



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 11, 2022 – 10:12 am BST

PDB ID : 7O5N  
Title : Crystal Structure of a Class D carbapenemase complexed with Avibactam  
Authors : Zhou, Q.; Zhang, Z.; He, Y.; Jin, Y.  
Deposited on : 2021-04-09  
Resolution : 1.60 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.27  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.27

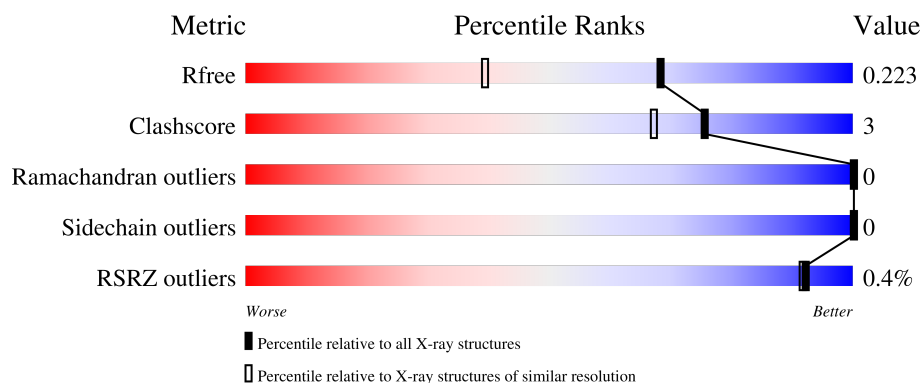
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	AAA	260	<div> <div>88%</div> <div>5%</div> <div>7%</div> </div>
1	BBB	260	<div> <div>88%</div> <div>5%</div> <div>7%</div> </div>
1	CCC	260	<div> <div>87%</div> <div>6%</div> <div>7%</div> </div>
1	DDD	260	<div> <div>%</div> <div>89%</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
2	1BO	AAA	402	-	-	X	-
4	CL	AAA	405[B]	-	-	X	-
4	CL	BBB	305[B]	-	-	X	-
4	CL	CCC	305[B]	-	-	X	-
4	CL	DDD	303[B]	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16886 atoms, of which 8024 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 Beta-lactamase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	243	Total	C	H	N	O	S	46	4	0
			4003	1285	1985	355	369	9			
1	BBB	242	Total	C	H	N	O	S	46	4	0
			3979	1279	1973	352	367	8			
1	CCC	242	Total	C	H	N	O	S	46	4	0
			3979	1279	1973	352	367	8			
1	DDD	242	Total	C	H	N	O	S	47	4	0
			3988	1282	1975	355	367	9			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	6	MET	-	initiating methionine	UNP Q6XEC0
AAA	7	HIS	-	expression tag	UNP Q6XEC0
AAA	8	HIS	-	expression tag	UNP Q6XEC0
AAA	9	HIS	-	expression tag	UNP Q6XEC0
AAA	10	HIS	-	expression tag	UNP Q6XEC0
AAA	11	HIS	-	expression tag	UNP Q6XEC0
AAA	12	HIS	-	expression tag	UNP Q6XEC0
AAA	13	SER	-	expression tag	UNP Q6XEC0
AAA	14	ALA	-	expression tag	UNP Q6XEC0
AAA	15	GLY	-	expression tag	UNP Q6XEC0
AAA	16	GLU	-	expression tag	UNP Q6XEC0
AAA	17	ASN	-	expression tag	UNP Q6XEC0
AAA	18	LEU	-	expression tag	UNP Q6XEC0
AAA	19	TYR	-	expression tag	UNP Q6XEC0
AAA	20	PHE	-	expression tag	UNP Q6XEC0
AAA	21	GLN	-	expression tag	UNP Q6XEC0
AAA	22	GLY	-	expression tag	UNP Q6XEC0
BBB	6	MET	-	initiating methionine	UNP Q6XEC0
BBB	7	HIS	-	expression tag	UNP Q6XEC0
BBB	8	HIS	-	expression tag	UNP Q6XEC0
BBB	9	HIS	-	expression tag	UNP Q6XEC0

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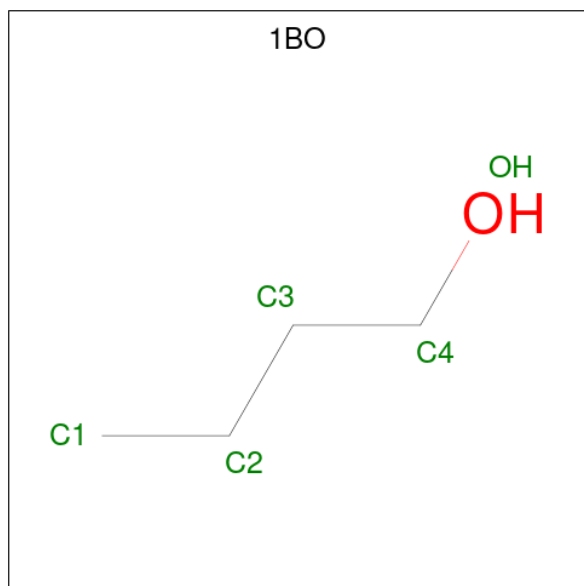
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	10	HIS	-	expression tag	UNP Q6XEC0
BBB	11	HIS	-	expression tag	UNP Q6XEC0
BBB	12	HIS	-	expression tag	UNP Q6XEC0
BBB	13	SER	-	expression tag	UNP Q6XEC0
BBB	14	ALA	-	expression tag	UNP Q6XEC0
BBB	15	GLY	-	expression tag	UNP Q6XEC0
BBB	16	GLU	-	expression tag	UNP Q6XEC0
BBB	17	ASN	-	expression tag	UNP Q6XEC0
BBB	18	LEU	-	expression tag	UNP Q6XEC0
BBB	19	TYR	-	expression tag	UNP Q6XEC0
BBB	20	PHE	-	expression tag	UNP Q6XEC0
BBB	21	GLN	-	expression tag	UNP Q6XEC0
BBB	22	GLY	-	expression tag	UNP Q6XEC0
CCC	6	MET	-	initiating methionine	UNP Q6XEC0
CCC	7	HIS	-	expression tag	UNP Q6XEC0
CCC	8	HIS	-	expression tag	UNP Q6XEC0
CCC	9	HIS	-	expression tag	UNP Q6XEC0
CCC	10	HIS	-	expression tag	UNP Q6XEC0
CCC	11	HIS	-	expression tag	UNP Q6XEC0
CCC	12	HIS	-	expression tag	UNP Q6XEC0
CCC	13	SER	-	expression tag	UNP Q6XEC0
CCC	14	ALA	-	expression tag	UNP Q6XEC0
CCC	15	GLY	-	expression tag	UNP Q6XEC0
CCC	16	GLU	-	expression tag	UNP Q6XEC0
CCC	17	ASN	-	expression tag	UNP Q6XEC0
CCC	18	LEU	-	expression tag	UNP Q6XEC0
CCC	19	TYR	-	expression tag	UNP Q6XEC0
CCC	20	PHE	-	expression tag	UNP Q6XEC0
CCC	21	GLN	-	expression tag	UNP Q6XEC0
CCC	22	GLY	-	expression tag	UNP Q6XEC0
DDD	6	MET	-	initiating methionine	UNP Q6XEC0
DDD	7	HIS	-	expression tag	UNP Q6XEC0
DDD	8	HIS	-	expression tag	UNP Q6XEC0
DDD	9	HIS	-	expression tag	UNP Q6XEC0
DDD	10	HIS	-	expression tag	UNP Q6XEC0
DDD	11	HIS	-	expression tag	UNP Q6XEC0
DDD	12	HIS	-	expression tag	UNP Q6XEC0
DDD	13	SER	-	expression tag	UNP Q6XEC0
DDD	14	ALA	-	expression tag	UNP Q6XEC0
DDD	15	GLY	-	expression tag	UNP Q6XEC0
DDD	16	GLU	-	expression tag	UNP Q6XEC0
DDD	17	ASN	-	expression tag	UNP Q6XEC0

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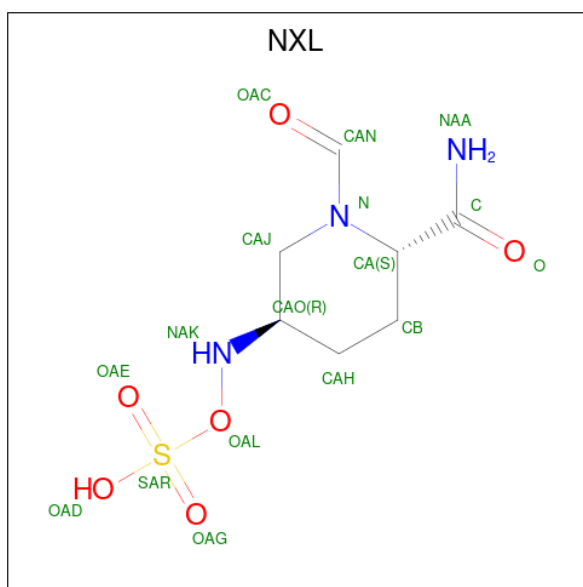
Chain	Residue	Modelled	Actual	Comment	Reference
DDD	18	LEU	-	expression tag	UNP Q6XEC0
DDD	19	TYR	-	expression tag	UNP Q6XEC0
DDD	20	PHE	-	expression tag	UNP Q6XEC0
DDD	21	GLN	-	expression tag	UNP Q6XEC0
DDD	22	GLY	-	expression tag	UNP Q6XEC0

- Molecule 2 is 1-BUTANOL (three-letter code: 1BO) (formula: C<sub>4</sub>H<sub>10</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	AAA	1	Total	C	H	O	0	0
			15	4	10	1		
2	AAA	1	Total	C	H	O	0	0
			15	4	10	1		
2	BBB	1	Total	C	H	O	0	0
			15	4	10	1		
2	BBB	1	Total	C	H	O	0	0
			15	4	10	1		
2	CCC	1	Total	C	H	O	0	0
			15	4	10	1		

- Molecule 3 is (2S,5R)-1-formyl-5-[(sulfooxy)amino]piperidine-2-carboxamide (three-letter code: NXL) (formula: C<sub>7</sub>H<sub>13</sub>N<sub>3</sub>O<sub>6</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	AAA	1	Total 28	C 7	H 11	N 3	O 6	S 1	0	0
3	BBB	1	Total 28	C 7	H 11	N 3	O 6	S 1	0	0
3	CCC	1	Total 28	C 7	H 11	N 3	O 6	S 1	0	0
3	DDD	1	Total 28	C 7	H 11	N 3	O 6	S 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	3	Total	Cl	0	2
			5	5		
4	BBB	1	Total	Cl	0	1
			2	2		
4	CCC	3	Total	Cl	0	2
			5	5		
4	DDD	1	Total	Cl	0	1
			2	2		

- Molecule 5 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
5	BBB	1	Total	C	H	O	2	0
			14	3	8	3		
5	CCC	1	Total	C	H	O	2	0
			14	3	8	3		
5	DDD	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	AAA	185	Total	O	0	0
			185	185		
6	BBB	144	Total	O	0	1
			145	145		
6	CCC	192	Total	O	0	0
			192	192		
6	DDD	170	Total	O	0	2
			172	172		



### 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: Beta-lactamase

Chain AAA: 



- Molecule 1: Beta-lactamase

Chain BBB: 



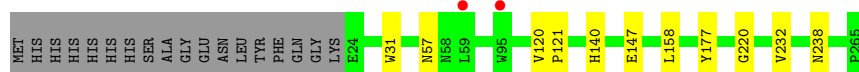
- Molecule 1: Beta-lactamase

Chain CCC: 



- Molecule 1: Beta-lactamase

Chain DDD: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.75Å 107.96Å 125.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.14 – 1.60 73.04 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (73.14-1.60) 99.9 (73.04-1.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.188 , 0.216 0.194 , 0.223	Depositor DCC
$R_{free}$ test set	7895 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.728	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	16886	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.04 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2117e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NXL, CL, GOL, 1BO

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	AAA	0.71	0/2067	0.82	0/2793
1	BBB	0.70	0/2058	0.82	0/2783
1	CCC	0.70	0/2058	0.82	0/2783
1	DDD	0.71	0/2063	0.81	0/2789
All	All	0.71	0/8246	0.82	0/11148

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 [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	AAA	2018	1985	1974	12	0
1	BBB	2006	1973	1964	13	0
1	CCC	2006	1973	1964	11	0
1	DDD	2013	1975	1963	8	0
2	AAA	10	20	20	7	0
2	BBB	10	20	20	2	0
2	CCC	5	10	10	1	0
3	AAA	17	11	11	0	0
3	BBB	17	11	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	CCC	17	11	11	0	0
3	DDD	17	11	11	0	0
4	AAA	5	0	0	5	0
4	BBB	2	0	0	4	0
4	CCC	5	0	0	5	0
4	DDD	2	0	0	3	0
5	BBB	6	8	8	1	0
5	CCC	6	8	8	0	0
5	DDD	6	8	8	0	0
6	AAA	185	0	0	4	0
6	BBB	145	0	0	2	0
6	CCC	192	0	0	0	0
6	DDD	172	0	0	1	0
All	All	8862	8024	7983	50	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.

The worst 5 of 50 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:BBB:158[B]:LEU:HD21	4:BBB:305[B]:CL:CL	1.07	1.59
1:DDD:158:LEU:HD21	4:DDD:303[B]:CL:CL	1.04	1.58
1:CCC:158[B]:LEU:HD21	4:CCC:305[B]:CL:CL	1.50	1.48
1:DDD:158:LEU:CD2	4:DDD:303[B]:CL:CL	1.97	1.46
1:BBB:158[B]:LEU:CD2	4:BBB:305[B]:CL:CL	2.03	1.41

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	AAA	245/260 (94%)	240 (98%)	5 (2%)	0	100	100
1	BBB	244/260 (94%)	239 (98%)	5 (2%)	0	100	100
1	CCC	244/260 (94%)	239 (98%)	5 (2%)	0	100	100
1	DDD	244/260 (94%)	240 (98%)	4 (2%)	0	100	100
All	All	977/1040 (94%)	958 (98%)	19 (2%)	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	AAA	216/226 (96%)	216 (100%)	0	100	100
1	BBB	215/226 (95%)	215 (100%)	0	100	100
1	CCC	215/226 (95%)	215 (100%)	0	100	100
1	DDD	215/226 (95%)	215 (100%)	0	100	100
All	All	861/904 (95%)	861 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 14 are monoatomic - leaving 12 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	1BO	BBB	302	-	4,4,4	0.25	0	3,3,3	0.26	0
5	GOL	BBB	301	-	5,5,5	0.10	0	5,5,5	0.25	0
3	NXL	CCC	303	1	14,17,17	0.52	0	17,24,24	2.11	7 (41%)
5	GOL	CCC	301	-	5,5,5	0.13	0	5,5,5	0.31	0
2	1BO	CCC	302	-	4,4,4	0.22	0	3,3,3	0.24	0
2	1BO	AAA	401	-	4,4,4	0.14	0	3,3,3	0.08	0
5	GOL	DDD	301	-	5,5,5	0.15	0	5,5,5	0.32	0
3	NXL	BBB	304	1	14,17,17	0.93	1 (7%)	17,24,24	1.33	2 (11%)
3	NXL	AAA	403	1	14,17,17	0.68	0	17,24,24	1.83	5 (29%)
3	NXL	DDD	302	1	14,17,17	0.60	0	17,24,24	1.55	2 (11%)
2	1BO	AAA	402	-	4,4,4	0.12	0	3,3,3	0.12	0
2	1BO	BBB	303	-	4,4,4	0.13	0	3,3,3	0.10	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	1BO	BBB	302	-	-	1/2/2/2	-
5	GOL	BBB	301	-	-	2/4/4/4	-
3	NXL	CCC	303	1	-	2/5/25/25	0/1/1/1
5	GOL	CCC	301	-	-	2/4/4/4	-
2	1BO	CCC	302	-	-	2/2/2/2	-
2	1BO	AAA	401	-	-	1/2/2/2	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	DDD	301	-	-	2/4/4/4	-
3	NXL	BBB	304	1	-	2/5/25/25	0/1/1/1
3	NXL	AAA	403	1	-	2/5/25/25	0/1/1/1
3	NXL	DDD	302	1	-	2/5/25/25	0/1/1/1
2	1BO	AAA	402	-	-	1/2/2/2	-
2	1BO	BBB	303	-	-	2/2/2/2	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	BBB	304	NXL	O-C	-2.18	1.19	1.23

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CCC	303	NXL	OAL-SAR-OAE	4.12	116.36	103.29
3	AAA	403	NXL	OAL-SAR-OAG	3.40	114.08	103.29
3	CCC	303	NXL	CB-CA-N	-3.35	105.46	110.31
3	DDD	302	NXL	O-C-CA	3.27	126.10	120.26
3	AAA	403	NXL	CAO-CAJ-N	-3.26	105.52	110.11

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

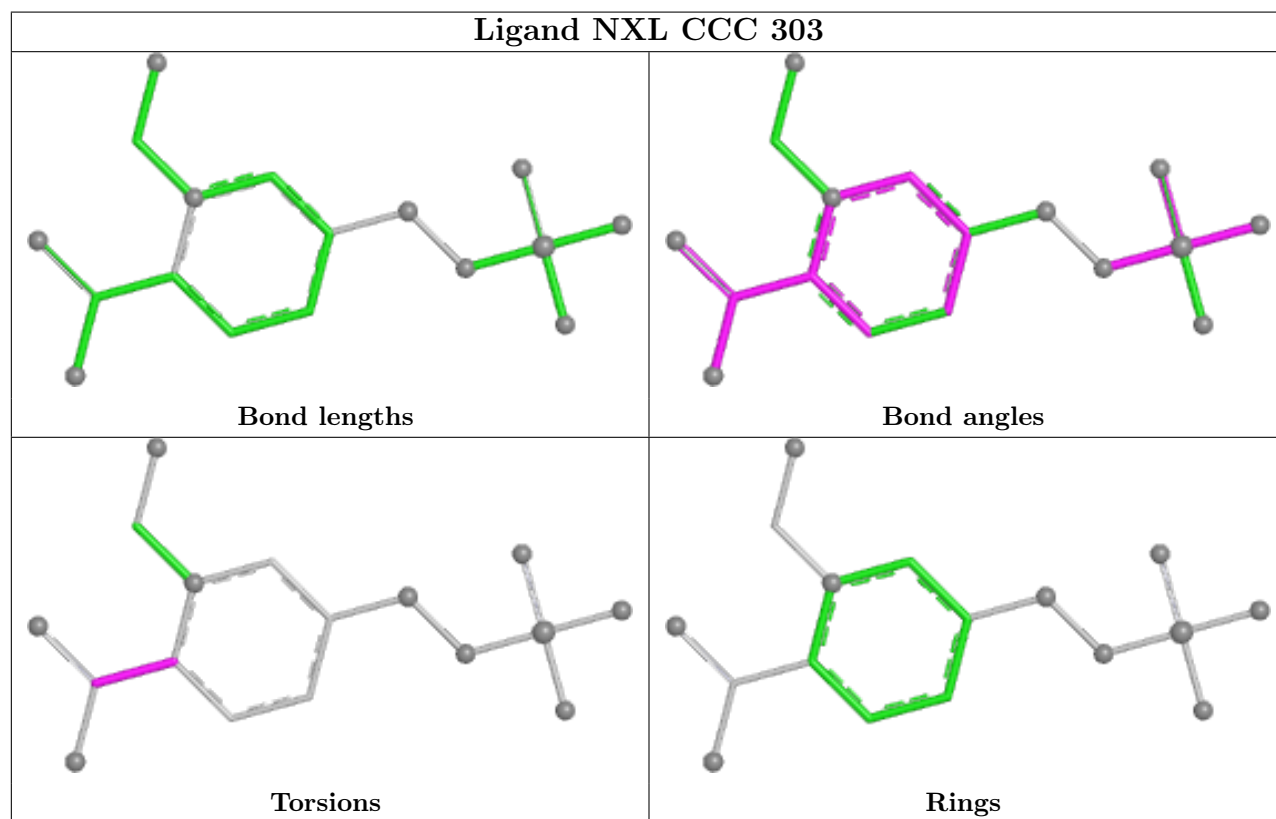
Mol	Chain	Res	Type	Atoms
3	BBB	304	NXL	O-C-CA-CB
3	BBB	304	NXL	NAA-C-CA-CB
3	DDD	302	NXL	NAA-C-CA-CB
5	BBB	301	GOL	C1-C2-C3-O3
5	CCC	301	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 11 short contacts:

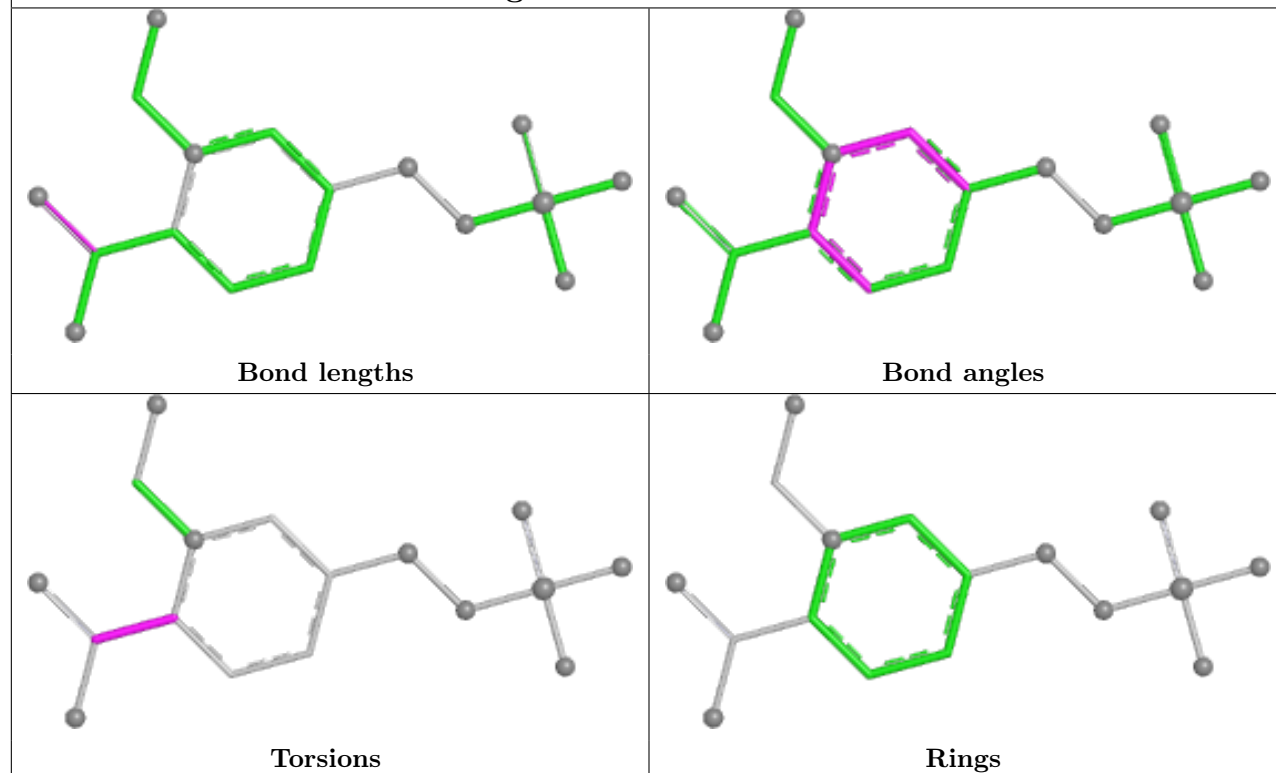
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	302	1BO	2	0
5	BBB	301	GOL	1	0
2	CCC	302	1BO	1	0
2	AAA	401	1BO	2	0
2	AAA	402	1BO	5	0

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.

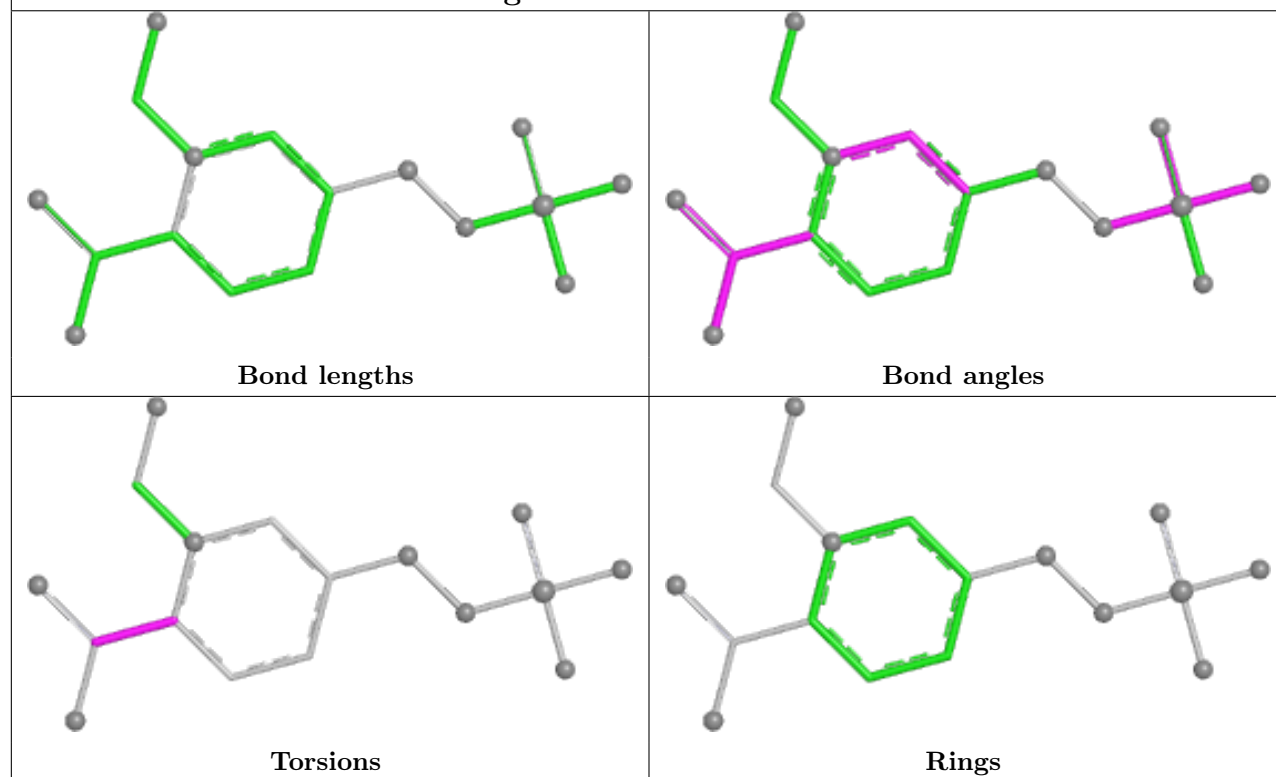


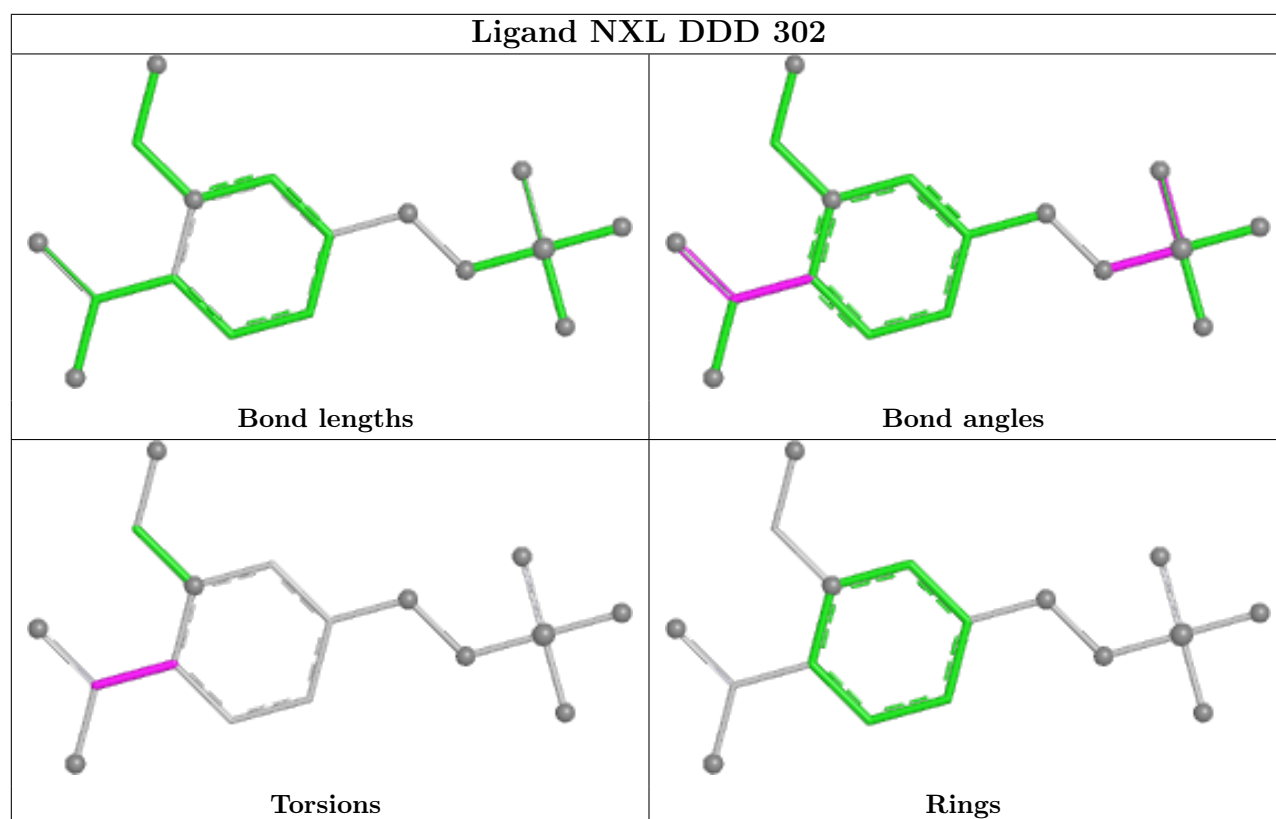


## Ligand NXL BBB 304



## Ligand NXL AAA 403





## 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	AAA	243/260 (93%)	-0.35	1 (0%) 92 92	22, 31, 45, 71	24 (9%)
1	BBB	242/260 (93%)	-0.29	1 (0%) 92 92	23, 35, 58, 78	2 (0%)
1	CCC	242/260 (93%)	-0.38	0 100 100	21, 31, 47, 59	1 (0%)
1	DDD	242/260 (93%)	-0.40	2 (0%) 86 86	22, 33, 54, 70	2 (0%)
All	All	969/1040 (93%)	-0.36	4 (0%) 92 92	21, 33, 52, 78	29 (2%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	DDD	59	LEU	2.5
1	AAA	23	LYS	2.4
1	BBB	59	LEU	2.2
1	DDD	95	TRP	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](#)

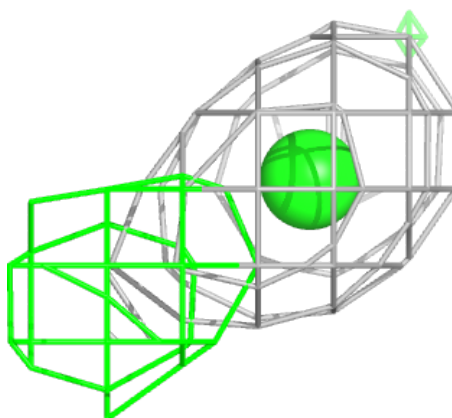
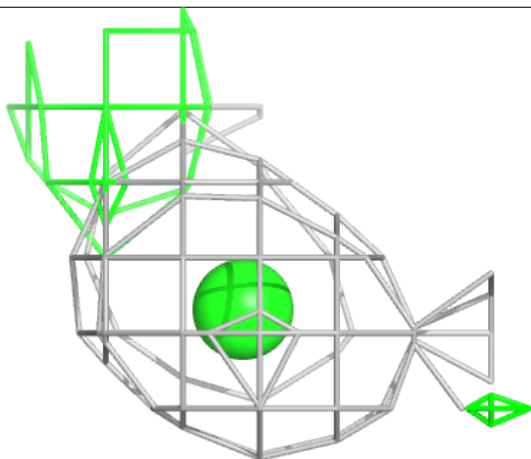
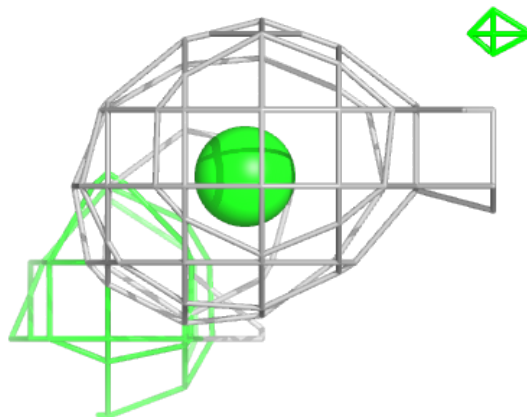
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	1BO	BBB	303	5/5	0.72	0.20	50,52,55,56	15
2	1BO	BBB	302	5/5	0.81	0.15	39,47,50,51	15
2	1BO	CCC	302	5/5	0.84	0.15	42,46,47,48	9
5	GOL	BBB	301	6/6	0.89	0.12	43,49,55,56	14
2	1BO	AAA	401	5/5	0.90	0.11	42,48,50,50	9
5	GOL	DDD	301	6/6	0.90	0.15	43,48,52,52	14
4	CL	CCC	306[B]	1/1	0.92	0.08	38,38,38,38	1
2	1BO	AAA	402	5/5	0.92	0.10	31,42,45,45	0
5	GOL	CCC	301	6/6	0.92	0.13	37,45,49,49	5
4	CL	CCC	306[A]	1/1	0.92	0.08	37,37,37,37	1
4	CL	AAA	405[B]	1/1	0.94	0.16	39,39,39,39	1
4	CL	AAA	405[A]	1/1	0.94	0.16	38,38,38,38	1
3	NXL	DDD	302	17/17	0.95	0.10	26,33,47,51	8
4	CL	CCC	305[A]	1/1	0.95	0.16	37,37,37,37	1
4	CL	CCC	305[B]	1/1	0.95	0.16	38,38,38,38	1
3	NXL	BBB	304	17/17	0.95	0.11	27,36,53,57	28
4	CL	AAA	406[B]	1/1	0.96	0.08	37,37,37,37	1
4	CL	BBB	305[A]	1/1	0.96	0.10	41,41,41,41	1
4	CL	BBB	305[B]	1/1	0.96	0.10	36,36,36,36	1
3	NXL	AAA	403	17/17	0.96	0.12	25,31,43,45	5
4	CL	AAA	406[A]	1/1	0.96	0.08	40,40,40,40	1
3	NXL	CCC	303	17/17	0.97	0.13	23,33,44,44	7
4	CL	DDD	303[A]	1/1	0.97	0.08	40,40,40,40	1
4	CL	DDD	303[B]	1/1	0.97	0.08	31,31,31,31	1
4	CL	CCC	304	1/1	0.99	0.08	27,27,27,27	0
4	CL	AAA	404	1/1	0.99	0.10	27,27,27,27	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.

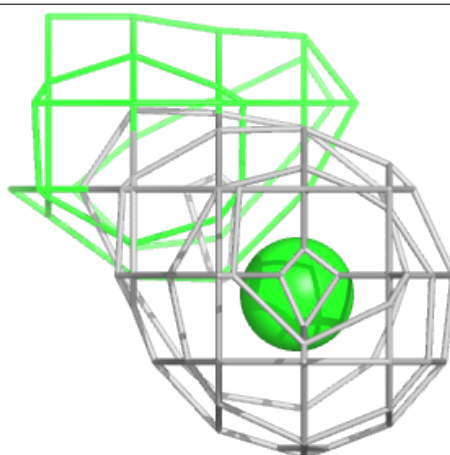
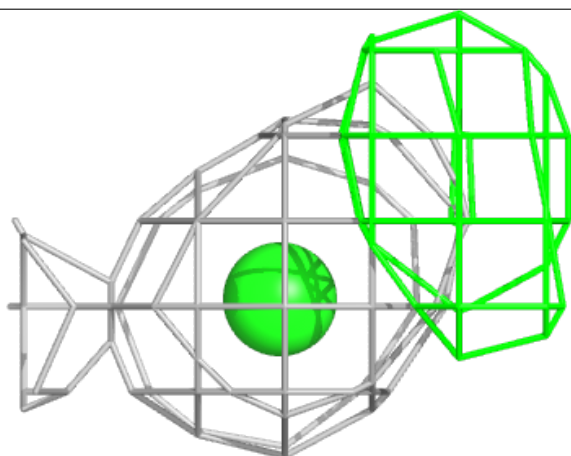
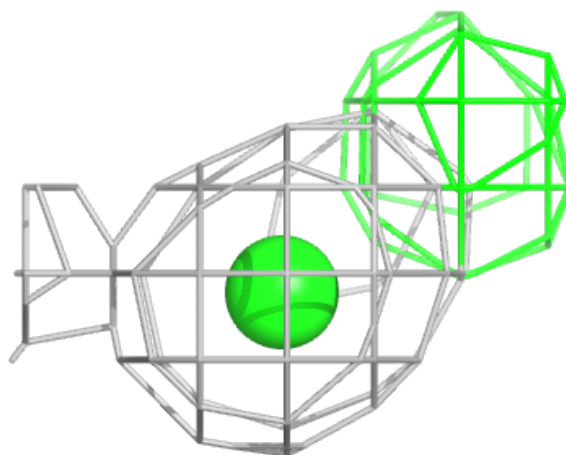
**Electron density around CL CCC 306 (B):**

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



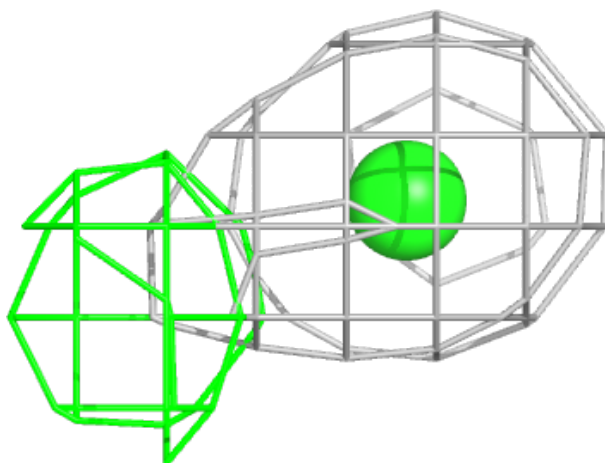
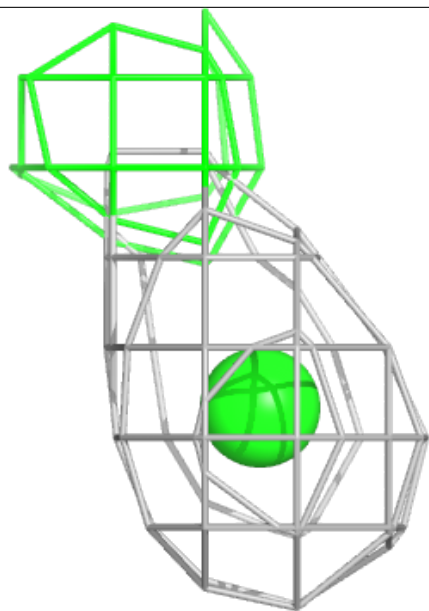
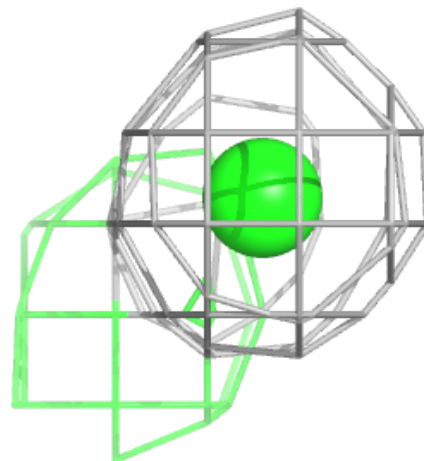
**Electron density around CL CCC 306 (A):**

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



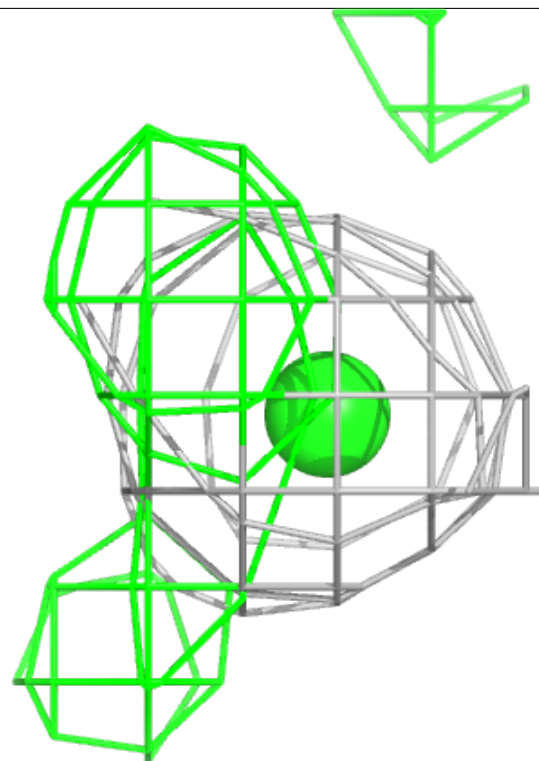
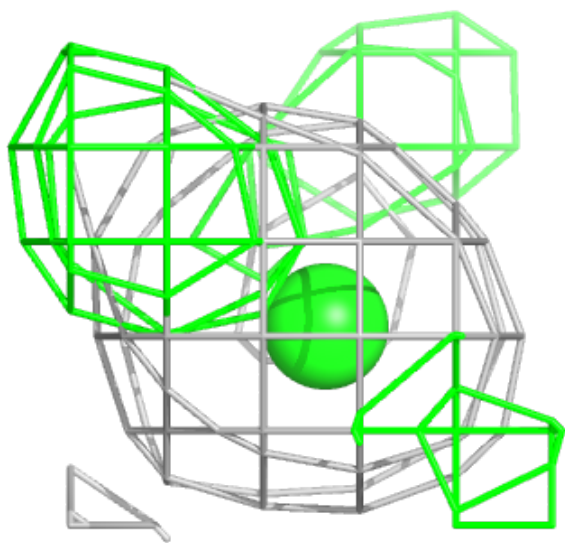
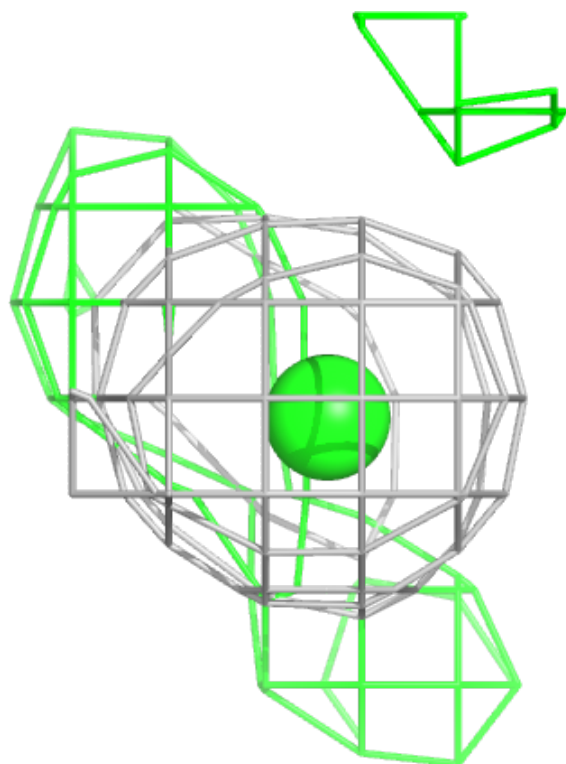
**Electron density around CL AAA 405 (B):**

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



**Electron density around CL AAA 405 (A):**

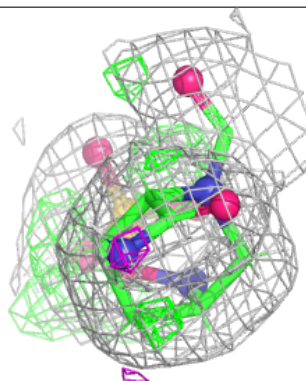
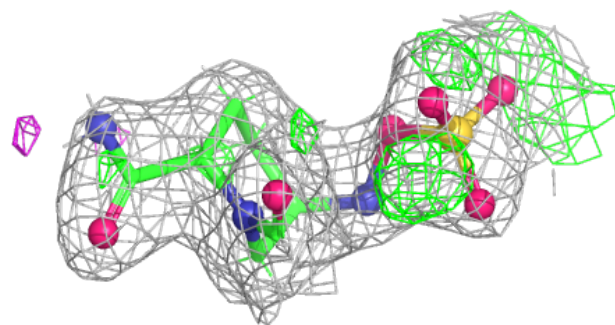
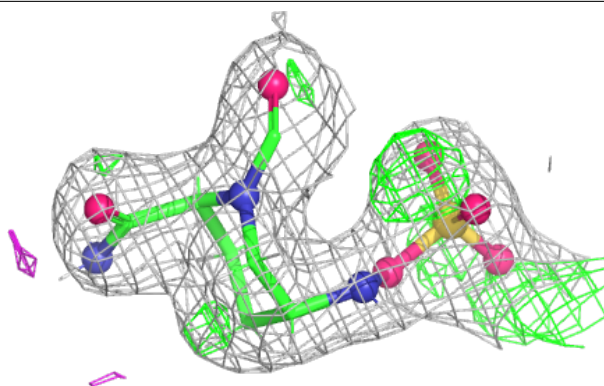
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





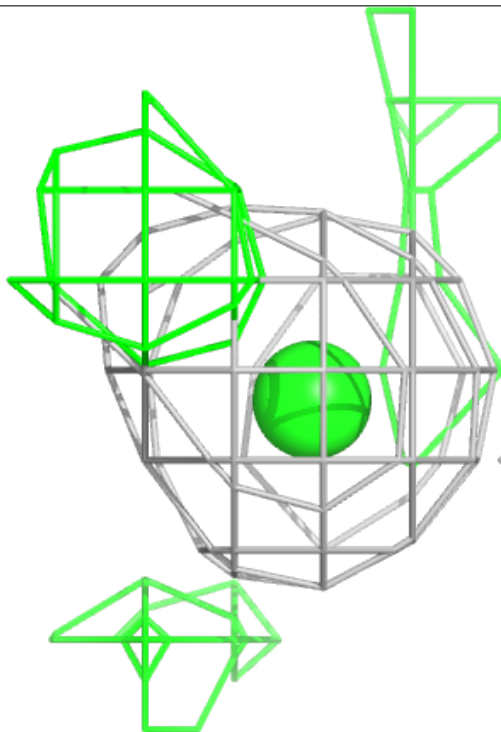
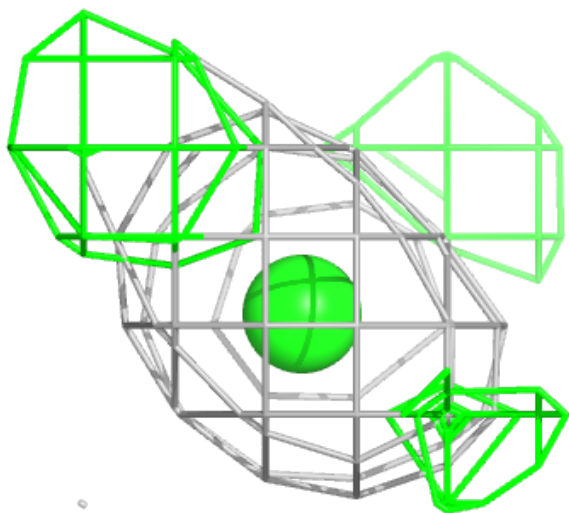
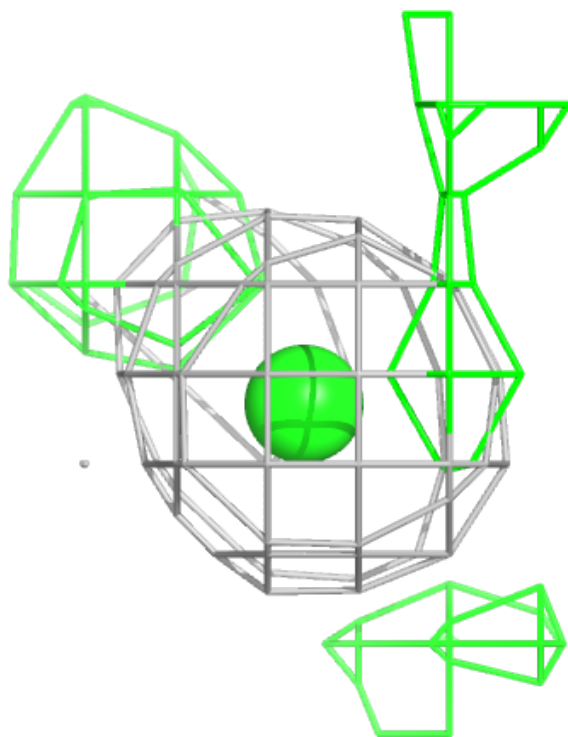
**Electron density around NXL DDD 302:**

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



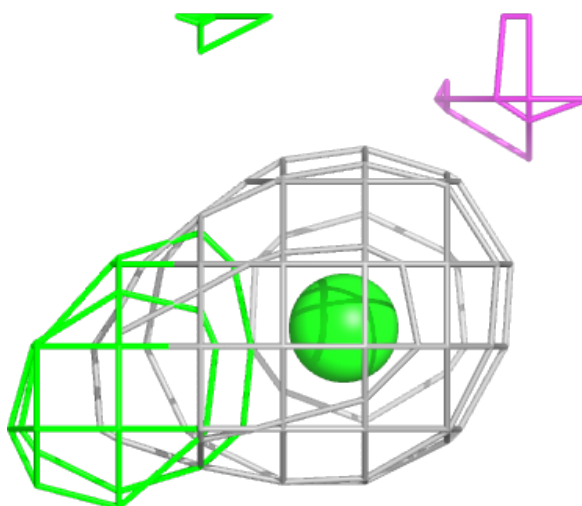
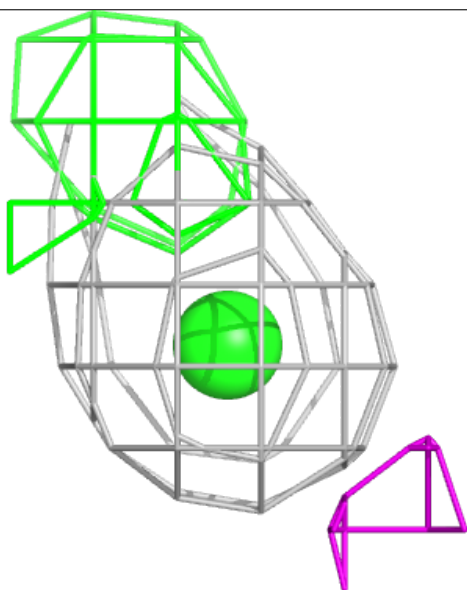
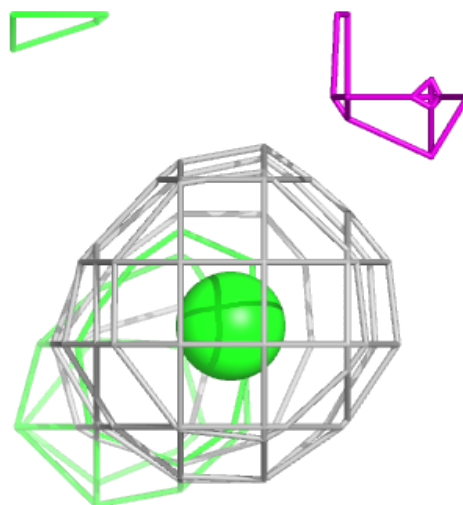
**Electron density around CL CCC 305 (A):**

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



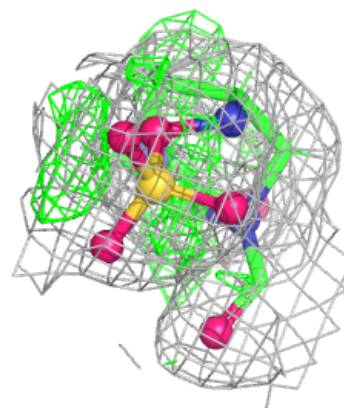
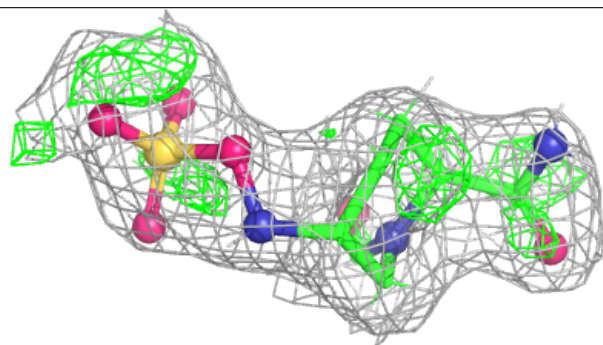
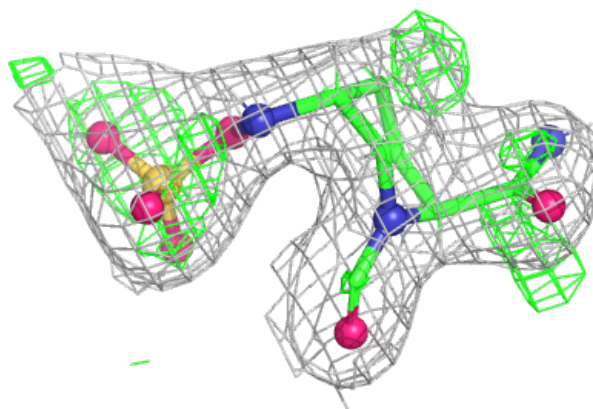
**Electron density around CL CCC 305 (B):**

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



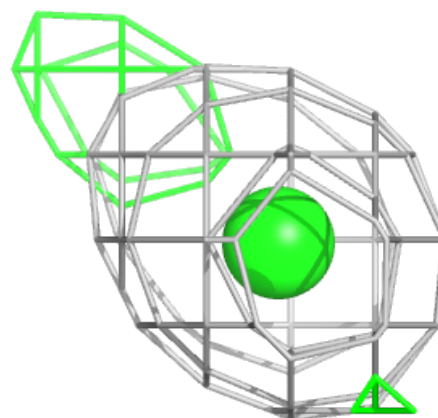
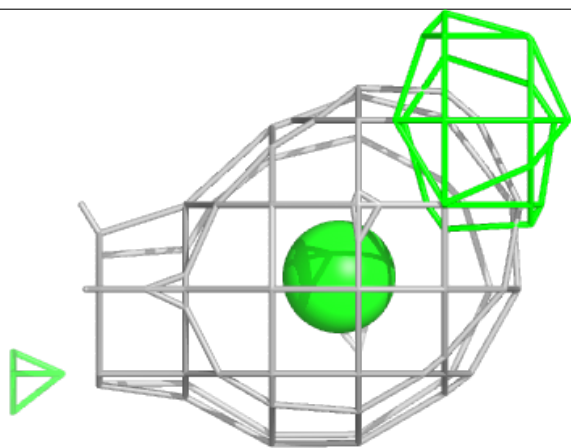
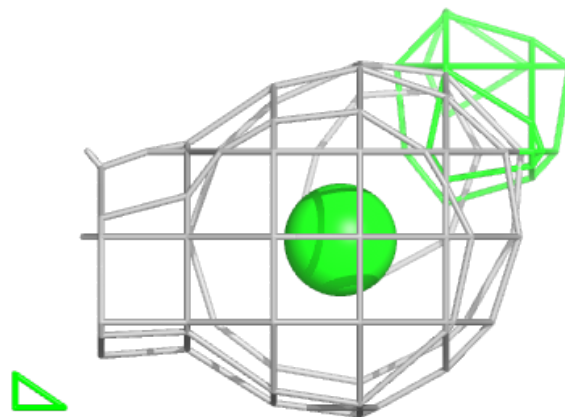
**Electron density around NXL BBB 304:**

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



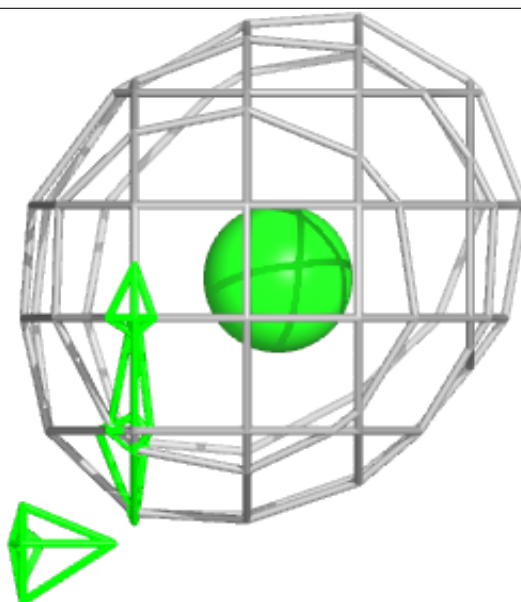
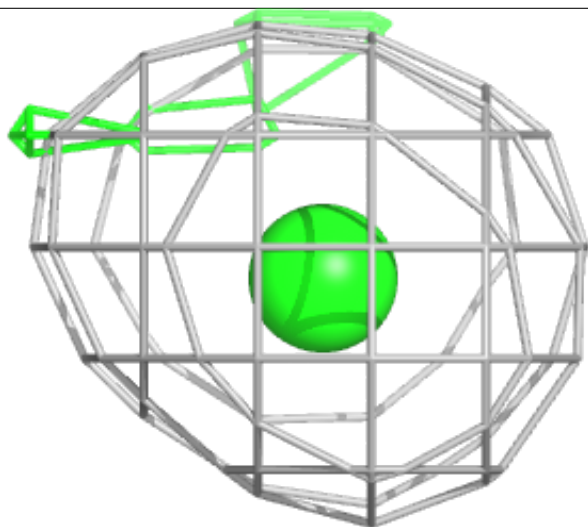
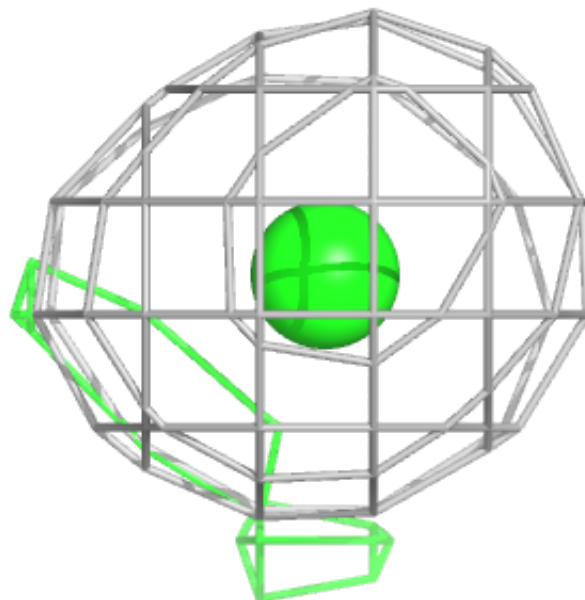
**Electron density around CL AAA 406 (B):**

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



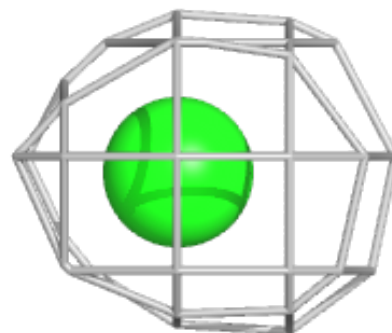
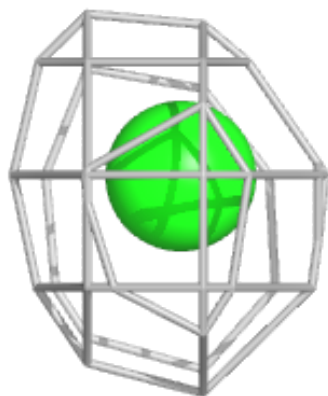
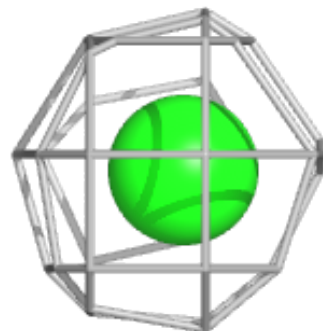
**Electron density around CL BBB 305 (A):**

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



**Electron density around CL BBB 305 (B):**

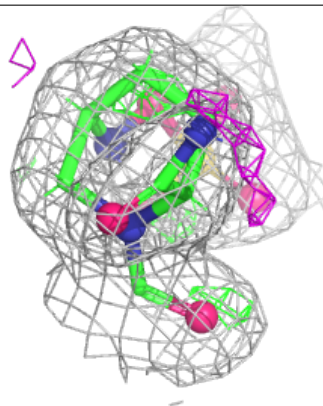
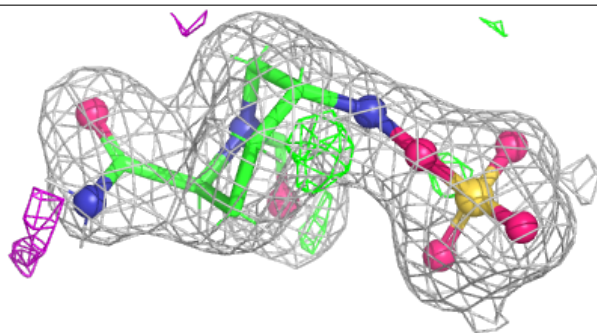
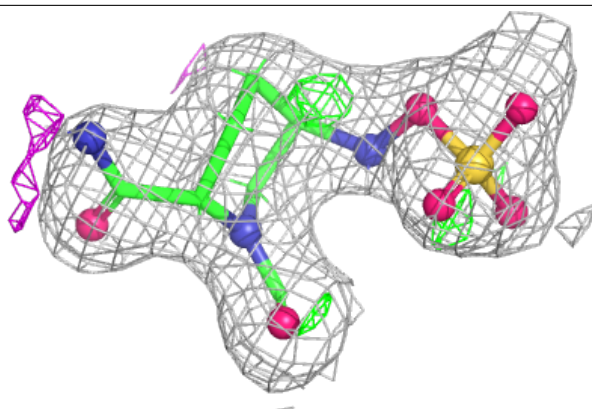
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around NXL AAA 403:**

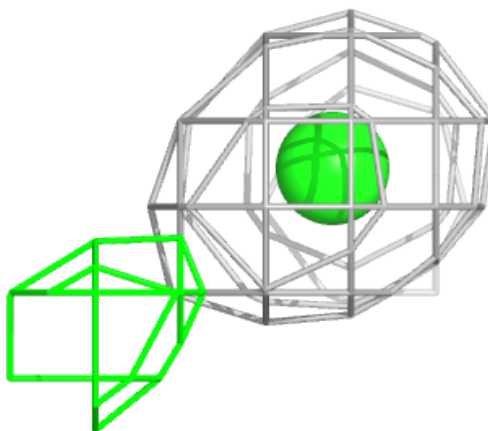
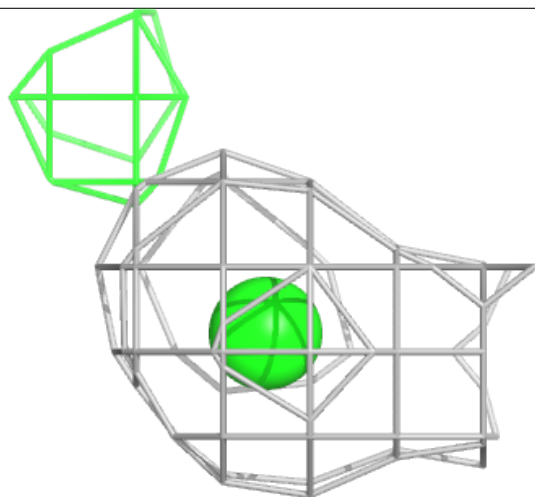
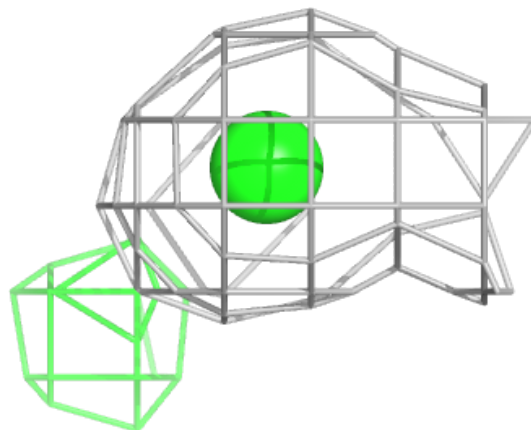
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





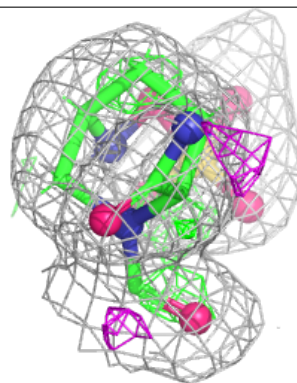
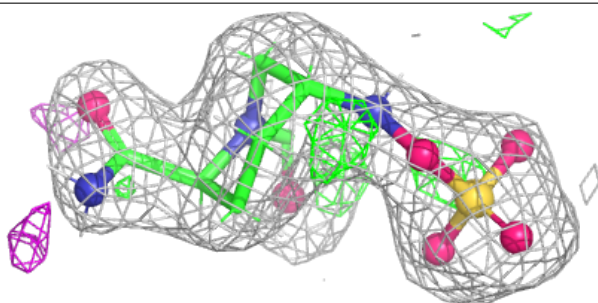
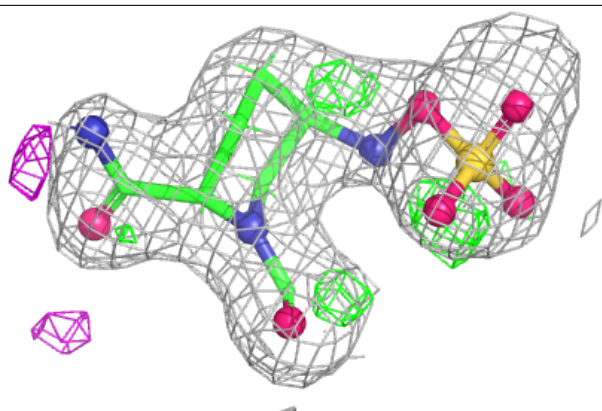
**Electron density around CL AAA 406 (A):**

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



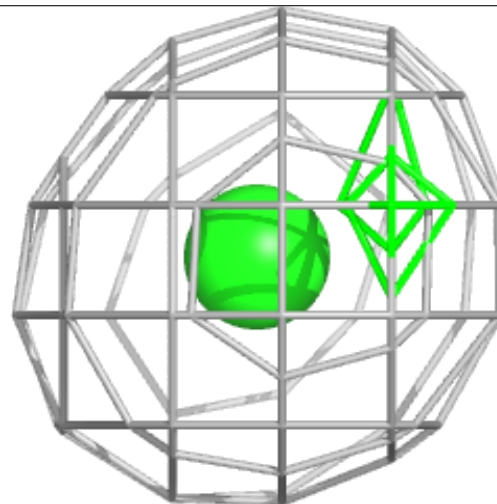
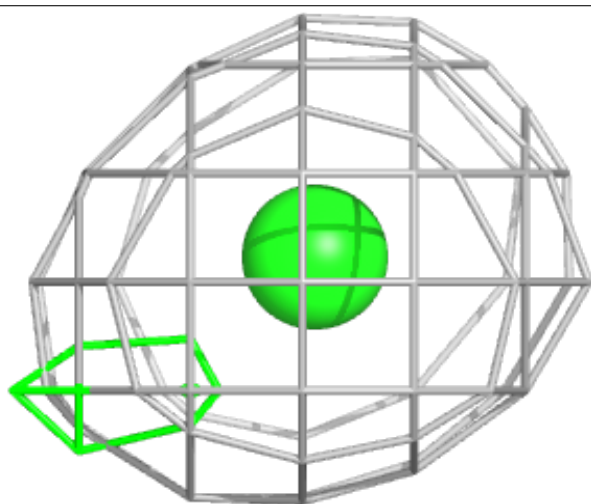
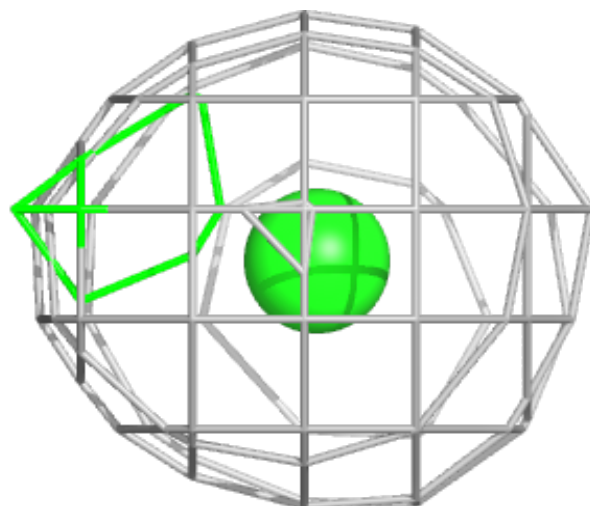
**Electron density around NXL CCC 303:**

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



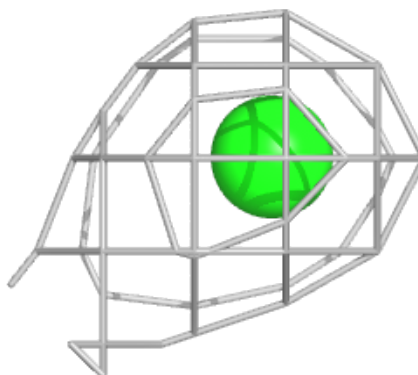
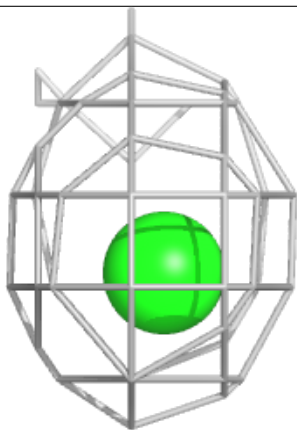
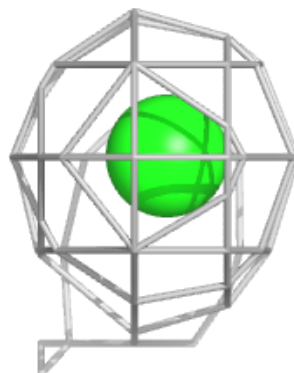
**Electron density around CL DDD 303 (A):**

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



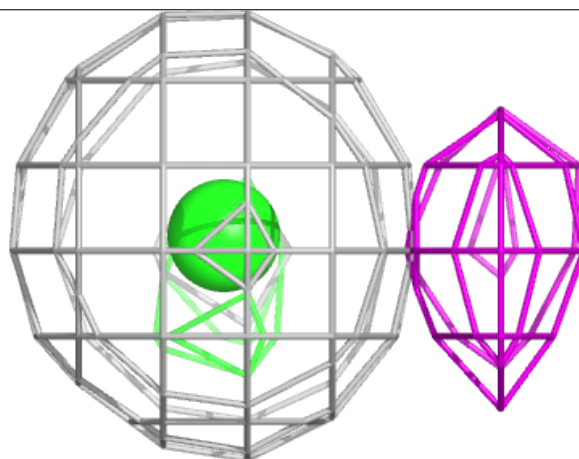
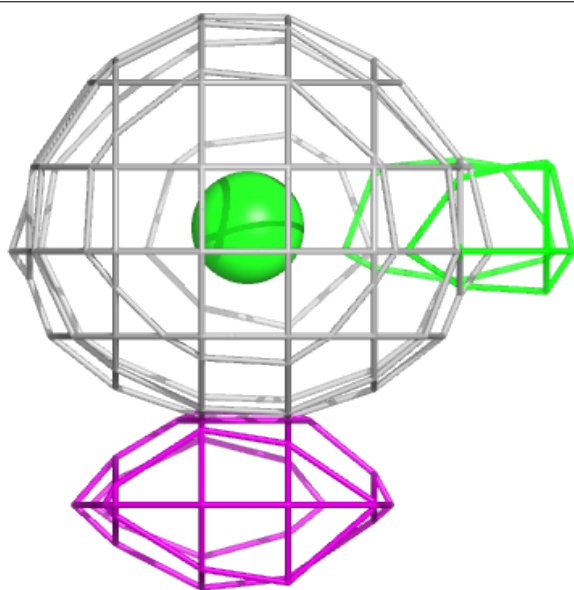
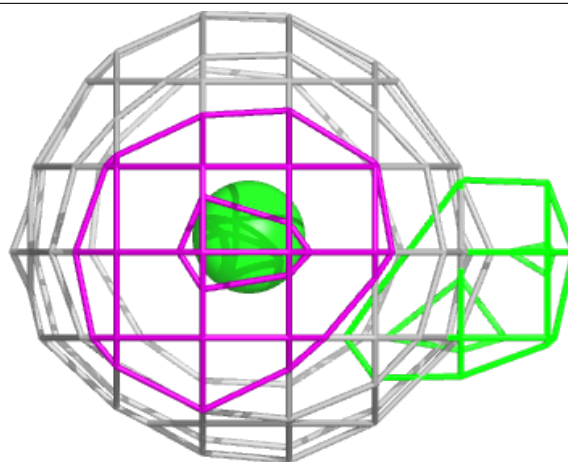
**Electron density around CL DDD 303 (B):**

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



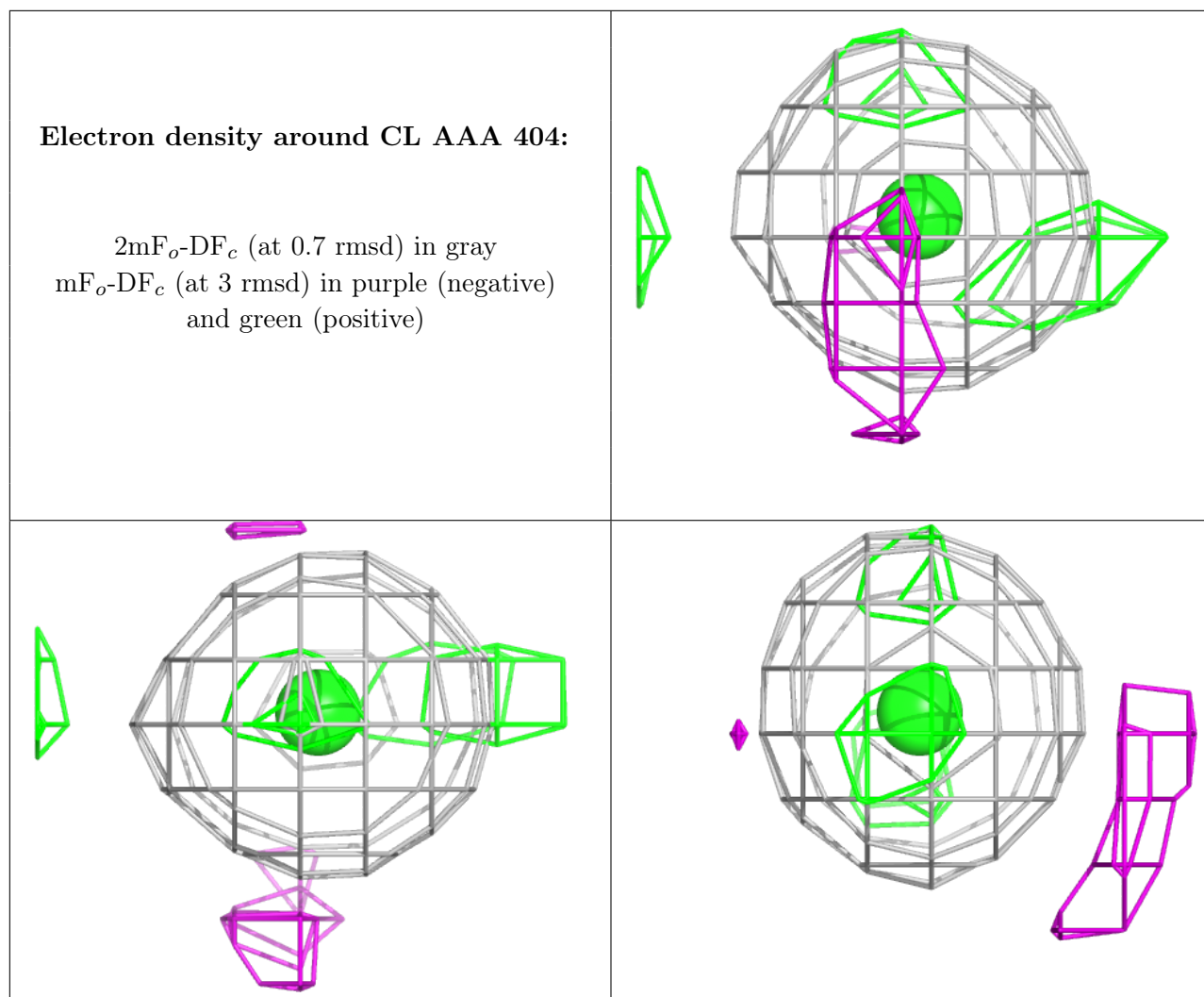
**Electron density around CL CCC 304:**

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



**Electron density around CL AAA 404:**

$2mF_o-DF_c$  (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.