



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 19, 2022 – 05:45 AM JST

PDB ID : 7WOK  
Title : Crystal structure of HSA soaked with cisplatin for one week  
Authors : Chen, S.L.; Yuan, C.; Jiang, L.G.; Luo, Z.P.; Huang, M.D.  
Deposited on : 2022-01-21  
Resolution : 2.90 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 : ?? (??), CSD ??CSD?? (????)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
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) : 2.29

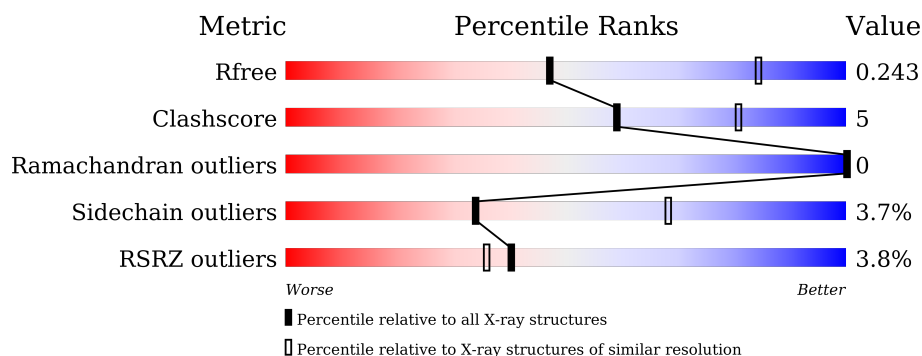
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	609	<div> <div>3%</div> <div> <div></div> <div>78%</div> <div>13%</div> <div>8%</div> </div> </div>
1	B	609	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>8%</div> </div> </div>

## 2 Entry composition [i](#)

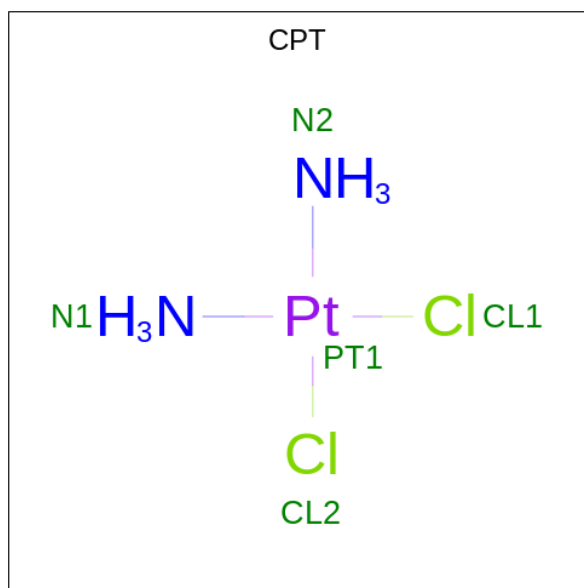
There are 4 unique types of molecules in this entry. The entry contains 8977 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4452	2812	753	847	40			
1	B	559	Total	C	N	O	S	0	0	0
			4468	2823	756	849	40			

- Molecule 2 is Cisplatin (three-letter code: CPT) (formula:  $\text{Cl}_2\text{H}_6\text{N}_2\text{Pt}$ ) (labeled as "Ligand of Interest" by depositor).



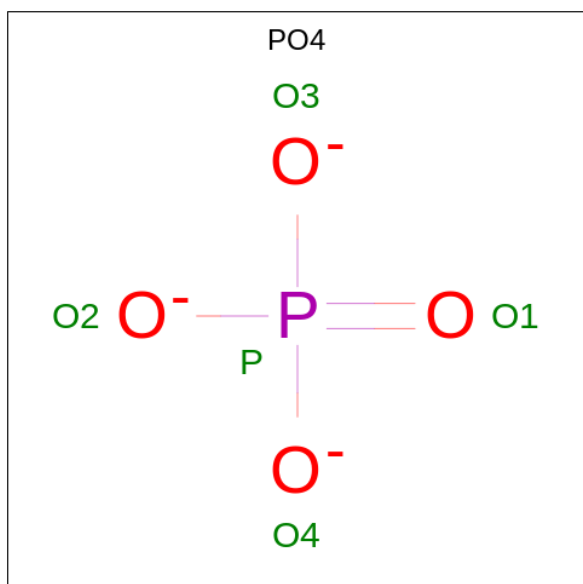
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	N	Pt		0	0
			3	2	1			
2	A	1	Total	Cl	N	Pt	0	0
			4	1	2	1		
2	A	1	Total	N	Pt		0	0
			3	2	1			
2	A	1	Total	N	Pt		0	0
			3	2	1			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	N	Pt			
			3	2	1	0	0	
2	B	1	Total	N	Pt			
			3	2	1	0	0	
2	B	1	Total	Cl	N	Pt		
			4	1	2	1	0	
2	B	1	Total	N	Pt			
			3	2	1	0	0	
2	B	1	Total	N	Pt			
			3	2	1	0	0	
2	B	1	Total	Pt				
			1	1		0	0	

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		

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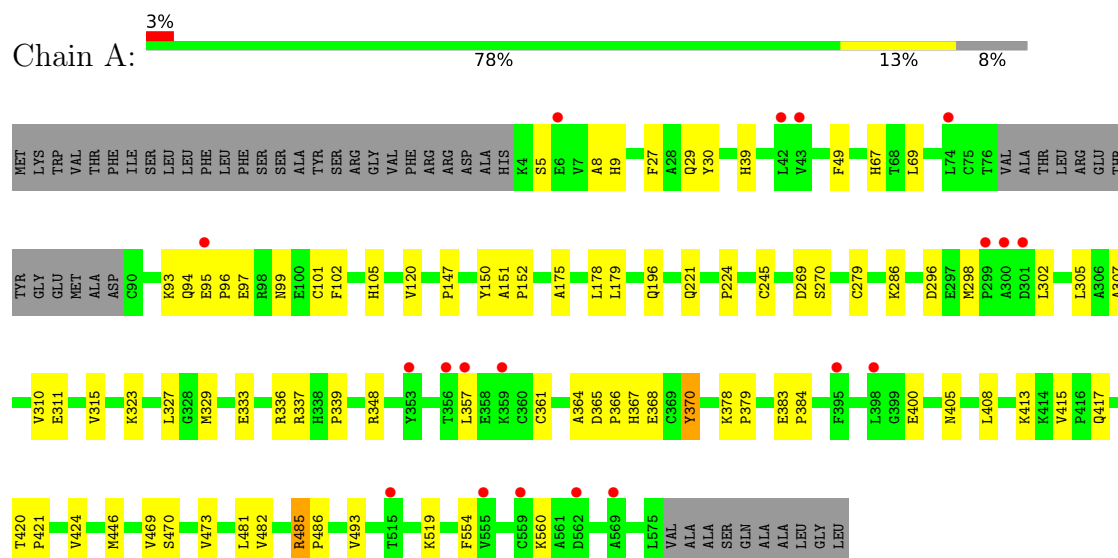
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	9	Total	O	0	0
			9	9		

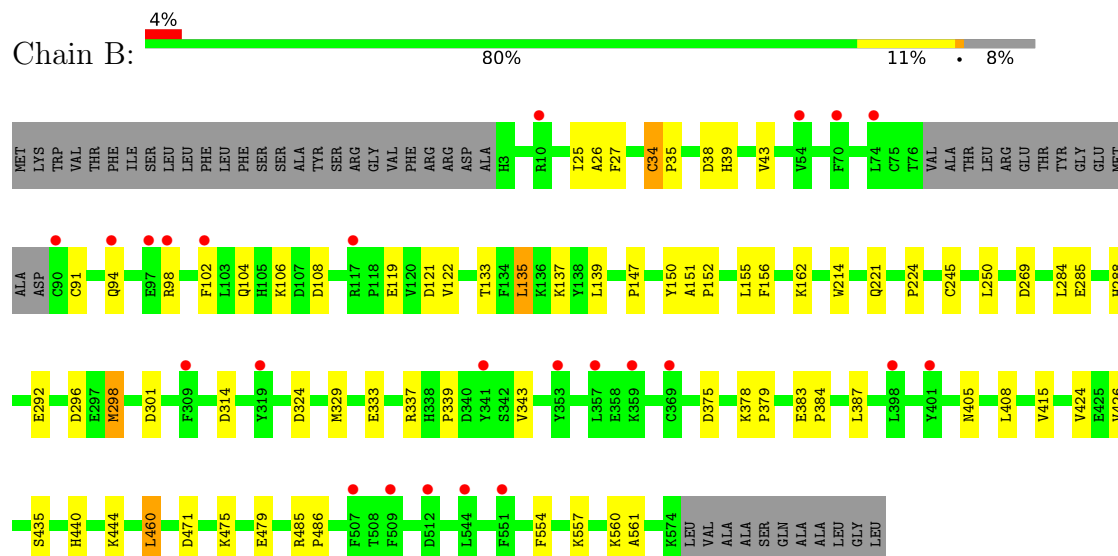
### 3 Residue-property plots [i](#)

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: Albumin



#### • Molecule 1: Albumin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.38Å 180.52Å 58.50Å 90.00° 103.87° 90.00°	Depositor
Resolution (Å)	36.55 – 2.90 36.55 – 2.91	Depositor EDS
% Data completeness (in resolution range)	98.9 (36.55-2.90) 98.9 (36.55-2.91)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.207 , 0.244 0.203 , 0.243	Depositor DCC
$R_{free}$ test set	1287 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	95.9	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 69.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.158 for l,-k,h	Xtriage
Reported twinning fraction	0.873 for H, K, L 0.127 for -L, -K, -H	Depositor
Outliers	0 of 25581 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8977	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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: PO4, CPT

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	0.75	0/4538	0.79	0/6118
1	B	0.73	0/4556	0.78	0/6141
All	All	0.74	0/9094	0.79	0/12259

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	4452	0	4370	48	0
1	B	4468	0	4390	36	0
2	A	16	0	0	3	0
2	B	14	0	0	4	0
3	A	5	0	0	1	0
3	B	5	0	0	0	0
4	A	8	0	0	1	0
4	B	9	0	0	0	0
All	All	8977	0	8760	84	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 5.



All (84) 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:417:GLN:HB3	1:A:469:VAL:HG22	1.69	0.73
1:A:49:PHE:HE2	1:A:69:LEU:HD11	1.56	0.69
1:B:151:ALA:HB3	1:B:152:PRO:HD3	1.74	0.69
1:A:364:ALA:O	1:A:366:PRO:HD3	1.93	0.69
1:B:329:MET:HG2	2:B:602:CPT:N2	2.11	0.65
1:B:224:PRO:HD2	1:B:296:ASP:HB3	1.81	0.62
1:B:26:ALA:HB2	1:B:250:LEU:HD12	1.82	0.61
1:A:269:ASP:OD1	1:A:270:SER:N	2.33	0.61
1:B:39:HIS:O	1:B:43:VAL:HG23	2.03	0.59
1:B:221:GLN:HE21	1:B:339:PRO:HA	1.68	0.58
1:B:94:GLN:O	1:B:98:ARG:HB2	2.02	0.58
1:A:95:GLU:N	1:A:96:PRO:HD2	2.19	0.57
1:A:49:PHE:CE2	1:A:69:LEU:HD11	2.40	0.56
1:A:9:HIS:NE2	4:A:701:HOH:O	2.27	0.56
1:A:93:LYS:HD2	1:A:97:GLU:CB	2.36	0.55
1:A:105:HIS:CE1	2:A:603:CPT:N1	2.75	0.55
1:A:348:ARG:HG3	1:A:482:VAL:HG22	1.89	0.55
1:A:378:LYS:N	1:A:379:PRO:HD2	2.23	0.54
1:A:67:HIS:HB3	1:A:95:GLU:CG	2.39	0.53
1:A:224:PRO:HD2	1:A:296:ASP:HB3	1.90	0.53
1:B:35:PRO:HB2	1:B:38:ASP:OD1	2.09	0.53
1:A:333:GLU:HB3	1:A:337:ARG:HH21	1.75	0.52
1:A:93:LYS:HD2	1:A:97:GLU:HB3	1.92	0.52
1:B:298:MET:O	2:B:601:CPT:N1	2.44	0.51
1:B:329:MET:CG	2:B:602:CPT:N2	2.72	0.51
1:A:417:GLN:HB2	1:A:470:SER:HB2	1.93	0.51
1:A:485:ARG:N	1:A:486:PRO:HD2	2.26	0.51
1:B:475:LYS:O	1:B:479:GLU:HB2	2.11	0.51
1:A:405:ASN:HA	1:A:408:LEU:HD12	1.92	0.50
1:B:426:VAL:HG21	1:B:460:LEU:HG	1.93	0.50
1:A:221:GLN:HE21	1:A:339:PRO:HA	1.76	0.50
1:A:94:GLN:HB2	1:A:96:PRO:HD2	1.94	0.50
1:B:156:PHE:HE1	1:B:285:GLU:HG3	1.77	0.49
1:A:415:VAL:HG11	1:A:473:VAL:HG23	1.94	0.49
1:A:307:ALA:HA	1:A:311:GLU:HB2	1.93	0.49
1:A:302:LEU:HD21	2:A:601:CPT:N2	2.28	0.48
1:B:155:LEU:HB3	1:B:284:LEU:HD21	1.96	0.48
1:B:27:PHE:HB3	1:B:39:HIS:ND1	2.27	0.48
1:B:329:MET:O	1:B:333:GLU:HG2	2.14	0.48
1:A:519:LYS:NZ	3:A:606:PO4:O3	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:PRO:CD	1:B:296:ASP:HB3	2.43	0.48
1:A:329:MET:O	1:A:333:GLU:HG2	2.14	0.47
1:A:27:PHE:HB3	1:A:39:HIS:ND1	2.30	0.47
1:A:30:TYR:CD2	1:A:102:PHE:HB3	2.50	0.47
1:B:383:GLU:HB3	1:B:384:PRO:HD3	1.96	0.47
1:A:120:VAL:HG21	1:A:175:ALA:HB2	1.97	0.47
1:A:365:ASP:OD2	1:A:368:GLU:HG2	2.14	0.46
1:A:310:VAL:HG23	1:A:370:TYR:HD1	1.80	0.46
1:A:151:ALA:N	1:A:152:PRO:HD2	2.31	0.46
1:A:323:LYS:O	1:A:327:LEU:HD12	2.17	0.46
1:A:408:LEU:HD21	1:A:424:VAL:HA	1.98	0.46
1:B:106:LYS:HD3	1:B:147:PRO:HB2	1.98	0.45
1:A:367:HIS:HA	1:A:370:TYR:CE1	2.51	0.45
1:A:105:HIS:HE1	2:A:603:CPT:N1	2.13	0.45
1:B:135:LEU:HD21	1:B:162:LYS:HB2	1.99	0.45
1:B:560:LYS:HD3	1:B:560:LYS:HA	1.71	0.45
1:B:98:ARG:HG2	1:B:102:PHE:CZ	2.51	0.45
1:B:133:THR:HG22	1:B:137:LYS:HD2	1.98	0.45
1:B:440:HIS:HB3	1:B:444:LYS:HB2	1.99	0.45
1:A:95:GLU:OE2	1:A:99:ASN:HB2	2.18	0.44
1:A:415:VAL:HG23	1:A:415:VAL:O	2.17	0.44
1:B:298:MET:HG3	2:B:601:CPT:N1	2.32	0.44
1:B:485:ARG:N	1:B:486:PRO:HD2	2.32	0.44
1:B:288:HIS:O	1:B:292:GLU:HG2	2.17	0.44
1:B:408:LEU:HD21	1:B:424:VAL:HA	2.00	0.44
1:A:5:SER:HB2	1:A:8:ALA:HB3	1.99	0.44
1:B:557:LYS:O	1:B:561:ALA:HB3	2.18	0.44
1:A:357:LEU:O	1:A:361:CYS:HB2	2.19	0.43
1:B:25:ILE:HD11	1:B:139:LEU:HD22	2.00	0.43
1:A:420:THR:N	1:A:421:PRO:CD	2.82	0.43
1:B:378:LYS:N	1:B:379:PRO:HD2	2.33	0.43
1:A:279:CYS:HA	1:A:286:LYS:HD2	2.01	0.42
1:A:95:GLU:N	1:A:96:PRO:CD	2.82	0.42
1:A:96:PRO:HG2	1:A:97:GLU:CD	2.39	0.42
1:A:413:LYS:HB3	1:A:493:VAL:HG13	2.02	0.42
1:B:405:ASN:HA	1:B:408:LEU:HD12	2.01	0.42
1:B:34:CYS:HA	1:B:35:PRO:HD3	1.90	0.41
1:B:214:TRP:HD1	1:B:343:VAL:HG11	1.85	0.41
1:A:93:LYS:HD2	1:A:97:GLU:HB2	2.01	0.41
1:B:119:GLU:HB2	1:B:122:VAL:HG23	2.03	0.41
1:A:333:GLU:OE1	1:A:336:ARG:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:VAL:HG23	1:B:415:VAL:O	2.21	0.40
1:A:29:GLN:HG2	1:A:147:PRO:HA	2.03	0.40
1:A:383:GLU:HB3	1:A:384:PRO:HD3	2.04	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	555/609 (91%)	530 (96%)	25 (4%)	0	100	100
1	B	555/609 (91%)	534 (96%)	21 (4%)	0	100	100
All	All	1110/1218 (91%)	1064 (96%)	46 (4%)	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	491/533 (92%)	475 (97%)	16 (3%)	38	72
1	B	494/533 (93%)	474 (96%)	20 (4%)	31	65
All	All	985/1066 (92%)	949 (96%)	36 (4%)	34	68

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	CYS
1	A	150	TYR
1	A	178	LEU
1	A	179	LEU
1	A	196	GLN
1	A	245	CYS
1	A	298	MET
1	A	305	LEU
1	A	315	VAL
1	A	370	TYR
1	A	400	GLU
1	A	446	MET
1	A	481	LEU
1	A	485	ARG
1	A	554	PHE
1	A	560	LYS
1	B	34	CYS
1	B	91	CYS
1	B	104	GLN
1	B	108	ASP
1	B	121	ASP
1	B	135	LEU
1	B	150	TYR
1	B	245	CYS
1	B	269	ASP
1	B	298	MET
1	B	301	ASP
1	B	314	ASP
1	B	324	ASP
1	B	337	ARG
1	B	375	ASP
1	B	387	LEU
1	B	435	SER
1	B	460	LEU
1	B	471	ASP
1	B	554	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	242	HIS
1	A	483	ASN

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Mol	Chain	Res	Type
1	B	33	GLN
1	B	204	GLN
1	B	221	GLN
1	B	247	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is modelled with single atom - leaving 11 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

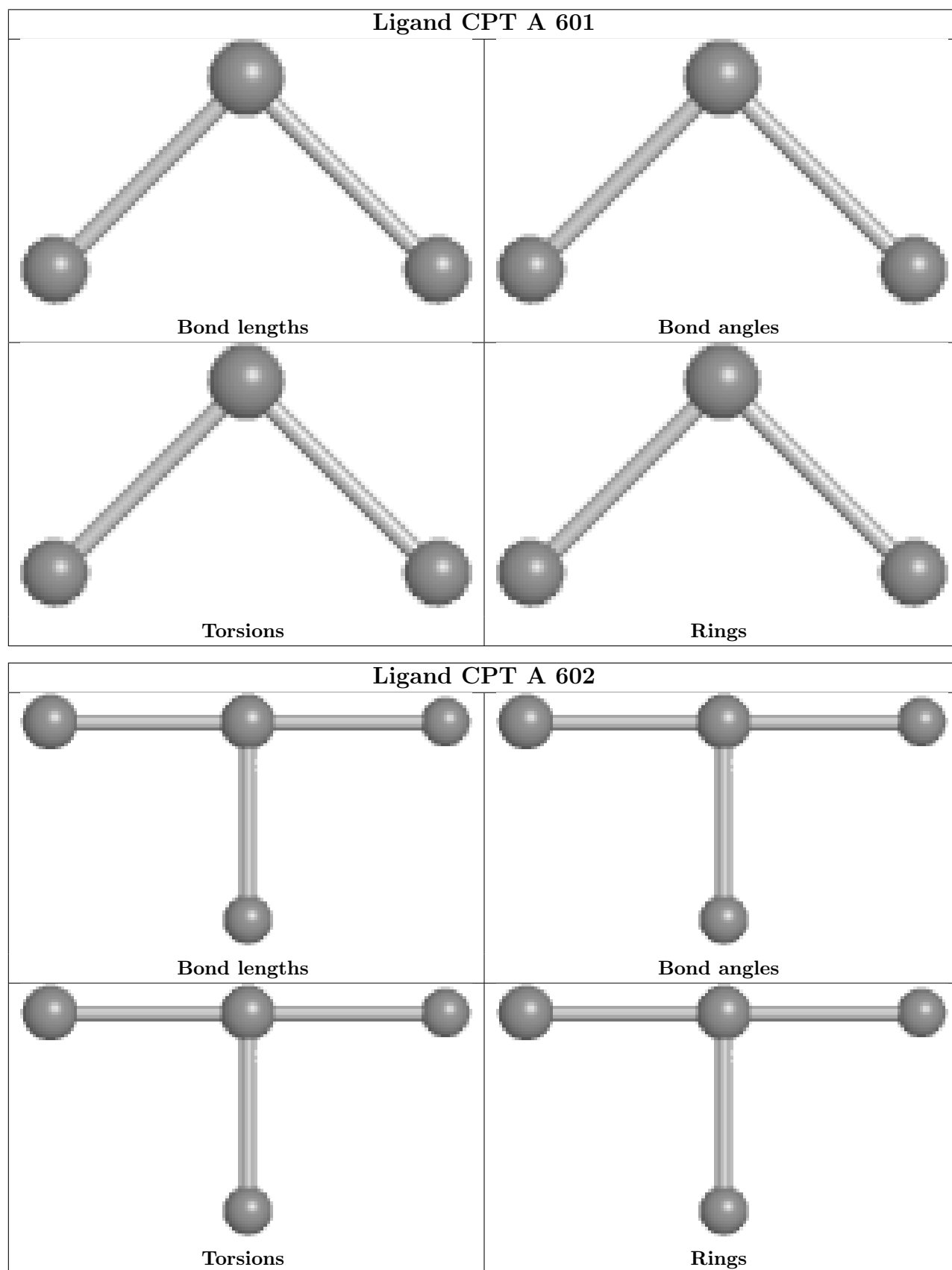
There are no torsion outliers.

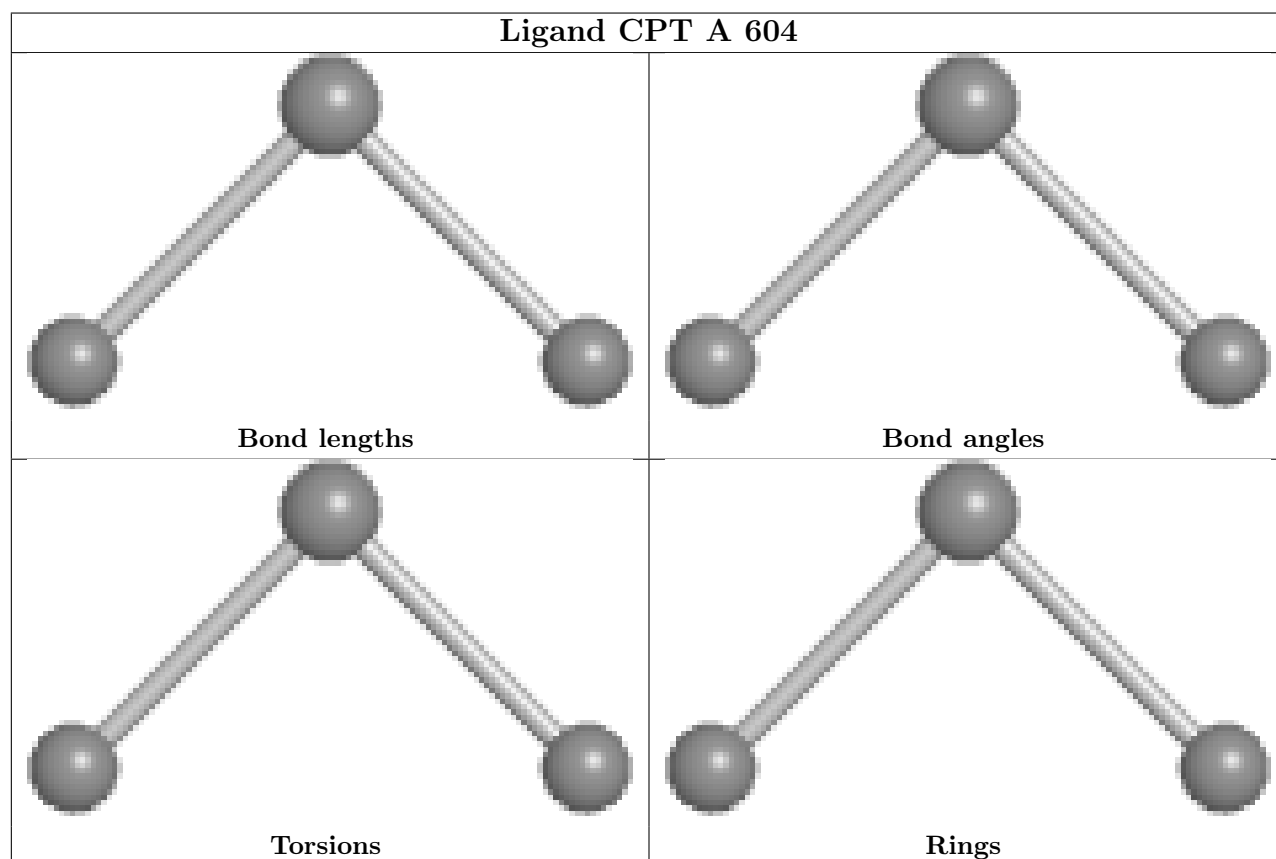
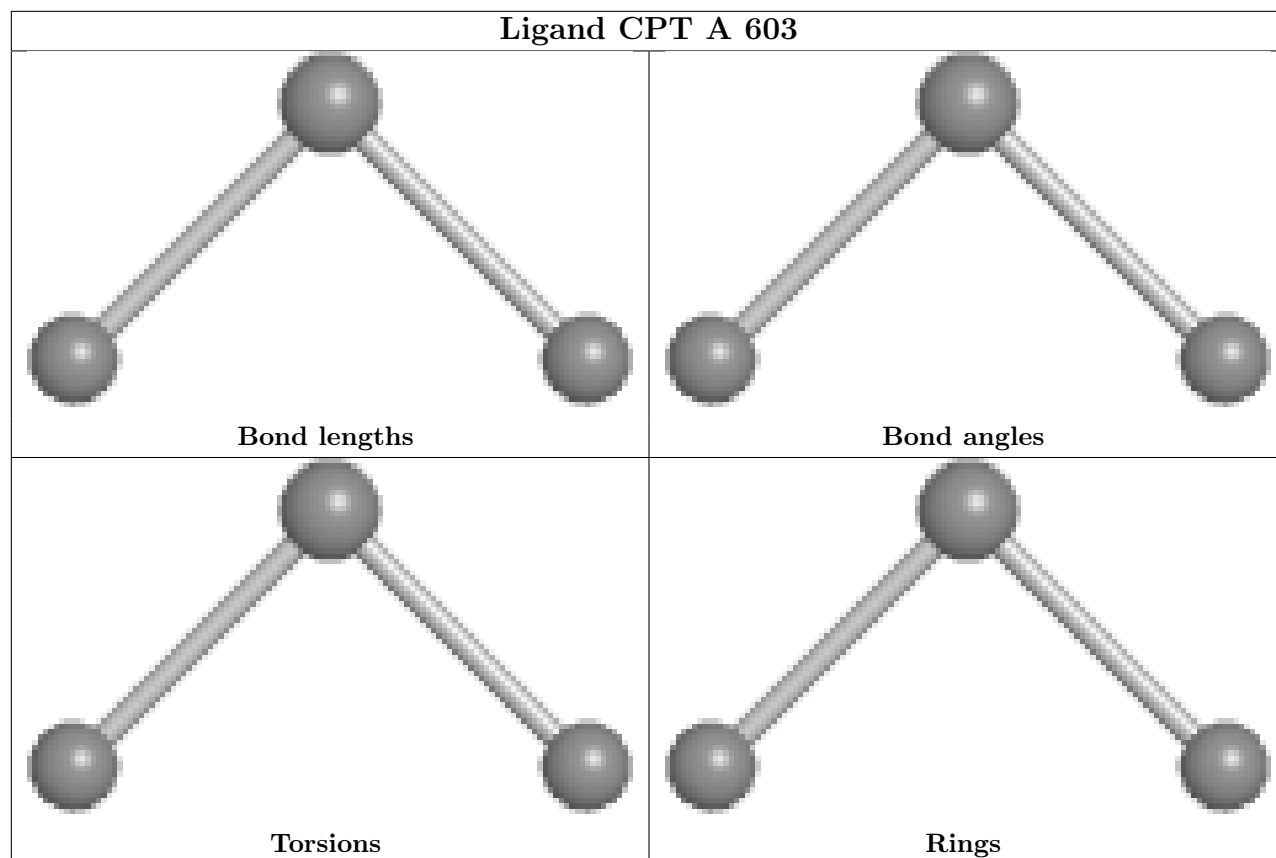
There are no ring outliers.

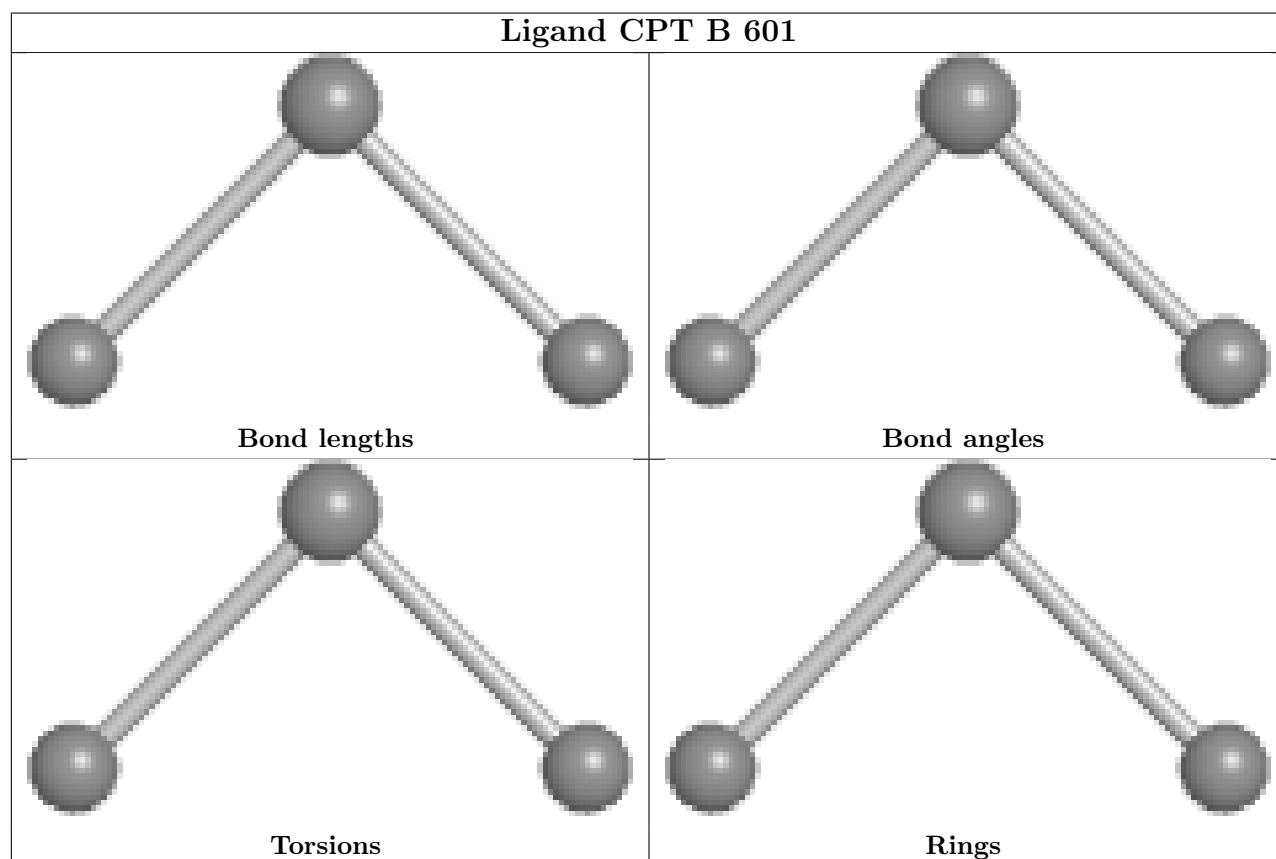
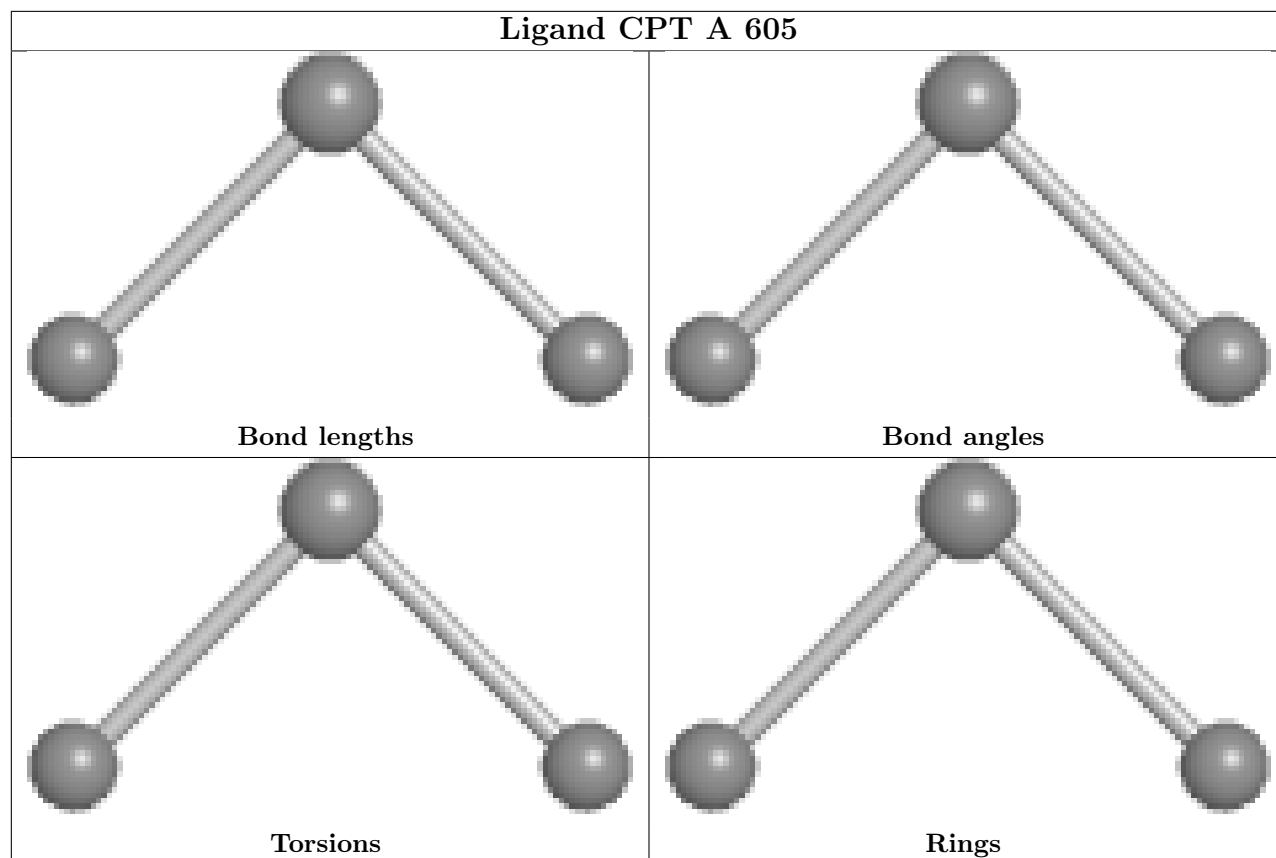
No monomer is involved in short contacts.

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.

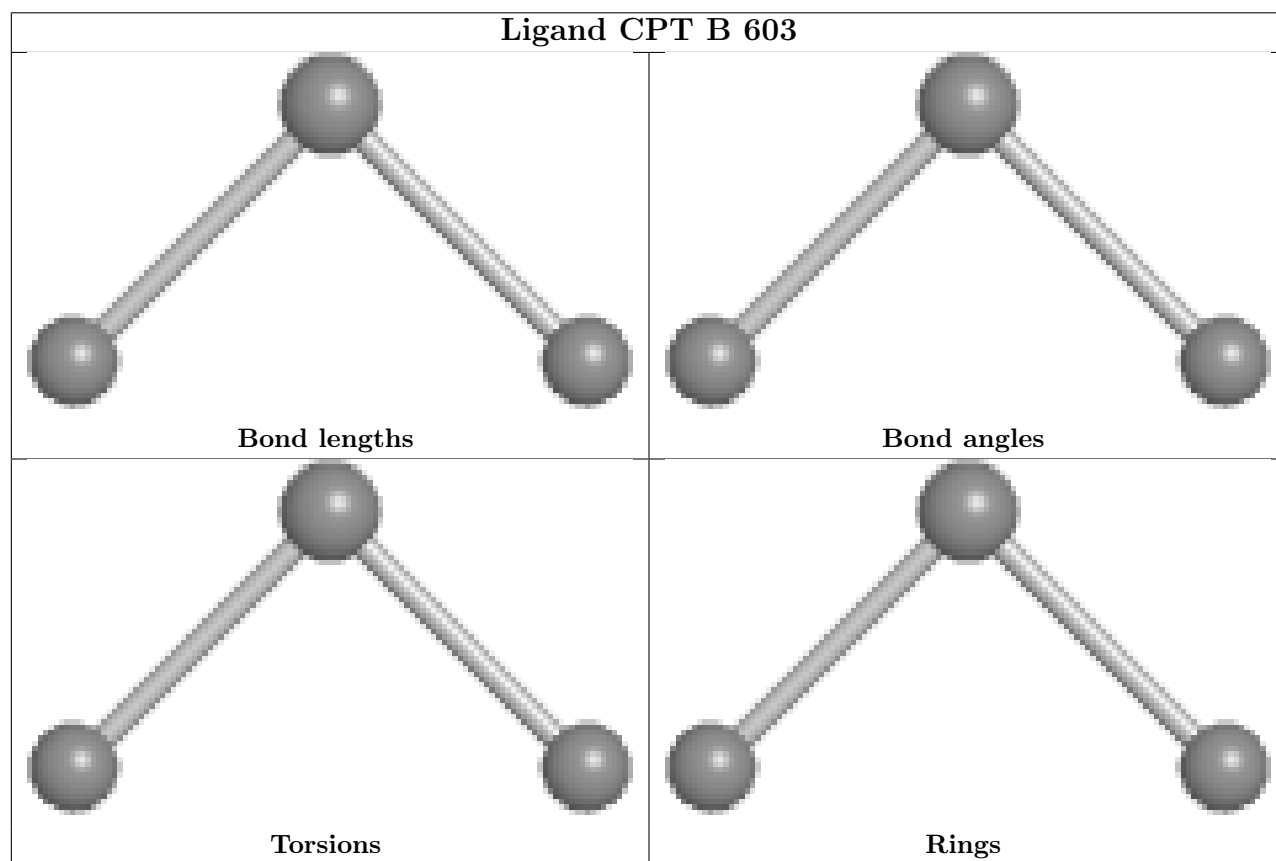
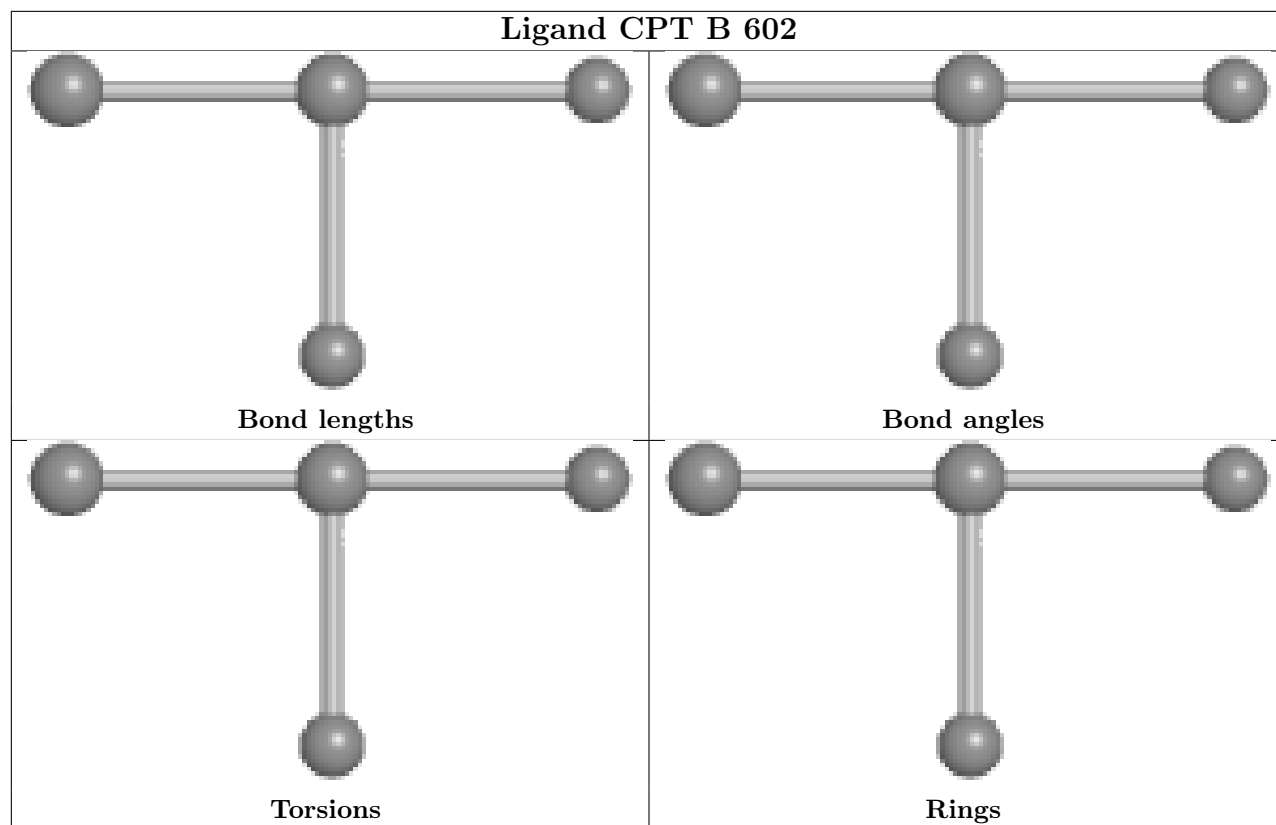
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

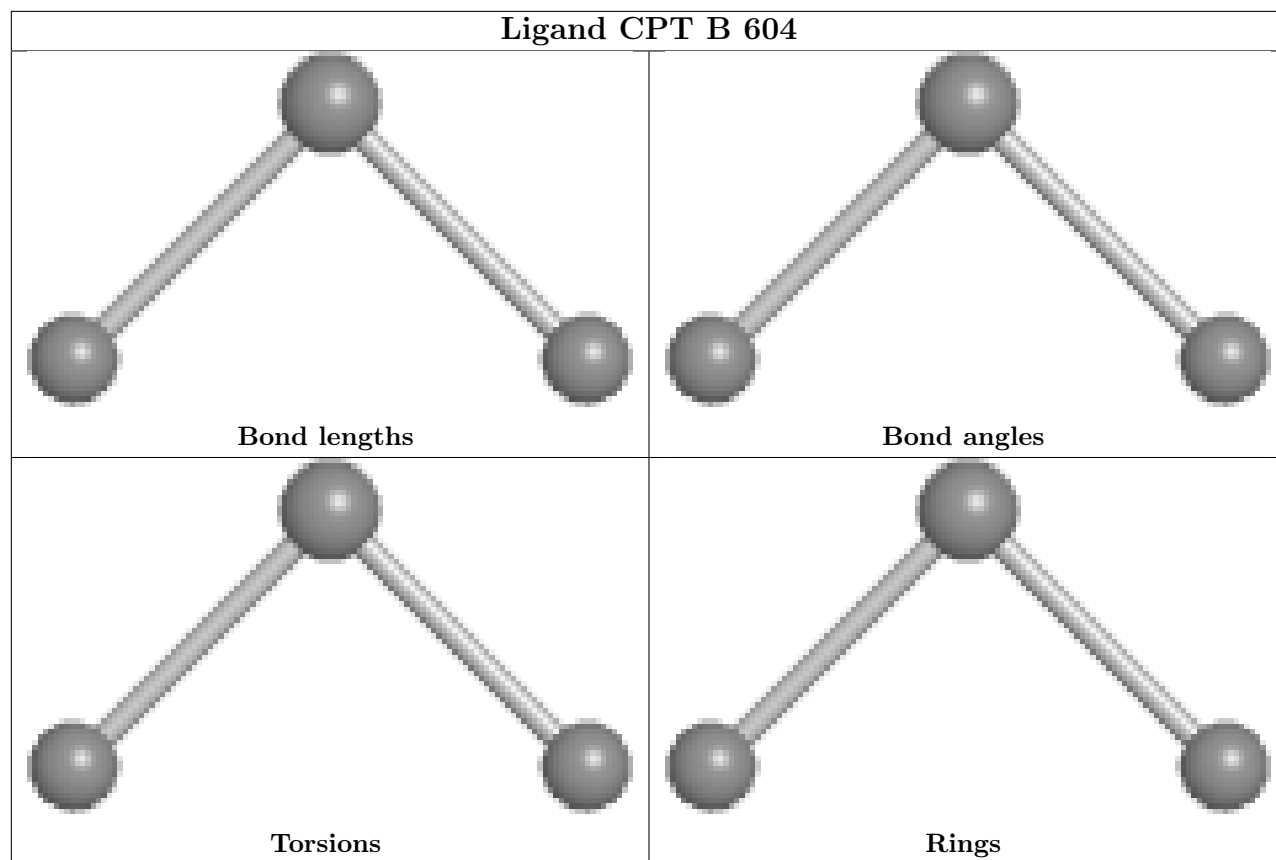












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	559/609 (91%)	-0.01	19 (3%)	45 40	69, 121, 180, 222	0
1	B	559/609 (91%)	0.03	24 (4%)	35 31	76, 121, 177, 241	0
All	All	1118/1218 (91%)	0.01	43 (3%)	40 36	69, 121, 179, 241	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	309	PHE	4.3
1	A	555	VAL	4.3
1	A	43	VAL	4.2
1	A	562	ASP	3.9
1	A	301	ASP	3.8
1	A	299	PRO	3.4
1	A	356	THR	3.4
1	B	398	LEU	3.2
1	A	353	TYR	3.1
1	B	97	GLU	3.1
1	A	359	LYS	3.1
1	A	398	LEU	3.0
1	A	357	LEU	3.0
1	B	94	GLN	3.0
1	B	551	PHE	2.7
1	B	544	LEU	2.7
1	B	359	LYS	2.6
1	A	74	LEU	2.6
1	A	42	LEU	2.6
1	A	95	GLU	2.5
1	B	509	PHE	2.5
1	A	559	CYS	2.5
1	B	117	ARG	2.4
1	B	70	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	300	ALA	2.3
1	B	54	VAL	2.3
1	B	341	TYR	2.3
1	B	357	LEU	2.3
1	B	98	ARG	2.3
1	B	90	CYS	2.3
1	A	515	THR	2.3
1	B	507	PHE	2.2
1	A	395	PHE	2.2
1	B	512	ASP	2.2
1	A	569	ALA	2.2
1	B	353	TYR	2.2
1	B	369	CYS	2.1
1	B	319	TYR	2.1
1	B	74	LEU	2.1
1	B	102	PHE	2.1
1	B	10	ARG	2.1
1	A	6	GLU	2.1
1	B	401	TYR	2.1

## 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.

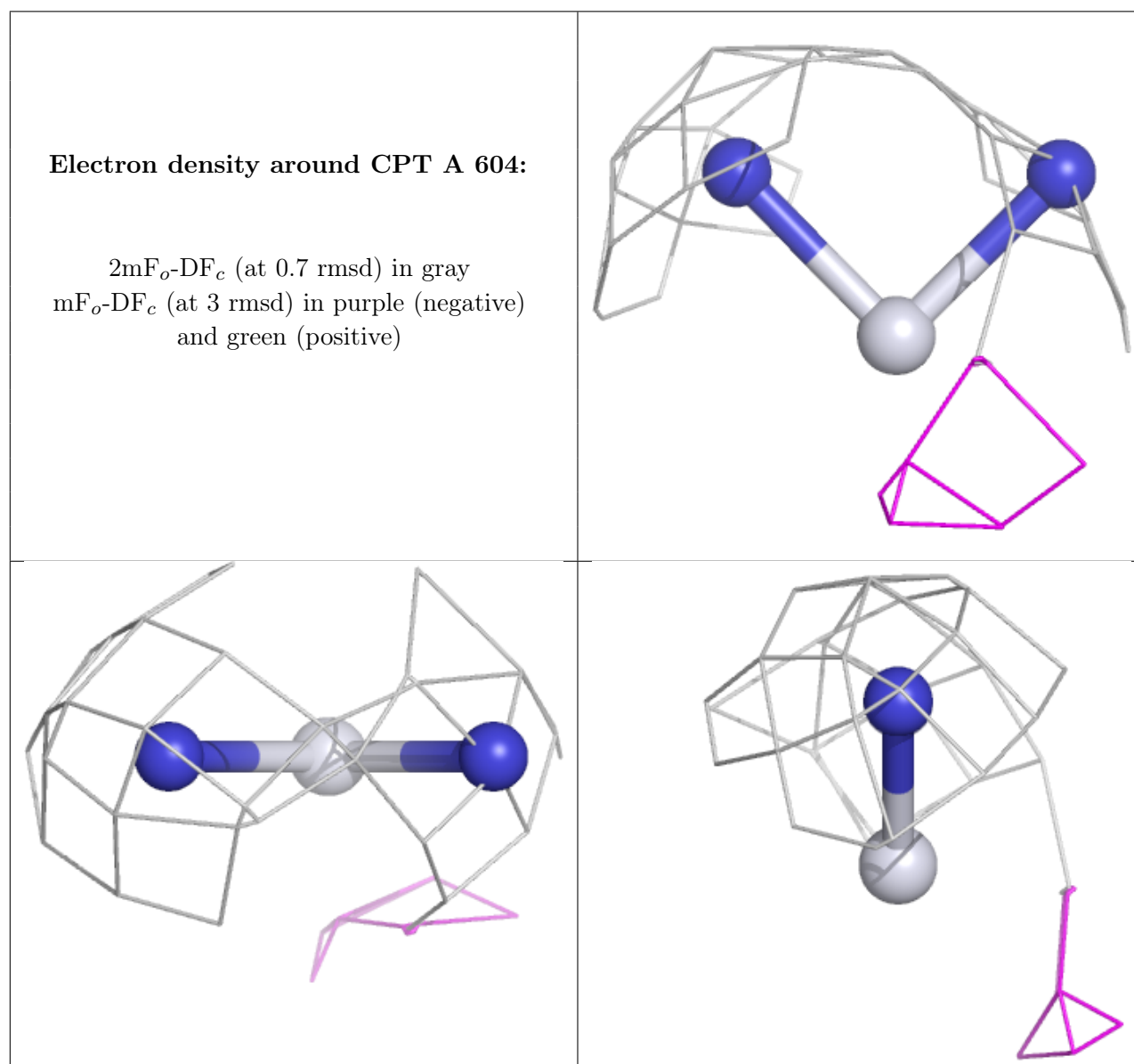
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	CPT	A	604	3/5	0.88	0.25	90,90,97,130	3
3	PO4	A	606	5/5	0.88	0.27	42,45,49,62	5
2	CPT	B	605	1/5	0.90	0.04	121,121,121,121	1
2	CPT	B	604	3/5	0.91	0.20	104,104,119,128	3

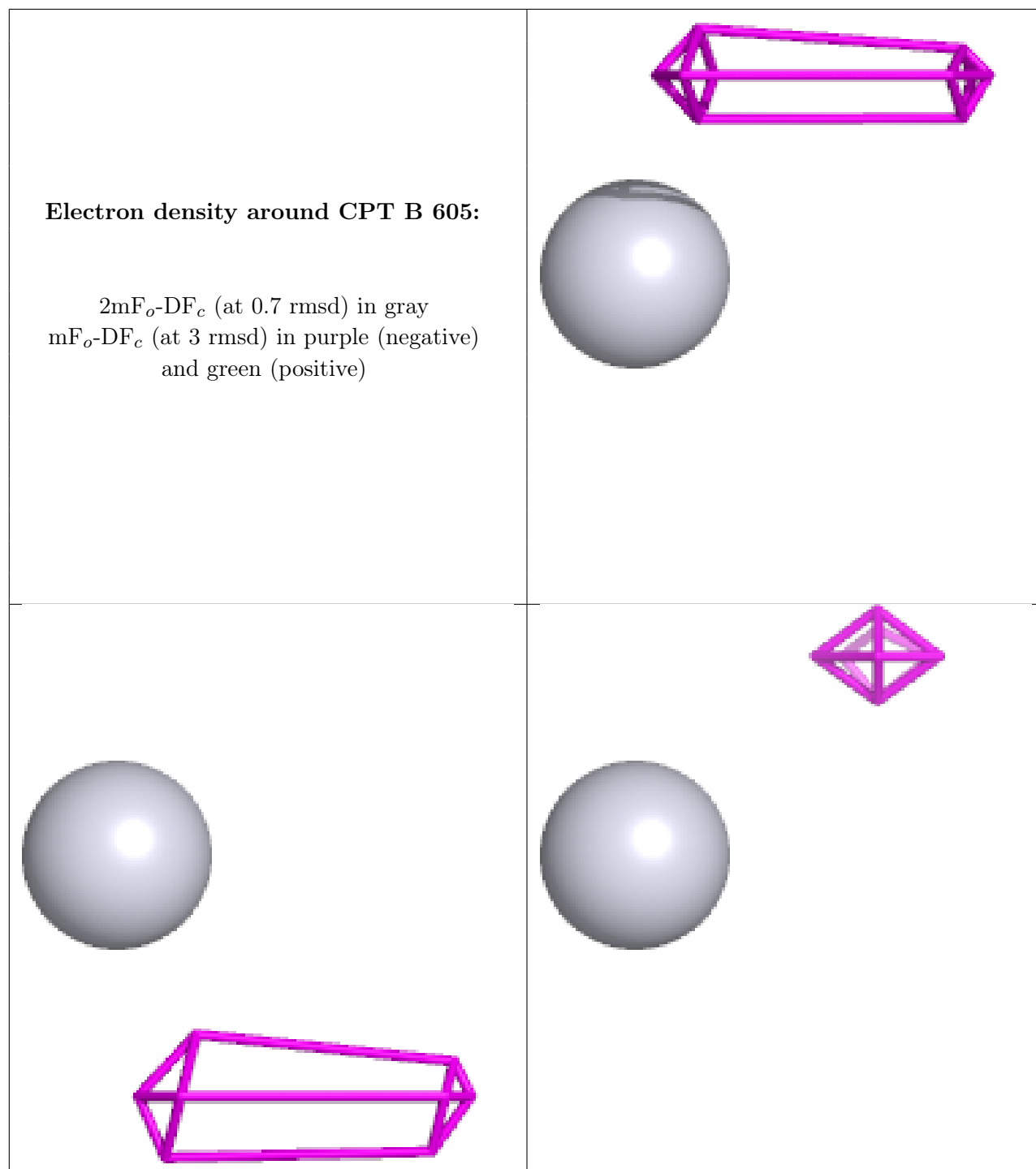
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	PO4	B	606	5/5	0.91	0.20	43,48,53,55	5
2	CPT	A	605	3/5	0.93	0.17	87,87,140,146	3
2	CPT	B	601	3/5	0.96	0.19	90,90,151,176	3
2	CPT	A	601	3/5	0.97	0.15	146,146,159,184	3
2	CPT	B	603	3/5	0.97	0.24	108,108,142,161	3
2	CPT	A	603	3/5	0.97	0.24	94,94,143,157	3
2	CPT	B	602	4/5	0.99	0.17	92,120,132,139	4
2	CPT	A	602	4/5	0.99	0.15	88,108,111,139	4

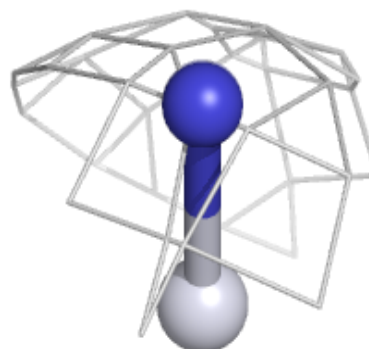
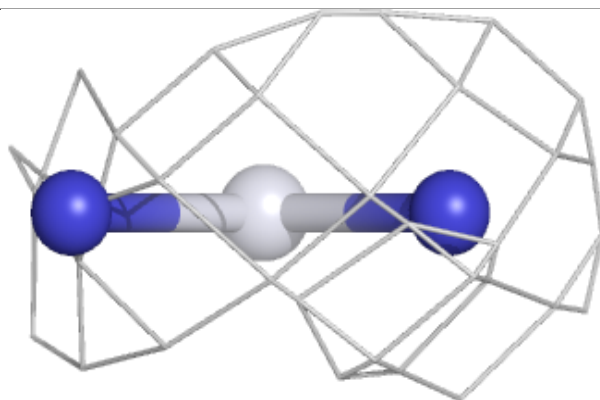
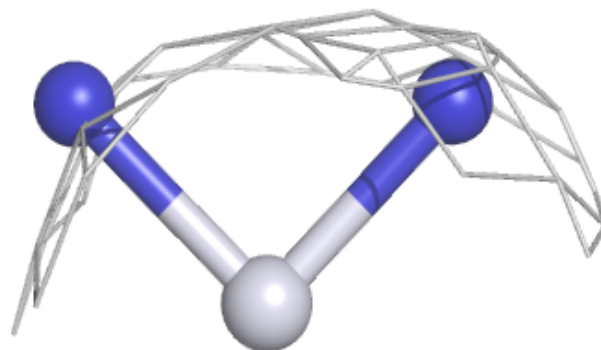
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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





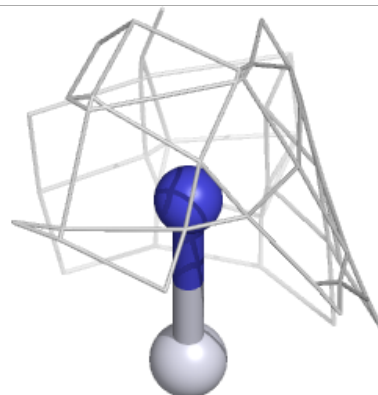
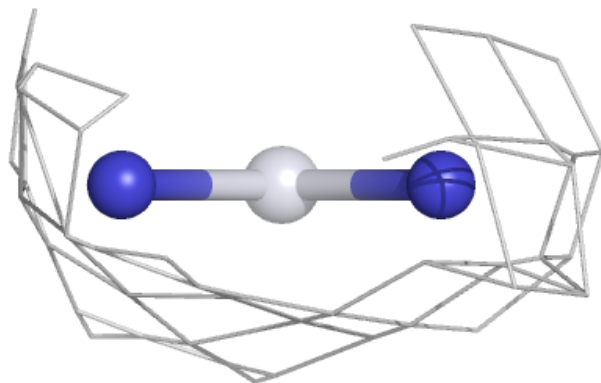
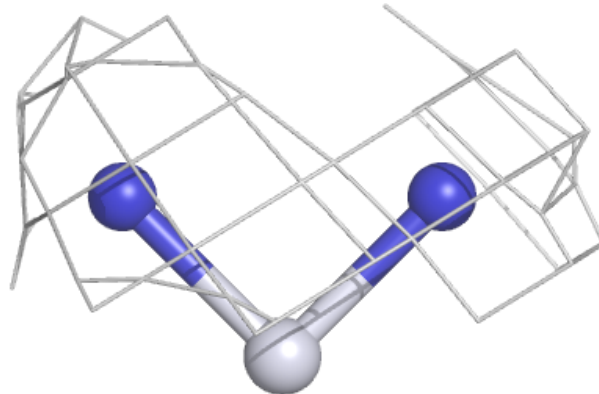
**Electron density around CPT B 604:**

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



**Electron density around CPT A 605:**

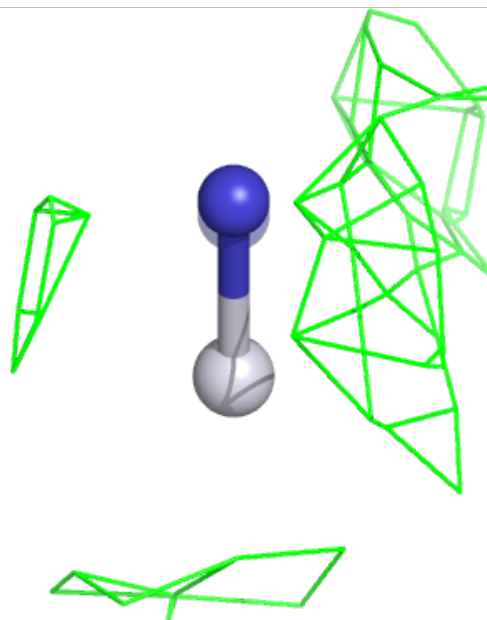
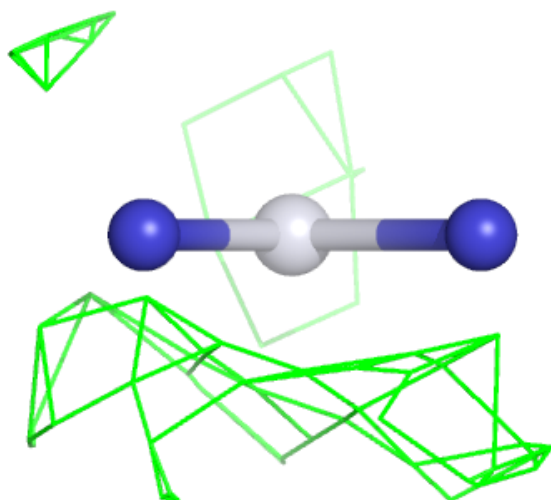
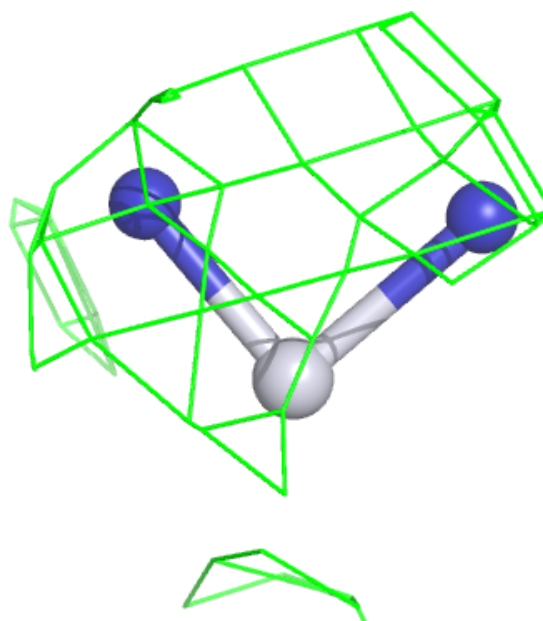
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





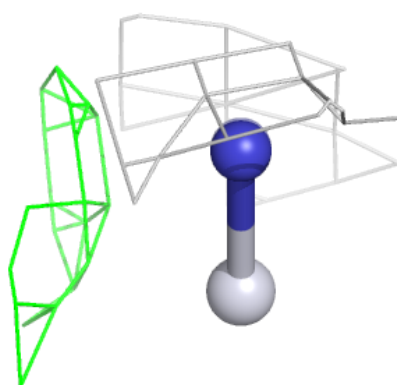
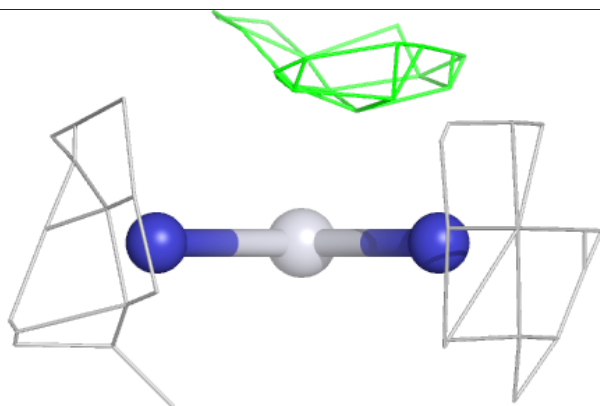
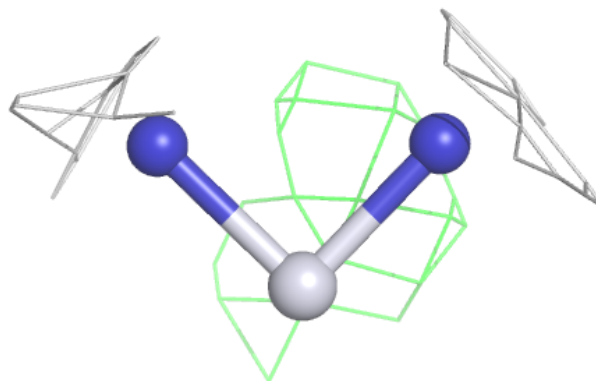
**Electron density around CPT B 601:**

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

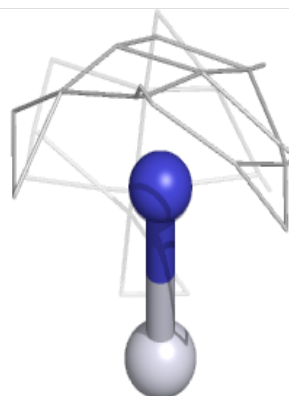
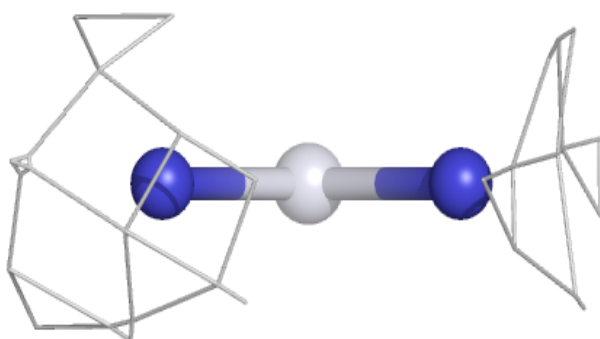
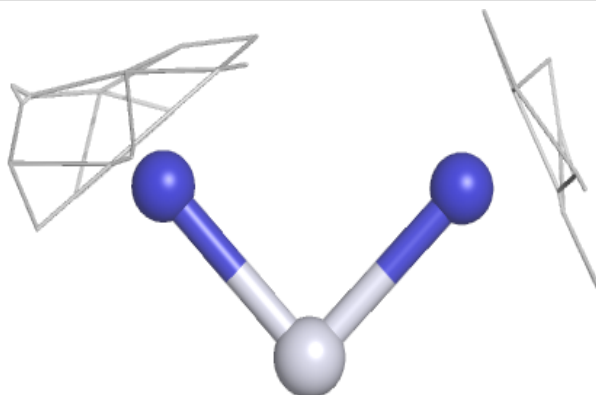


**Electron density around CPT A 601:**

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

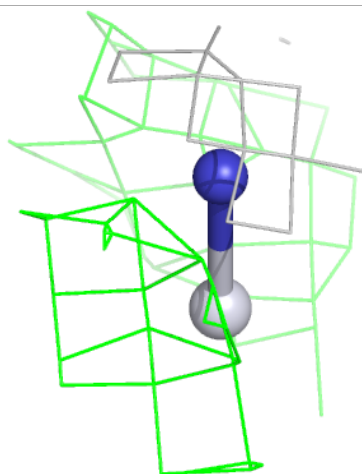
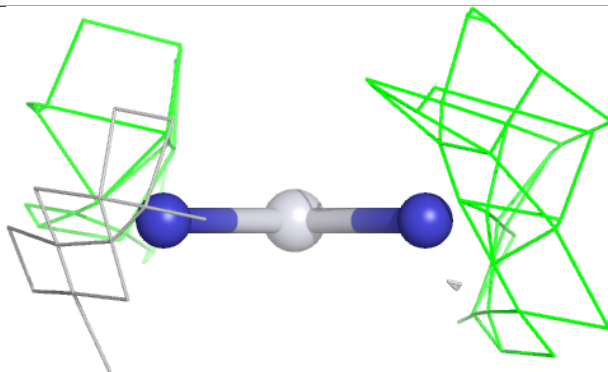
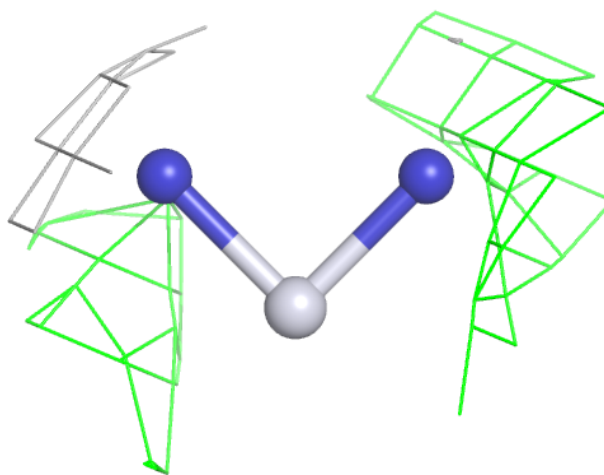
**Electron density around CPT B 603:**

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



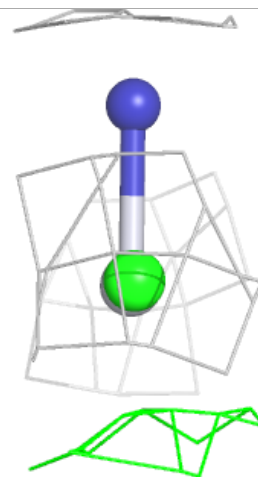
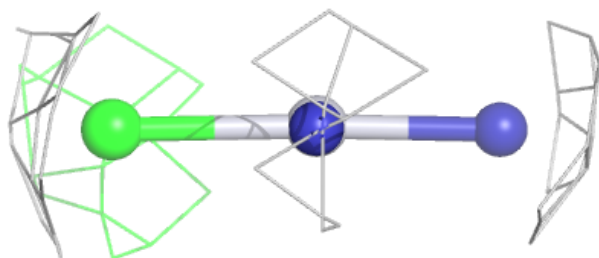
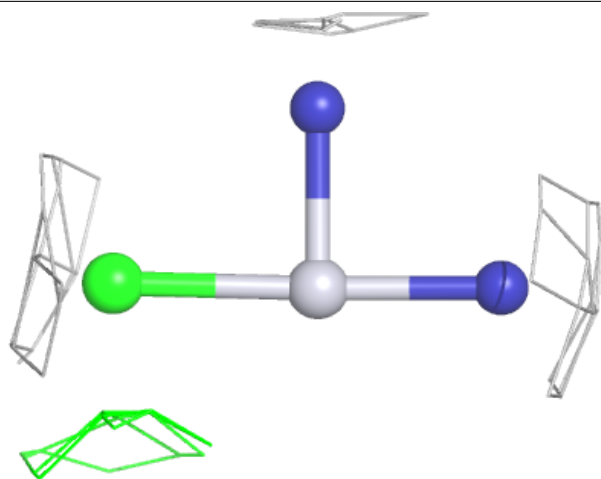
**Electron density around CPT A 603:**

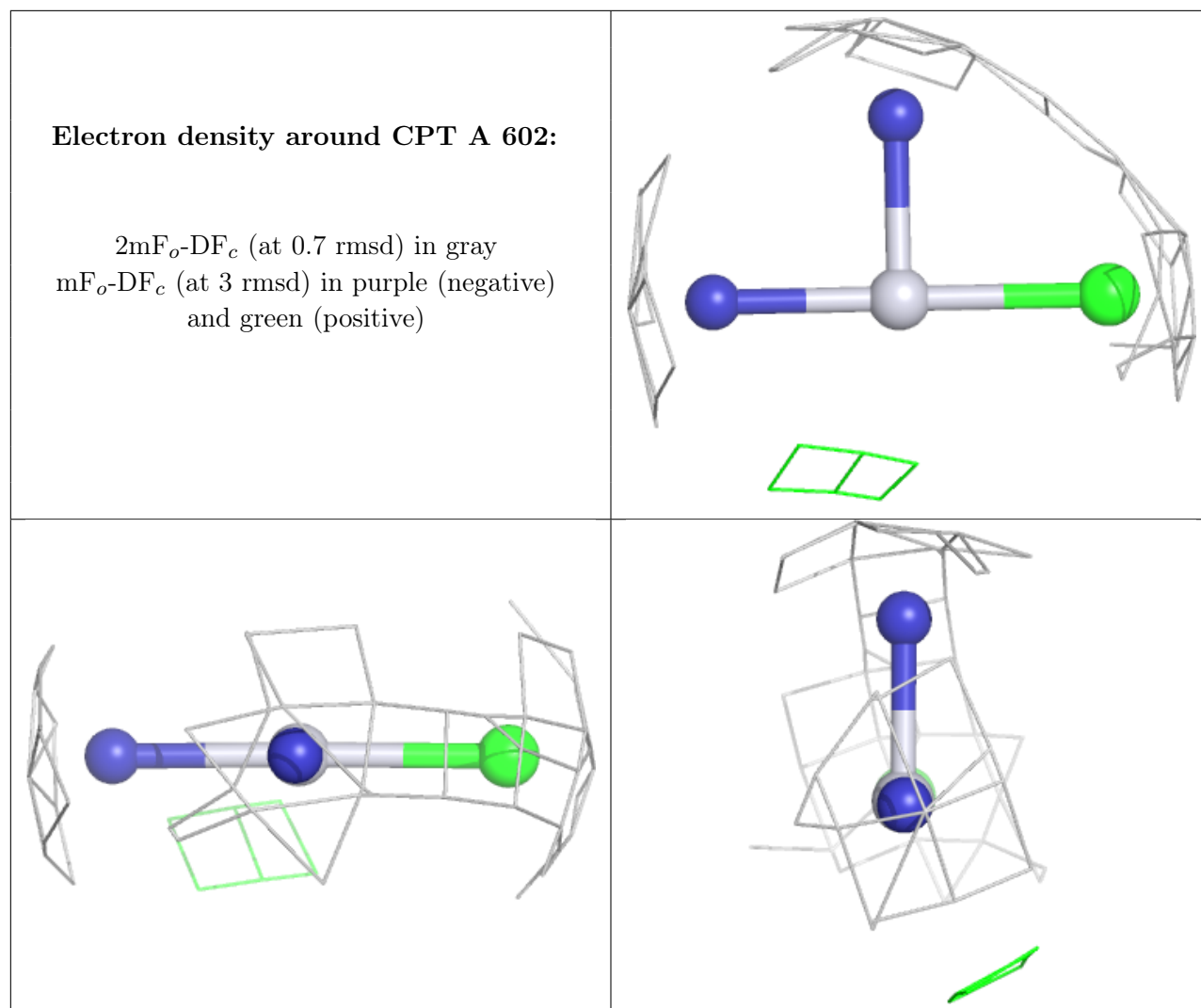
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CPT B 602:**

$2mF_o-DF_c$  (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.