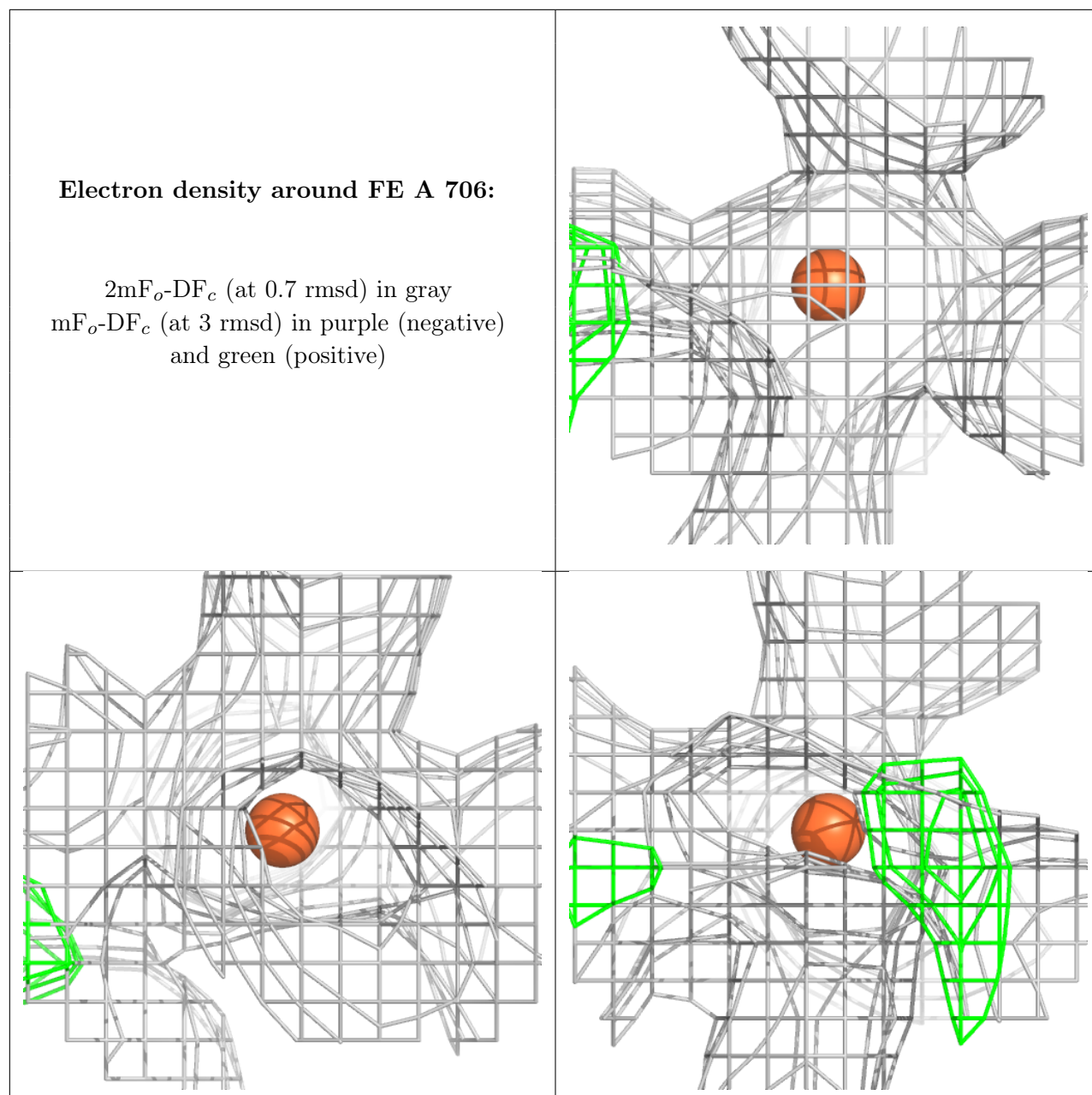




**Electron density around PO4 A 701:**

$2mF_o-DF_c$  (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.