



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 19, 2022 – 06:57 AM JST

PDB ID : 7WOJ  
Title : Crystal structure of HSA-Myr complex 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 : 2.89 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

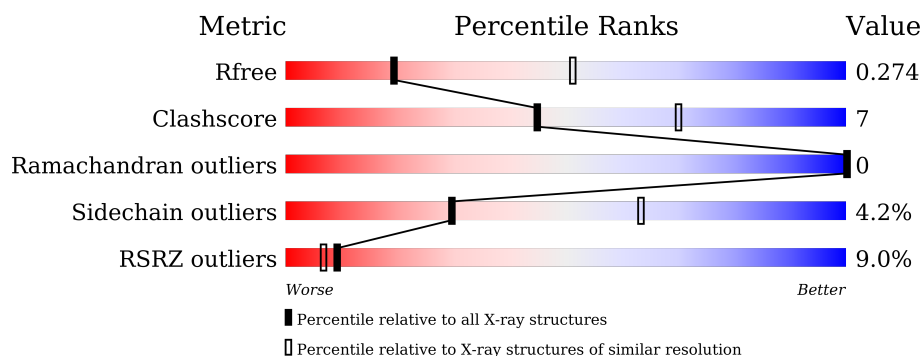
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.89 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>8%</div> <div>77%</div> <div>16%</div> <div>7%</div> </div>

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
3	MYR	A	610	-	-	-	X
3	MYR	A	613	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MYR	A	614	-	-	-	X

## 2 Entry composition [i](#)

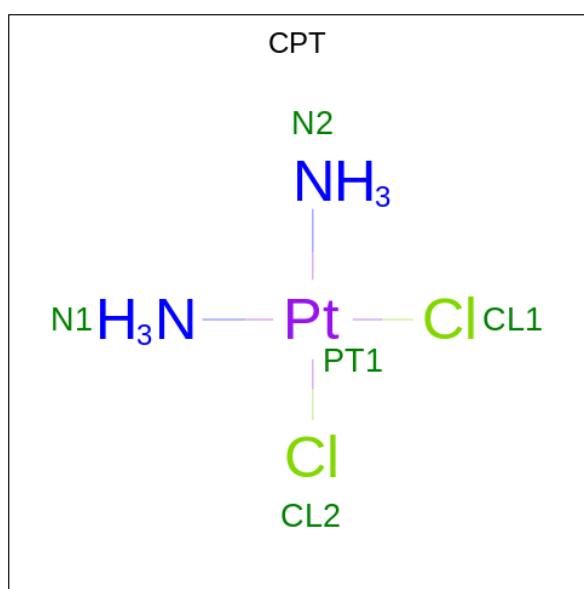
There are 3 unique types of molecules in this entry. The entry contains 4478 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	567	Total	C	N	O	S	0	0	0
			4360	2753	747	820	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).



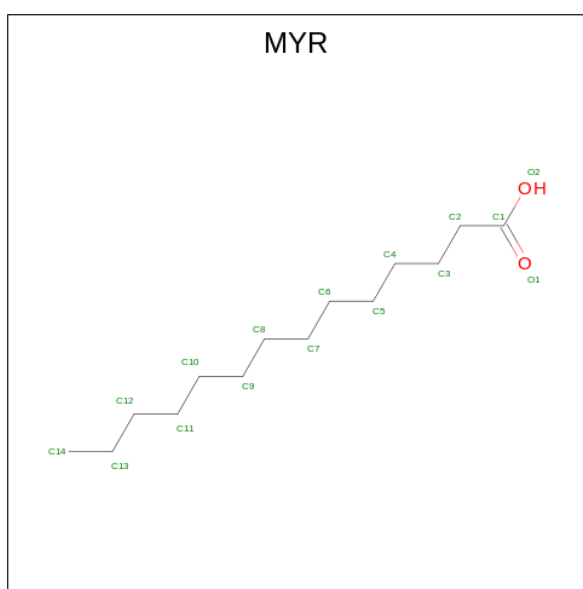
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	Cl	N	Pt	0	0
			4	1	2	1		
2	A	1	Total	Cl	N	Pt	0	0
			4	1	2	1		
2	A	1	Total	N	Pt		0	0
			3	2	1			
2	A	1	Total	Cl	N	Pt	0	0
			4	1	2	1		
2	A	1	Total	N	Pt		0	0
			3	2	1			

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

- Molecule 3 is MYRISTIC ACID (three-letter code: MYR) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>2</sub>).

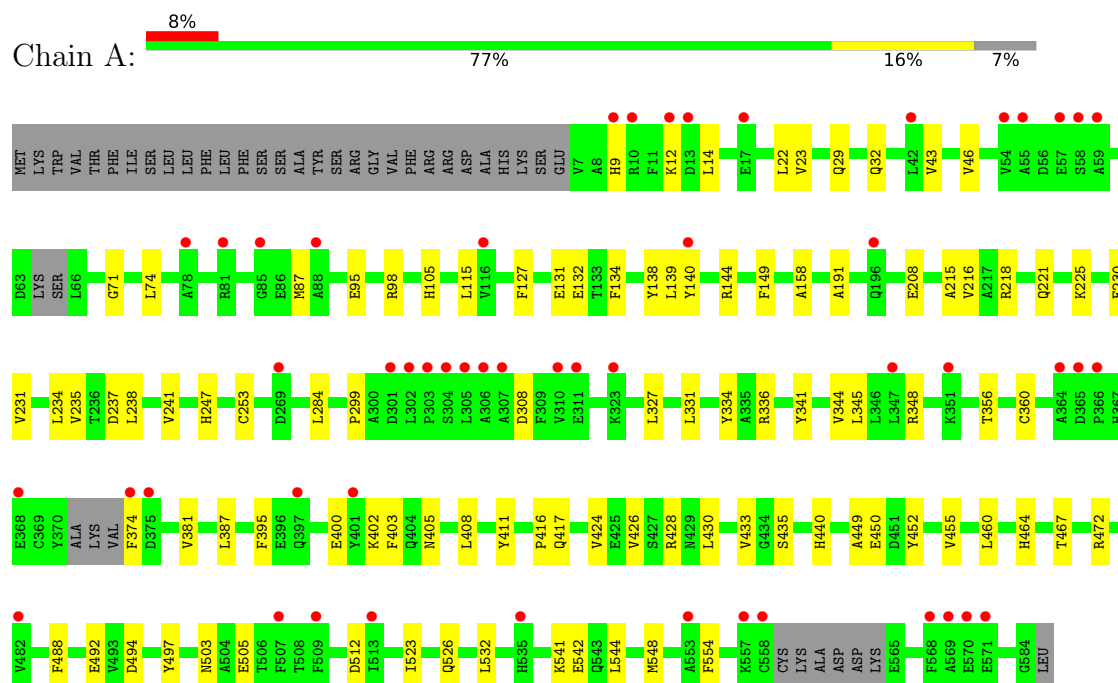


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	12	2		
3	A	1	Total	C	O	0	0
			13	11	2		
3	A	1	Total	C	O	0	0
			13	11	2		
3	A	1	Total	C	O	0	0
			16	14	2		
3	A	1	Total	C	O	0	0
			16	14	2		
3	A	1	Total	C	O	0	0
			16	14	2		

### 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



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.91Å 36.69Å 90.01Å 90.00° 105.41° 90.00°	Depositor
Resolution (Å)	43.41 – 2.89 43.41 – 2.89	Depositor EDS
% Data completeness (in resolution range)	86.6 (43.41-2.89) 86.6 (43.41-2.89)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.89 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.258 , 0.284 0.253 , 0.274	Depositor DCC
$R_{free}$ test set	562 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.9	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 35.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4478	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% 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: MYR, 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	0.79	0/4443	1.06	0/5997

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	4360	0	4147	57	0
2	A	30	0	0	0	0
3	A	88	0	137	8	0
All	All	4478	0	4284	57	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 7.

All (57) 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:327:LEU:HB3	3:A:614:MYR:H81	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ARG:HG2	3:A:615:MYR:H41	1.76	0.66
1:A:408:LEU:HD21	1:A:526:GLN:O	2.04	0.58
1:A:472:ARG:NH2	1:A:492:GLU:O	2.36	0.58
1:A:131:GLU:HG3	1:A:132:GLU:N	2.19	0.57
1:A:215:ALA:HB3	1:A:235:VAL:HG13	1.86	0.55
1:A:9:HIS:HA	1:A:12:LYS:HE2	1.89	0.54
1:A:14:LEU:HD13	1:A:22:LEU:HD12	1.88	0.54
1:A:449:ALA:O	1:A:450:GLU:C	2.45	0.54
1:A:532:LEU:HD13	3:A:613:MYR:H131	1.90	0.53
1:A:238:LEU:O	1:A:241:VAL:HG22	2.08	0.53
1:A:95:GLU:HA	1:A:98:ARG:HB3	1.91	0.52
1:A:127:PHE:O	1:A:131:GLU:HB3	2.10	0.52
1:A:131:GLU:HG3	1:A:132:GLU:H	1.75	0.52
1:A:402:LYS:HA	1:A:405:ASN:HD22	1.75	0.52
1:A:216:VAL:CG2	1:A:235:VAL:HG21	2.40	0.52
1:A:23:VAL:HG21	1:A:46:VAL:HG11	1.92	0.51
1:A:231:VAL:O	1:A:235:VAL:HG23	2.12	0.49
1:A:139:LEU:HD13	1:A:158:ALA:HB2	1.95	0.49
1:A:237:ASP:O	1:A:241:VAL:HG13	2.13	0.49
1:A:216:VAL:HG22	1:A:235:VAL:HG21	1.95	0.49
1:A:426:VAL:HG21	1:A:460:LEU:HD13	1.96	0.48
1:A:395:PHE:CE2	1:A:400:GLU:HA	2.48	0.47
1:A:411:TYR:OH	3:A:612:MYR:O1	2.32	0.47
1:A:345:LEU:HD21	1:A:381:VAL:HA	1.97	0.47
1:A:433:VAL:HG22	1:A:452:TYR:HB3	1.97	0.47
1:A:139:LEU:HA	3:A:610:MYR:H111	1.96	0.47
1:A:14:LEU:HD22	1:A:284:LEU:HD13	1.97	0.46
1:A:416:PRO:HG2	1:A:497:TYR:CG	2.50	0.46
1:A:488:PHE:HB3	3:A:612:MYR:H51	1.98	0.46
1:A:344:VAL:O	1:A:348:ARG:HG3	2.16	0.46
1:A:115:LEU:HD23	1:A:115:LEU:HA	1.84	0.45
1:A:225:LYS:HG2	1:A:299:PRO:HG3	1.99	0.45
1:A:417:GLN:NE2	1:A:494:ASP:OD2	2.48	0.45
1:A:395:PHE:HD2	1:A:403:PHE:CD2	2.35	0.45
1:A:71:GLY:HA2	1:A:74:LEU:HD12	1.98	0.44
1:A:87:MET:HA	1:A:105:HIS:CD2	2.52	0.44
1:A:221:GLN:NE2	1:A:341:TYR:O	2.47	0.44
1:A:230:GLU:O	1:A:234:LEU:HG	2.17	0.44
1:A:238:LEU:HD11	3:A:615:MYR:O2	2.18	0.44
1:A:395:PHE:CZ	1:A:435:SER:HA	2.53	0.44
1:A:23:VAL:HG13	1:A:43:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:MET:HG2	3:A:613:MYR:H62	2.01	0.43
1:A:29:GLN:NE2	1:A:149:PHE:O	2.44	0.42
1:A:428:ARG:HD2	1:A:523:ILE:HG12	1.99	0.42
1:A:22:LEU:HD23	1:A:22:LEU:HA	1.81	0.42
1:A:87:MET:HG3	1:A:105:HIS:HB2	2.01	0.42
1:A:408:LEU:HD11	1:A:424:VAL:HA	2.01	0.42
1:A:134:PHE:O	1:A:138:TYR:HD1	2.02	0.42
1:A:32:GLN:NE2	1:A:144:ARG:O	2.50	0.41
1:A:216:VAL:HG23	1:A:235:VAL:HG11	2.02	0.41
1:A:544:LEU:HD23	1:A:544:LEU:HA	1.97	0.41
1:A:216:VAL:HA	1:A:235:VAL:HG21	2.02	0.41
1:A:356:THR:O	1:A:360:CYS:N	2.50	0.41
1:A:191:ALA:HA	1:A:455:VAL:HG11	2.03	0.41
1:A:416:PRO:HB2	1:A:497:TYR:CZ	2.56	0.41
1:A:430:LEU:HD23	1:A:430:LEU:HA	1.90	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	559/609 (92%)	535 (96%)	24 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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	455/533 (85%)	436 (96%)	19 (4%)	30 63

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	TYR
1	A	208	GLU
1	A	247	HIS
1	A	253	CYS
1	A	308	ASP
1	A	331	LEU
1	A	334	TYR
1	A	336	ARG
1	A	374	PHE
1	A	387	LEU
1	A	440	HIS
1	A	464	HIS
1	A	467	THR
1	A	503	ASN
1	A	505	GLU
1	A	512	ASP
1	A	541	LYS
1	A	542	GLU
1	A	554	PHE

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	268	GLN
1	A	464	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

15 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

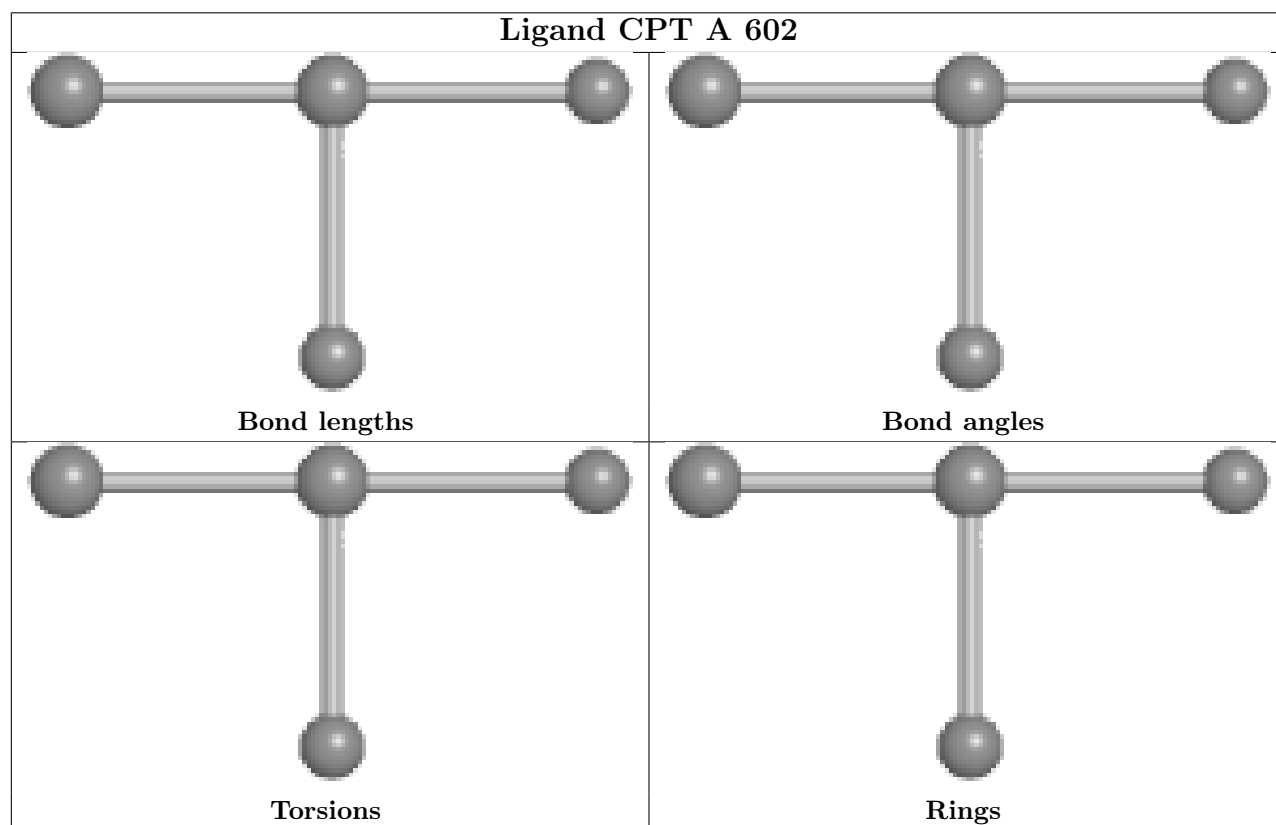
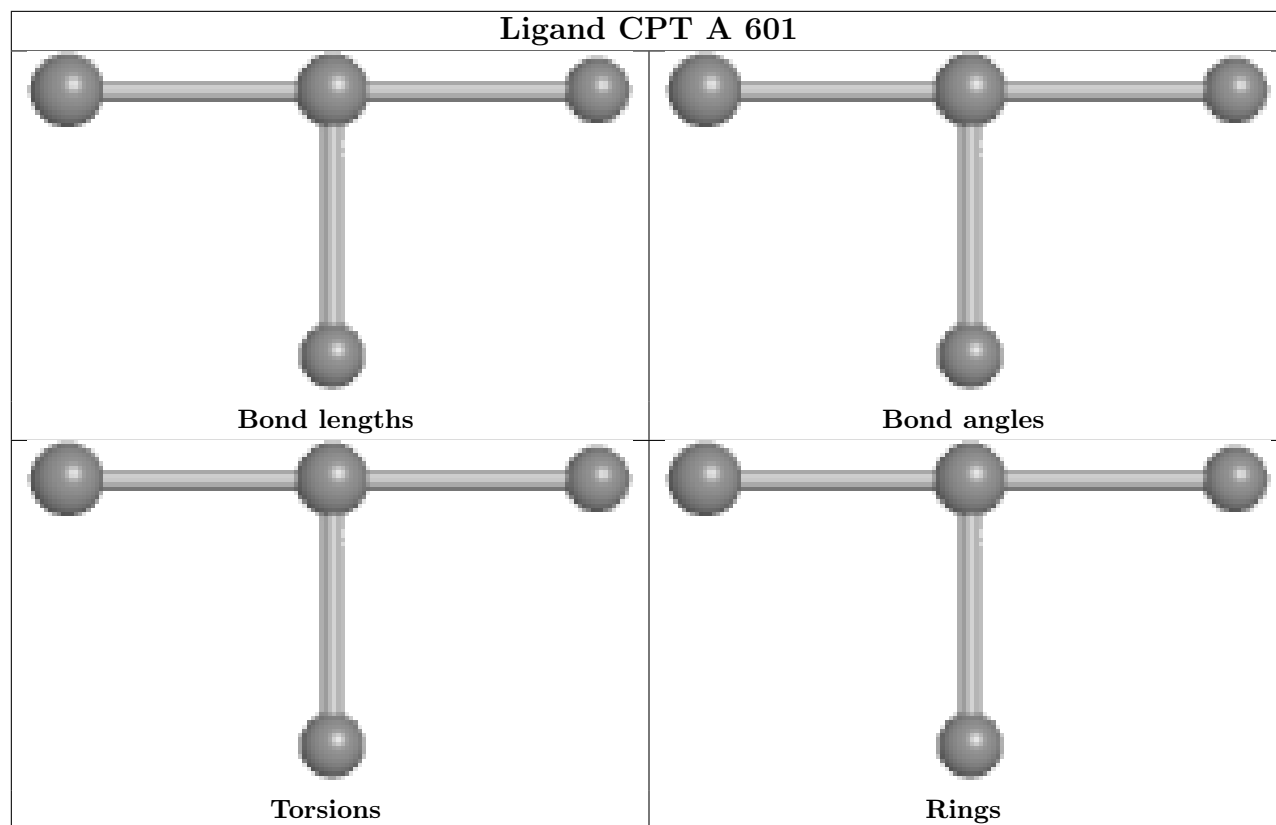
There are no chirality outliers.

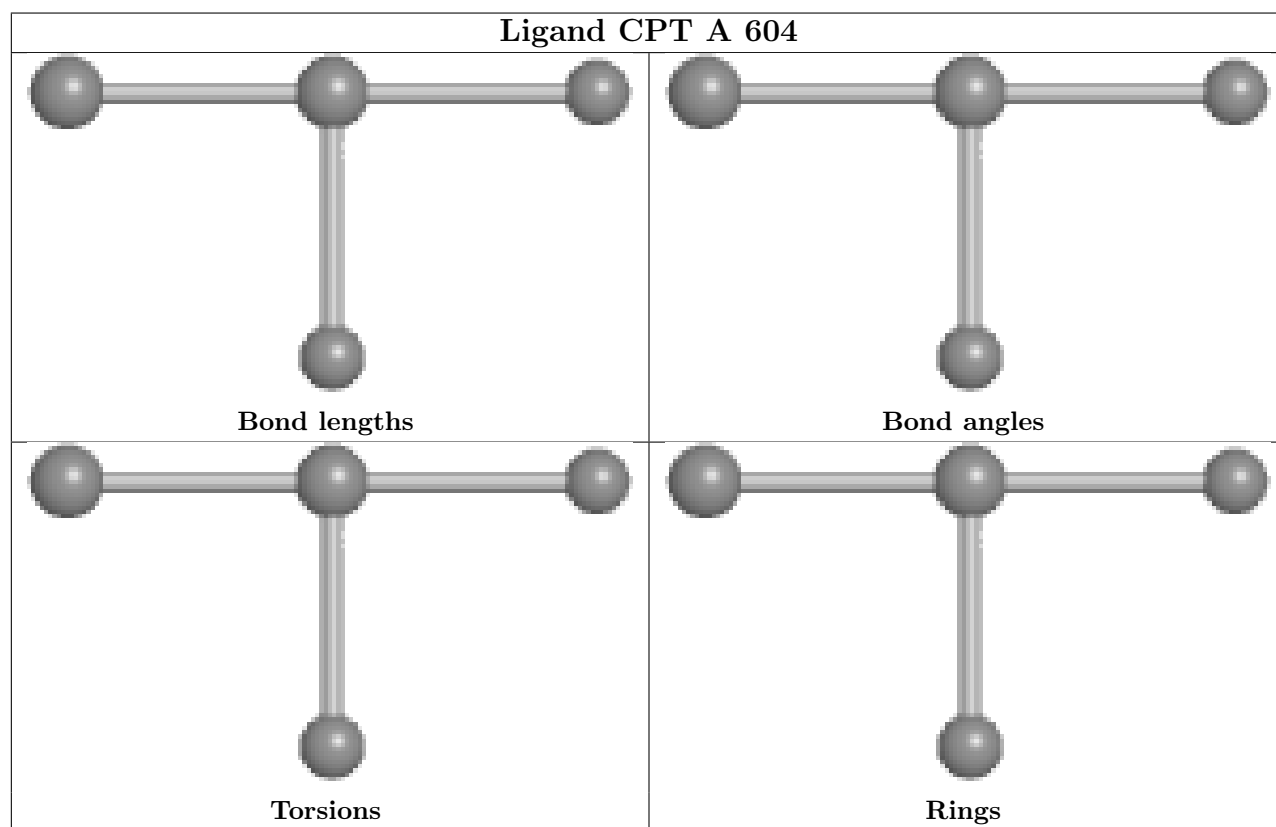
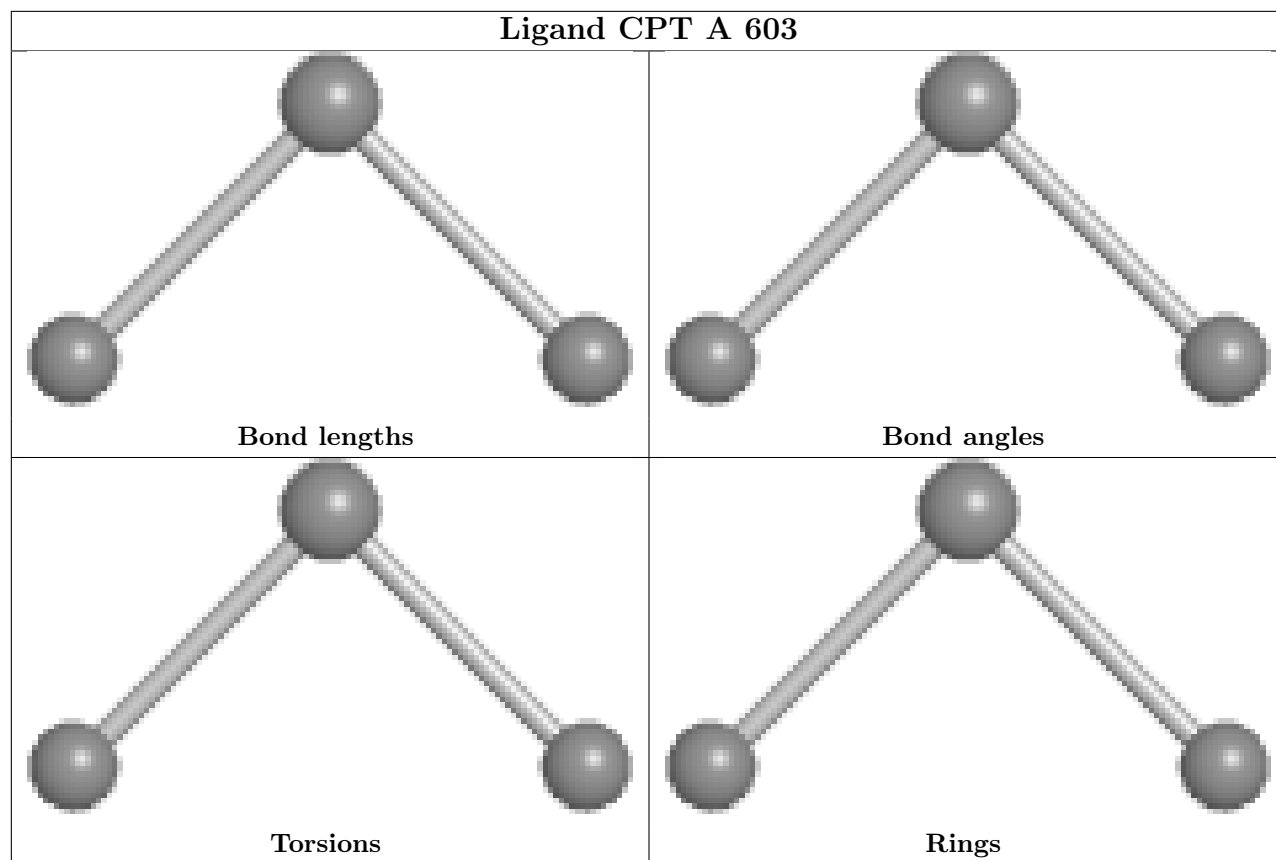
There are no torsion outliers.

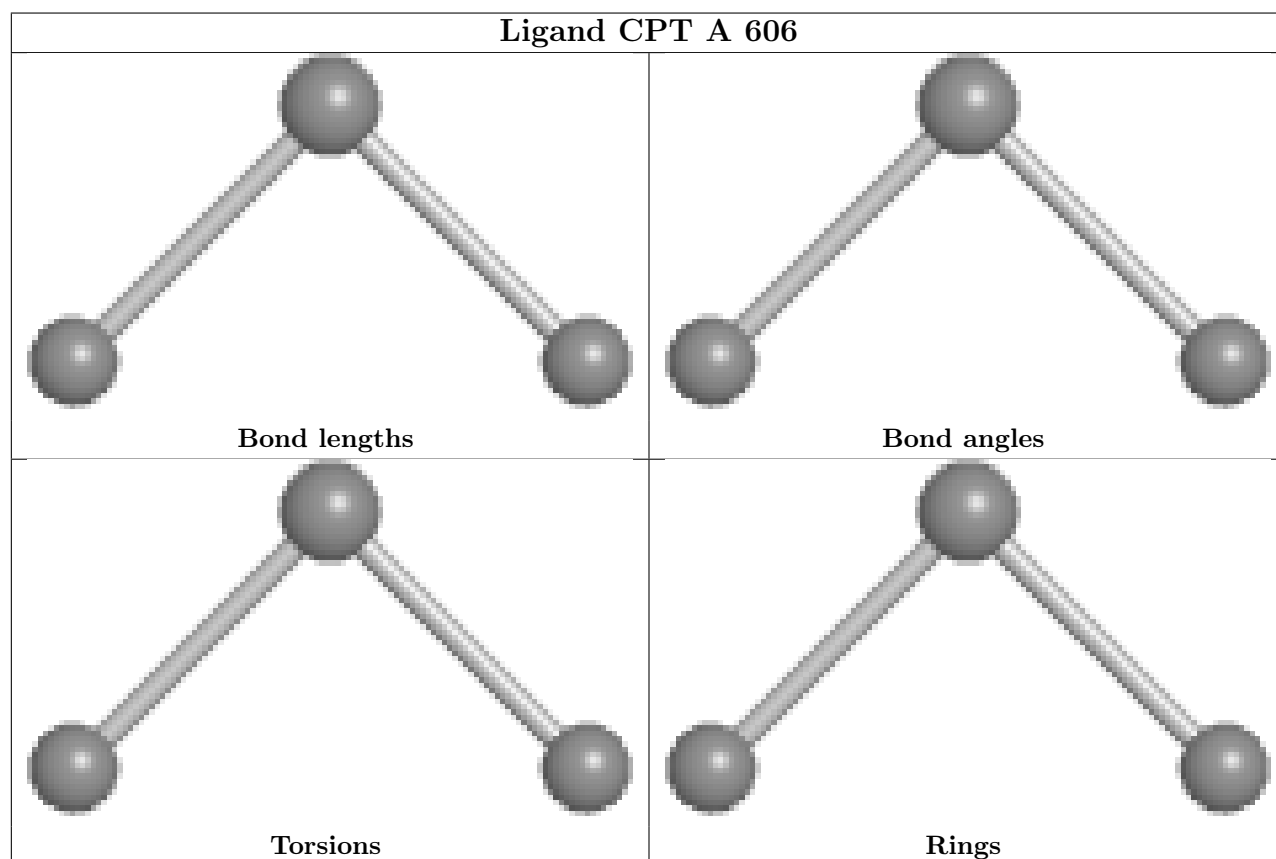
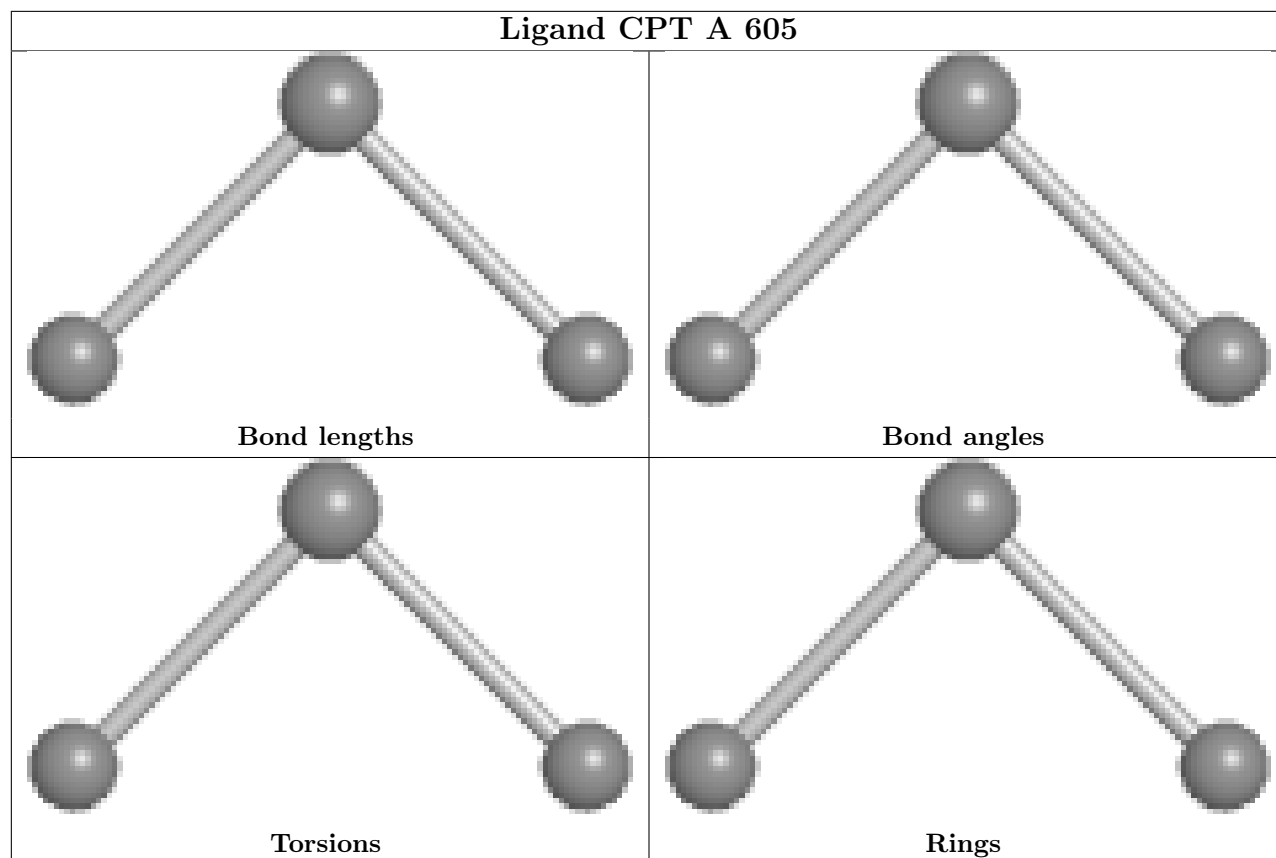
There are no ring outliers.

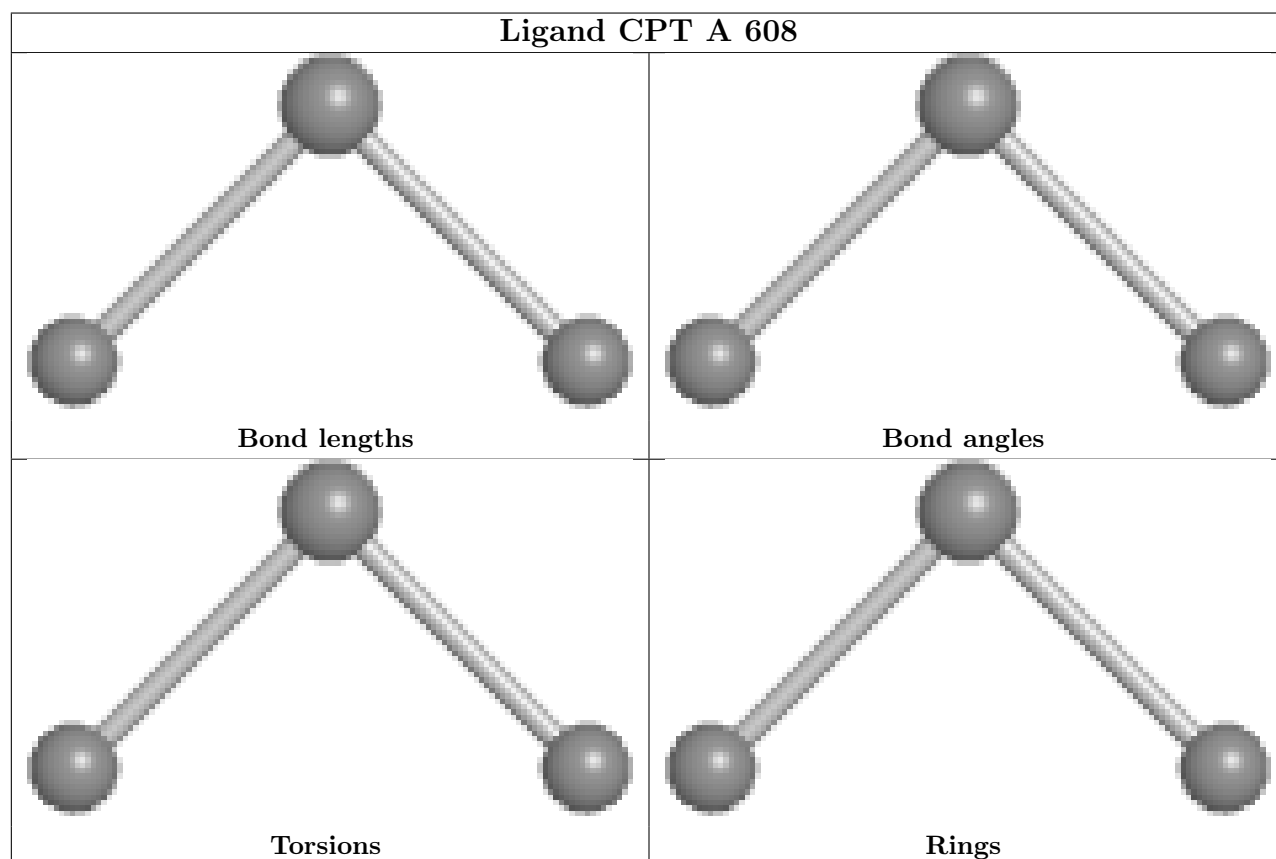
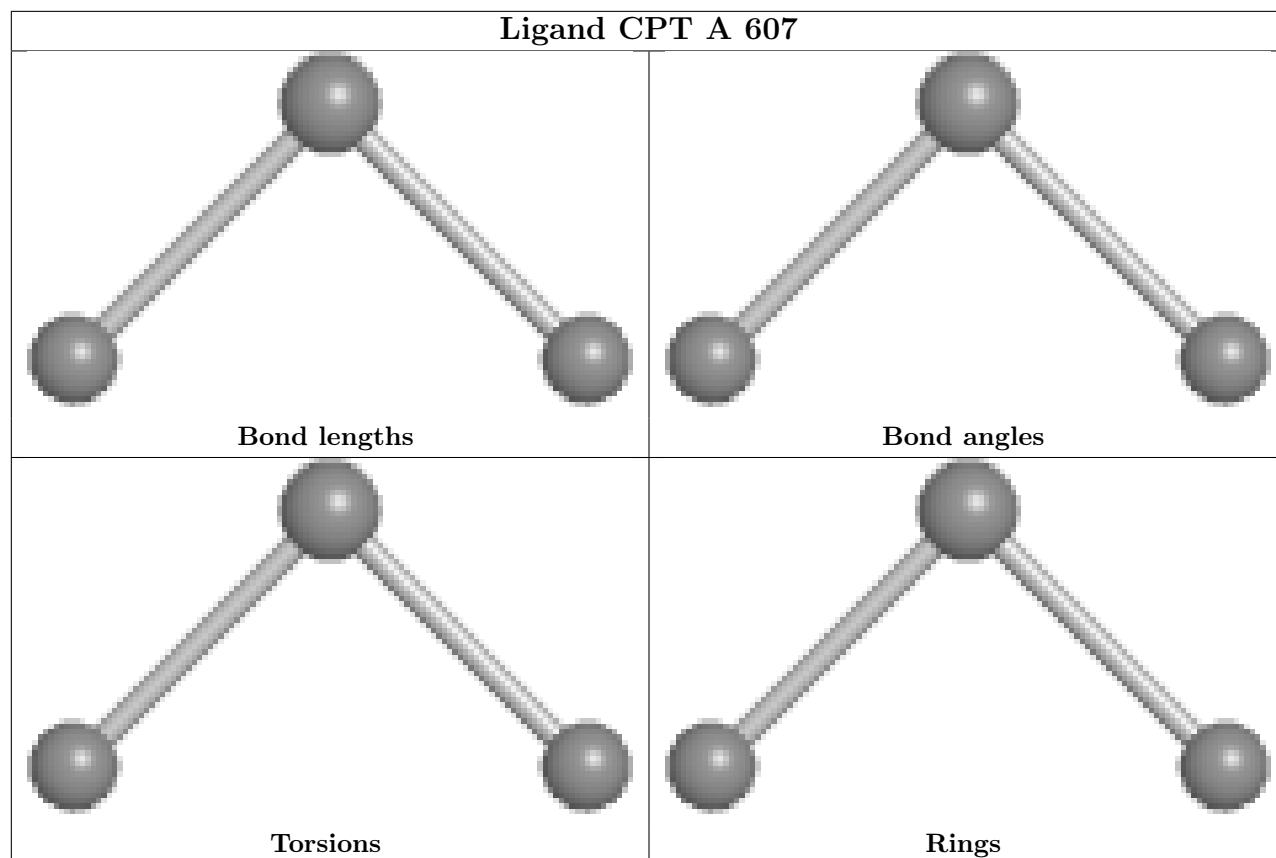
No monomer is involved in short contacts.

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.

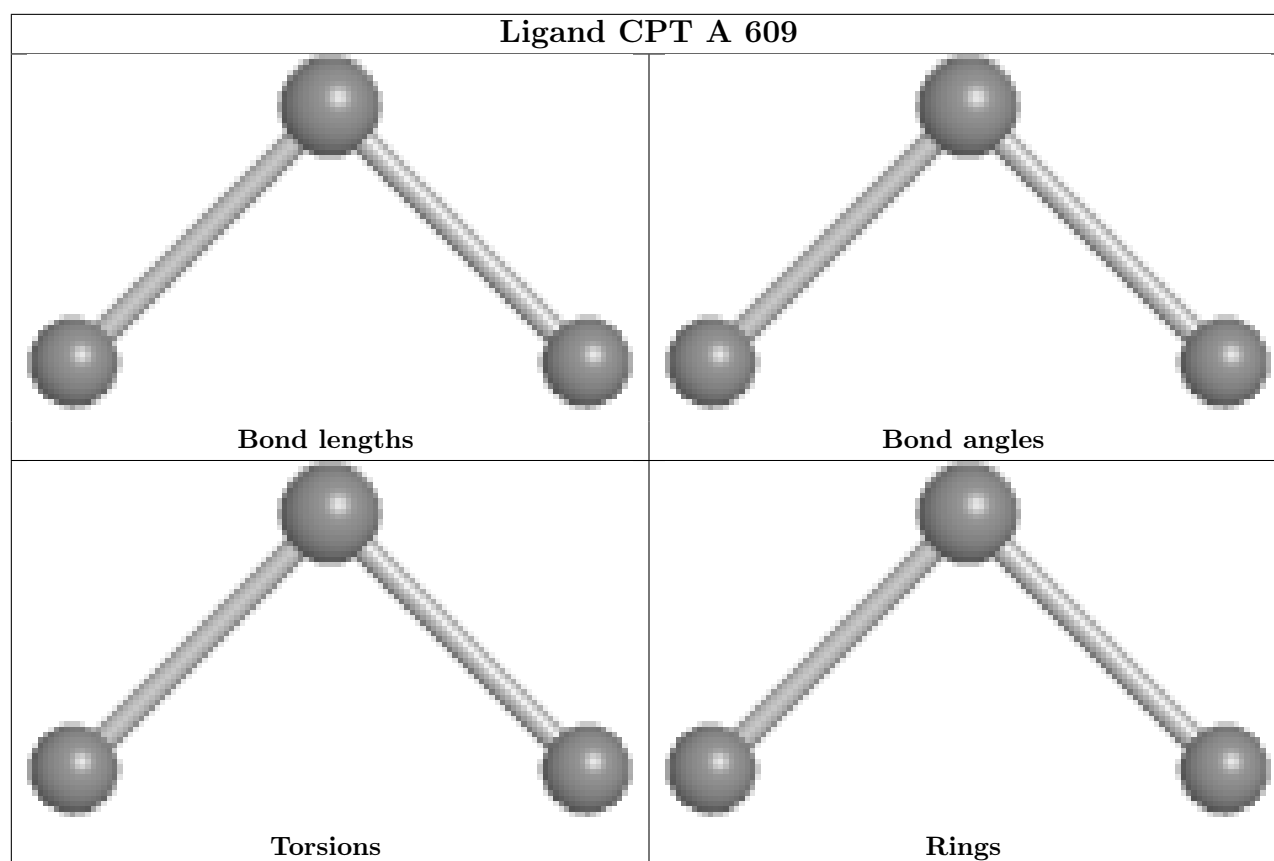












## 5.7 Other polymers [i](#)

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	567/609 (93%)	0.42	51 (8%) <b>9</b> <b>7</b>	47, 95, 149, 195	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	366	PRO	5.0
1	A	55	ALA	5.0
1	A	301	ASP	4.9
1	A	58	SER	4.7
1	A	302	LEU	4.5
1	A	57	GLU	4.5
1	A	303	PRO	4.4
1	A	85	GLY	4.3
1	A	374	PHE	4.2
1	A	553	ALA	4.0
1	A	310	VAL	4.0
1	A	306	ALA	3.9
1	A	9	HIS	3.7
1	A	571	GLU	3.6
1	A	307	ALA	3.5
1	A	568	PHE	3.5
1	A	351	LYS	3.5
1	A	347	LEU	3.4
1	A	509	PHE	3.3
1	A	311	GLU	3.3
1	A	78	ALA	3.1
1	A	81	ARG	3.1
1	A	12	LYS	3.0
1	A	13	ASP	3.0
1	A	507	PHE	3.0
1	A	10	ARG	2.9
1	A	557	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	569	ALA	2.9
1	A	196	GLN	2.8
1	A	368	GLU	2.8
1	A	558	CYS	2.7
1	A	59	ALA	2.7
1	A	304	SER	2.6
1	A	364	ALA	2.6
1	A	375	ASP	2.6
1	A	482	VAL	2.6
1	A	570	GLU	2.6
1	A	323	LYS	2.6
1	A	305	LEU	2.5
1	A	42	LEU	2.4
1	A	116	VAL	2.4
1	A	140	TYR	2.3
1	A	88	ALA	2.2
1	A	269	ASP	2.2
1	A	401	TYR	2.2
1	A	365	ASP	2.2
1	A	54	VAL	2.2
1	A	17	GLU	2.1
1	A	535	HIS	2.1
1	A	513	ILE	2.1
1	A	397	GLN	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](#)

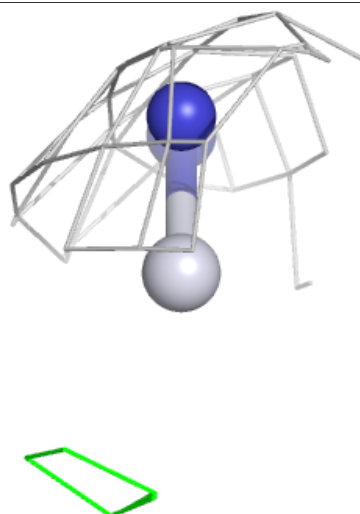
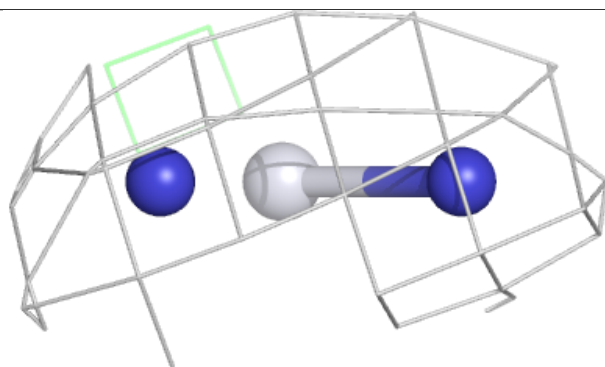
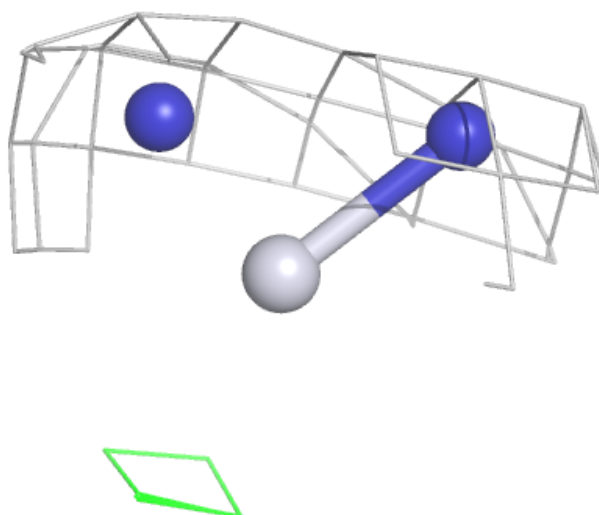
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MYR	A	614	16/16	0.70	0.66	72,89,140,144	0
3	MYR	A	613	16/16	0.71	0.87	82,94,119,122	0
3	MYR	A	610	14/16	0.77	0.63	76,102,114,116	0
3	MYR	A	615	16/16	0.79	0.38	92,106,128,133	0
3	MYR	A	611	13/16	0.82	0.30	58,77,101,107	0
3	MYR	A	612	13/16	0.89	0.28	59,69,103,106	0
2	CPT	A	607	3/5	0.92	0.26	56,56,58,97	3
2	CPT	A	609	3/5	0.94	0.20	48,48,48,86	3
2	CPT	A	606	3/5	0.95	0.18	56,56,65,110	3
2	CPT	A	608	3/5	0.98	0.18	51,51,52,88	3
2	CPT	A	601	4/5	0.99	0.12	99,126,155,161	0
2	CPT	A	602	4/5	0.99	0.10	85,86,100,131	4
2	CPT	A	603	3/5	0.99	0.14	57,57,58,101	3
2	CPT	A	604	4/5	0.99	0.07	90,97,101,113	4
2	CPT	A	605	3/5	0.99	0.24	72,72,76,121	3

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.

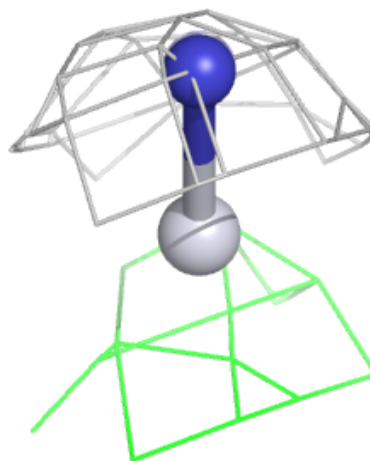
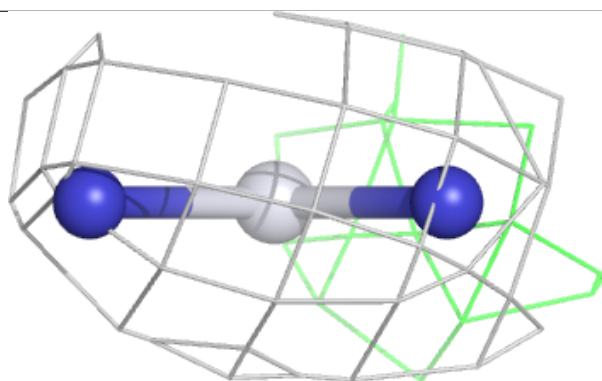
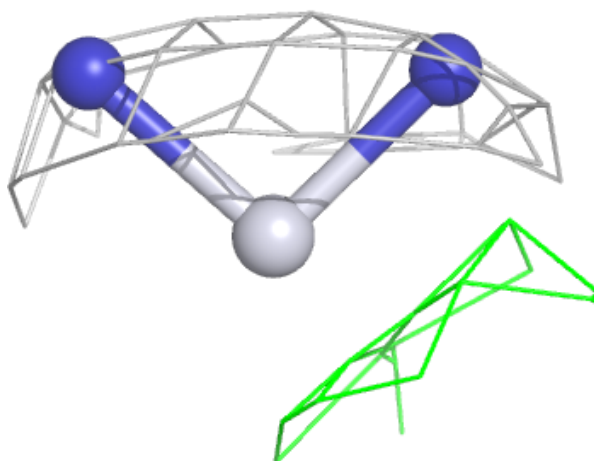
**Electron density around CPT A 607:**

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



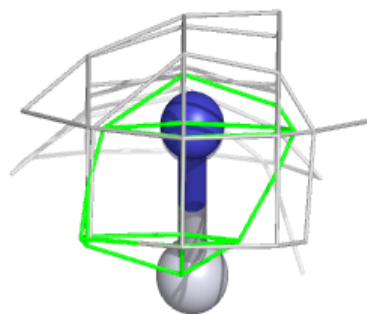
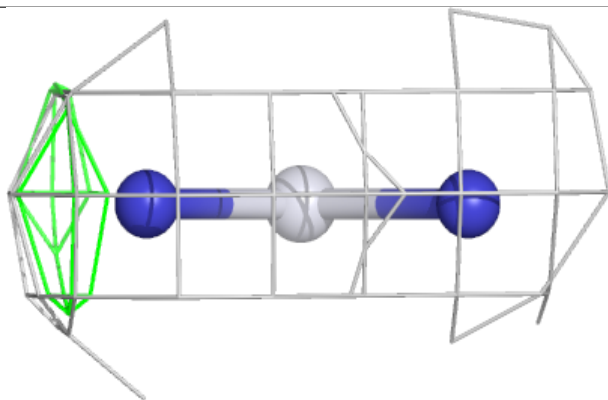
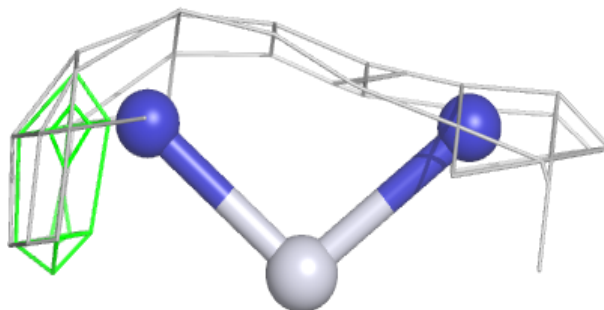
**Electron density around CPT A 609:**

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

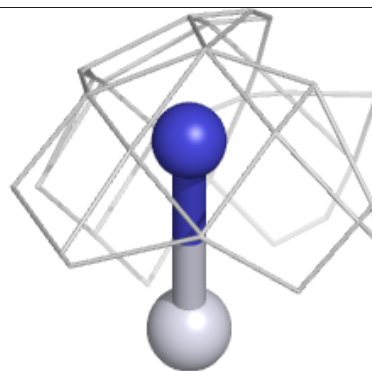
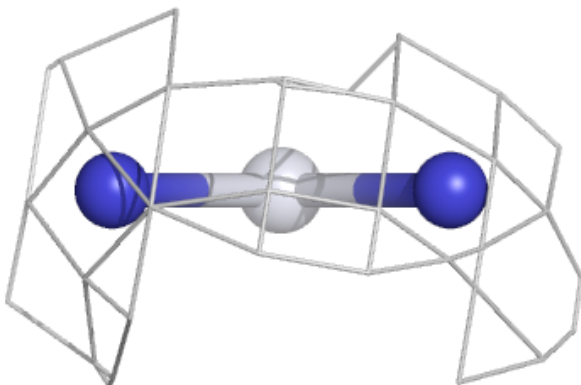
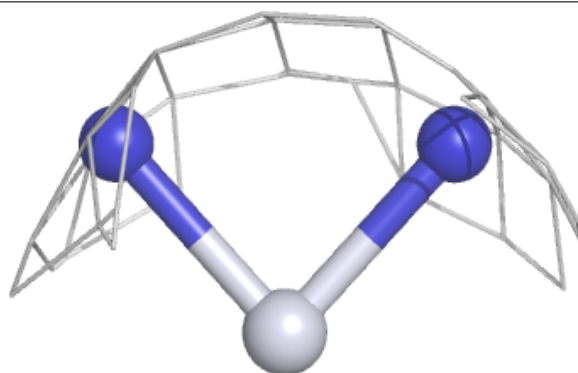


**Electron density around CPT A 606:**

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

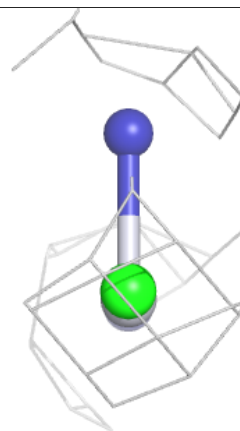
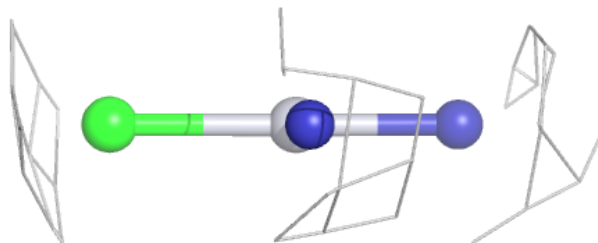
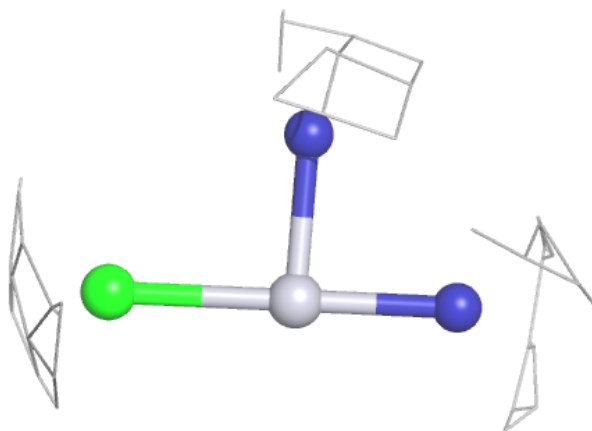
**Electron density around CPT A 608:**

$2mF_o-DF_c$  (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:**

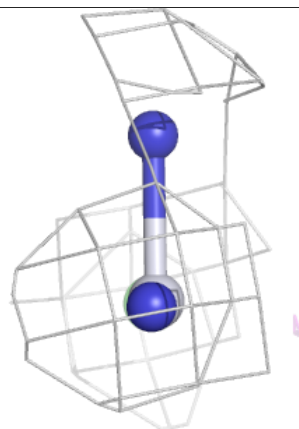
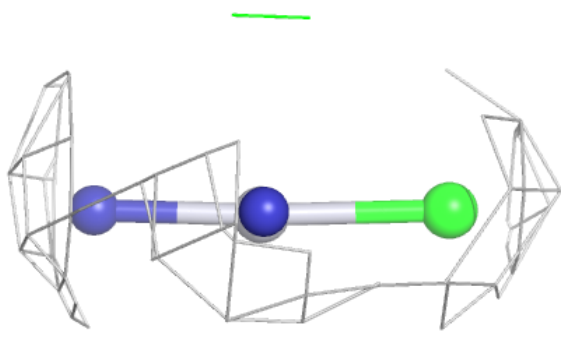
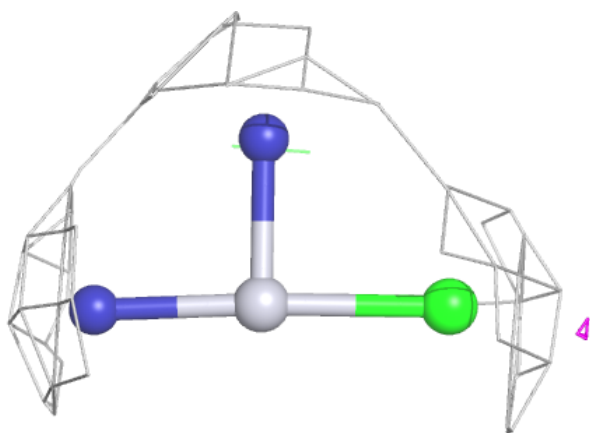
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





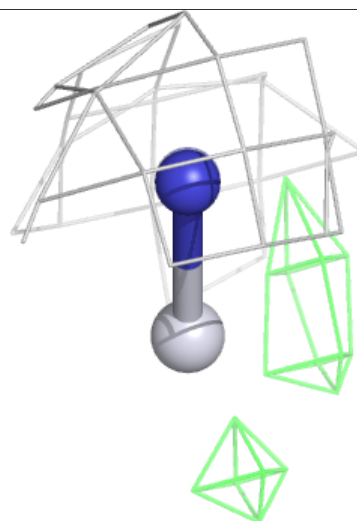
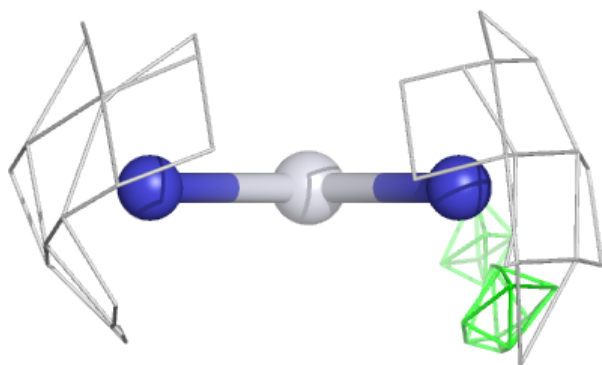
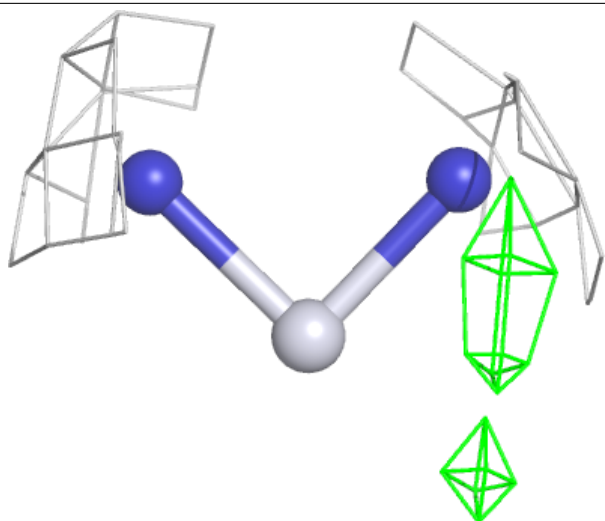
**Electron density around CPT A 602:**

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



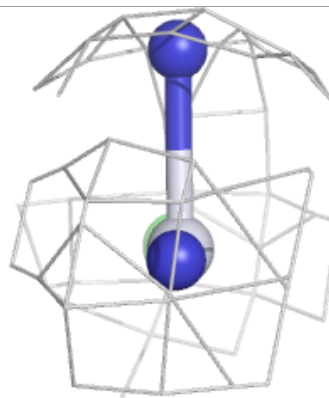
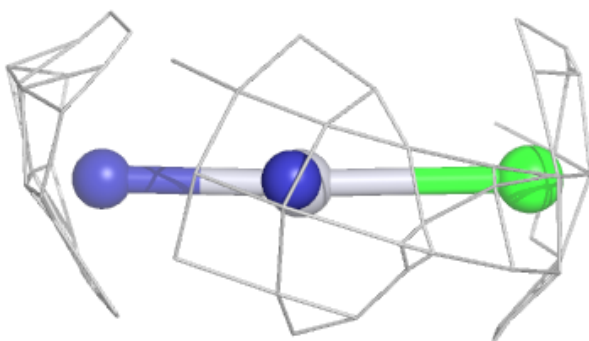
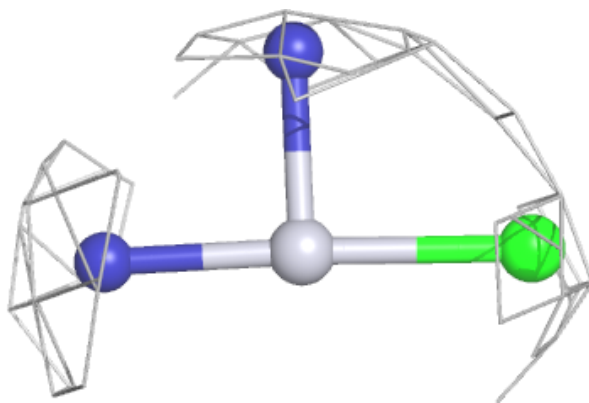
**Electron density around CPT A 603:**

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

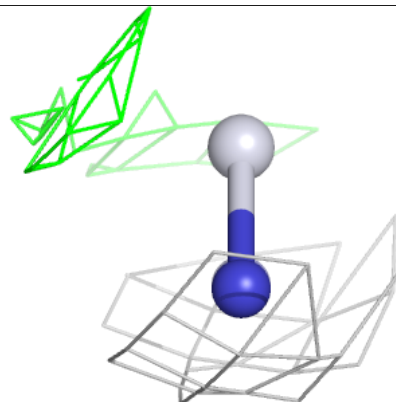
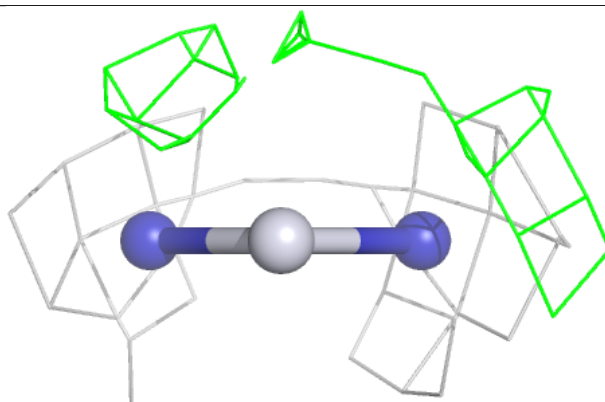
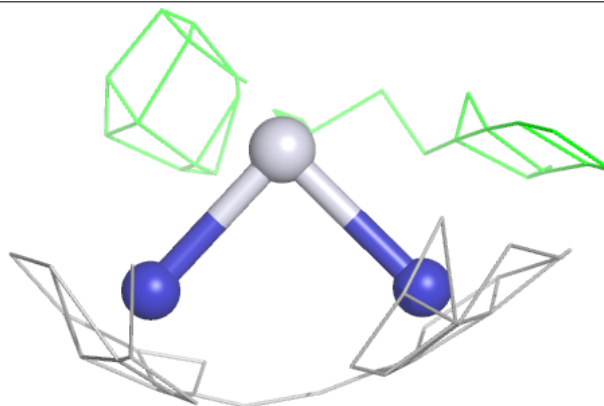


**Electron density around CPT A 604:**

$2mF_o - DF_c$  (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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.