



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2021 – 02:19 PM JST

PDB ID : 7V3C  
Title : Crystal structure of NP exonuclease C409A-PCMB complex  
Authors : Hsiao, Y.Y.; Huang, K.W.  
Deposited on : 2021-08-10  
Resolution : 1.90 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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.24  
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) : 2.24

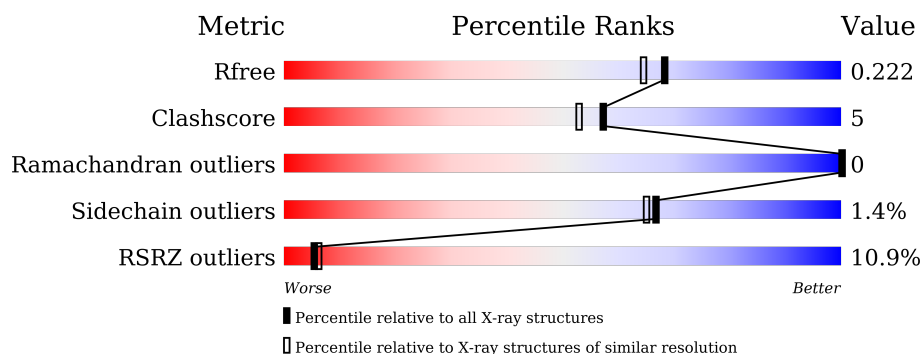
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	249	<div> <div>8%</div> <div>71%</div> <div>9%</div> <div>19%</div> </div>
1	B	249	<div> <div>10%</div> <div>71%</div> <div>9%</div> <div>19%</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
4	HGB	B	602	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3361 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	0	0	0
			1577	995	268	302	12			
1	B	201	Total	C	N	O	S	0	0	0
			1577	995	268	302	12			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	321	MET	-	initiating methionine	UNP P13699
A	322	GLY	-	expression tag	UNP P13699
A	323	SER	-	expression tag	UNP P13699
A	324	SER	-	expression tag	UNP P13699
A	325	HIS	-	expression tag	UNP P13699
A	326	HIS	-	expression tag	UNP P13699
A	327	HIS	-	expression tag	UNP P13699
A	328	HIS	-	expression tag	UNP P13699
A	329	HIS	-	expression tag	UNP P13699
A	330	HIS	-	expression tag	UNP P13699
A	331	SER	-	expression tag	UNP P13699
A	332	SER	-	expression tag	UNP P13699
A	333	GLY	-	expression tag	UNP P13699
A	334	LEU	-	expression tag	UNP P13699
A	335	VAL	-	expression tag	UNP P13699
A	336	PRO	-	expression tag	UNP P13699
A	337	ARG	-	expression tag	UNP P13699
A	338	GLY	-	expression tag	UNP P13699
A	339	SER	-	expression tag	UNP P13699
A	340	HIS	-	expression tag	UNP P13699
A	341	MET	-	expression tag	UNP P13699
A	409	ALA	CYS	engineered mutation	UNP P13699
B	321	MET	-	initiating methionine	UNP P13699
B	322	GLY	-	expression tag	UNP P13699
B	323	SER	-	expression tag	UNP P13699

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Chain	Residue	Modelled	Actual	Comment	Reference
B	324	SER	-	expression tag	UNP P13699
B	325	HIS	-	expression tag	UNP P13699
B	326	HIS	-	expression tag	UNP P13699
B	327	HIS	-	expression tag	UNP P13699
B	328	HIS	-	expression tag	UNP P13699
B	329	HIS	-	expression tag	UNP P13699
B	330	HIS	-	expression tag	UNP P13699
B	331	SER	-	expression tag	UNP P13699
B	332	SER	-	expression tag	UNP P13699
B	333	GLY	-	expression tag	UNP P13699
B	334	LEU	-	expression tag	UNP P13699
B	335	VAL	-	expression tag	UNP P13699
B	336	PRO	-	expression tag	UNP P13699
B	337	ARG	-	expression tag	UNP P13699
B	338	GLY	-	expression tag	UNP P13699
B	339	SER	-	expression tag	UNP P13699
B	340	HIS	-	expression tag	UNP P13699
B	341	MET	-	expression tag	UNP P13699
B	409	ALA	CYS	engineered mutation	UNP P13699

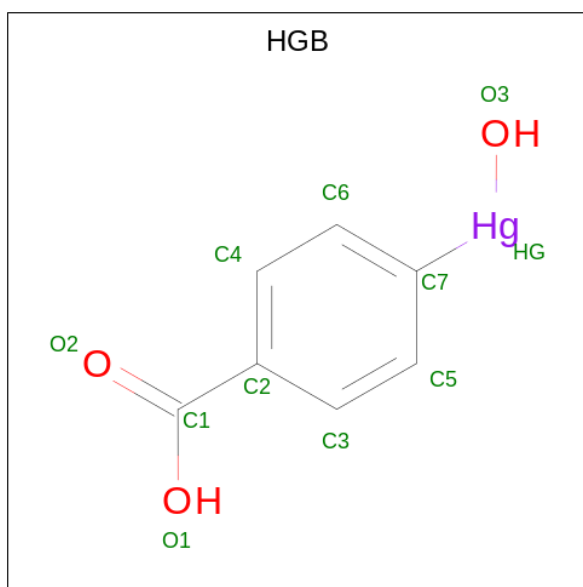
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is 4-(HYDROXYMERCURY)BENZOIC ACID (three-letter code: HGB) (formula: C<sub>7</sub>H<sub>6</sub>HgO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	Hg	O	0	0
			10	7	1	2		

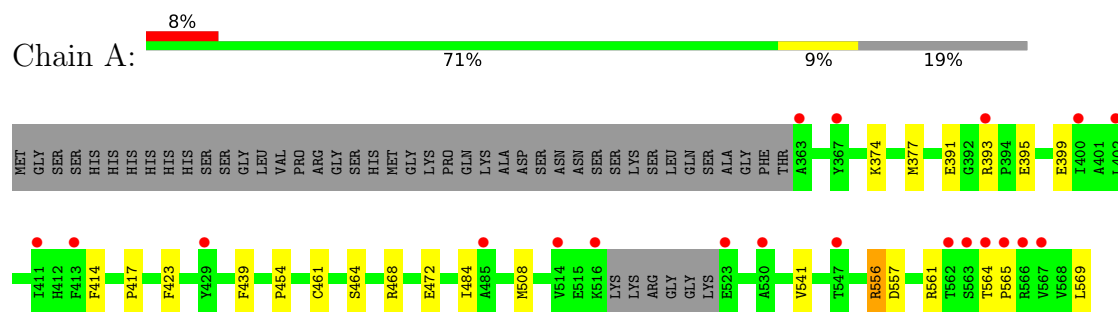
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	103	Total	O	0	0
			103	103		
5	B	90	Total	O	0	0
			90	90		

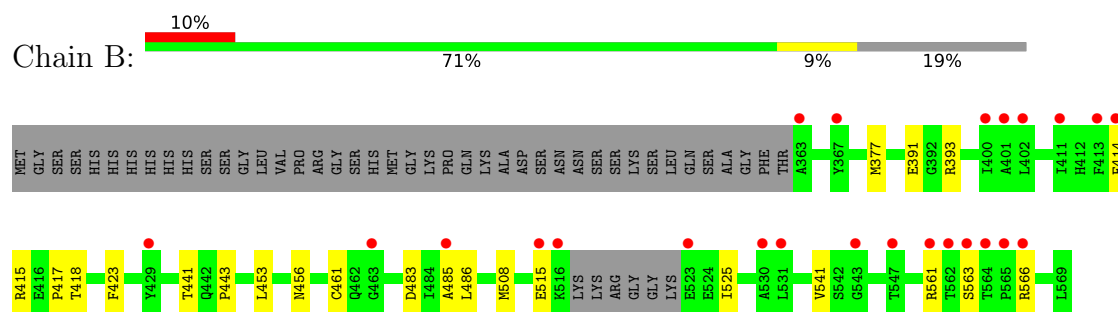
### 3 Residue-property plots [i](#)

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: Nucleoprotein



#### • Molecule 1: Nucleoprotein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.85Å 58.81Å 68.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.44 – 1.90 26.44 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (26.44-1.90) 99.4 (26.44-1.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.81 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.187 , 0.222 0.188 , 0.222	Depositor DCC
$R_{free}$ test set	3096 reflections (7.67%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.5	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 50.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3361	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	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 28.91 % 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 1.6987e-03. 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, HGB

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	0.59	0/1606	0.68	0/2175
1	B	0.58	0/1606	0.70	0/2175
All	All	0.59	0/3212	0.69	0/4350

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	1577	0	1574	16	0
1	B	1577	0	1573	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	10	0	4	4	0
5	A	103	0	0	3	0
5	B	90	0	0	2	0
All	All	3361	0	3151	31	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 (31) 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:439:PHE:O	1:A:561:ARG:NH1	2.14	0.80
1:A:556:ARG:HD3	1:A:556:ARG:H	1.54	0.72
1:A:569:LEU:O	5:A:701:HOH:O	2.11	0.69
1:B:483:ASP:HB3	4:B:602:HGB:C7	2.30	0.61
1:A:484:ILE:HG12	1:A:541:VAL:HG21	1.84	0.59
1:A:468:ARG:O	1:A:472:GLU:HG3	2.05	0.56
1:B:483:ASP:HB3	4:B:602:HGB:C5	2.35	0.56
1:B:415:ARG:HH22	1:B:418:THR:HG23	1.71	0.56
1:A:393:ARG:HG3	5:A:762:HOH:O	2.06	0.54
1:A:414:PHE:CZ	1:A:508:MET:HG3	2.44	0.53
1:A:556:ARG:HD3	1:A:556:ARG:N	2.26	0.50
1:A:564:THR:HG22	1:A:565:PRO:O	2.13	0.49
1:B:391:GLU:OE2	5:B:701:HOH:O	2.20	0.47
1:B:485:ALA:HA	4:B:602:HGB:HC3	1.97	0.46
1:B:414:PHE:CZ	1:B:508:MET:HG3	2.50	0.46
1:B:441:THR:O	1:B:443:PRO:HD3	2.16	0.46
1:A:374:LYS:HD2	5:A:715:HOH:O	2.15	0.45
1:B:515:GLU:HB2	1:B:525:ILE:HD13	1.97	0.45
1:B:417:PRO:HG3	1:B:423:PHE:CD1	2.52	0.45
1:A:461:CYS:SG	1:A:464:SER:HA	2.57	0.45
1:B:486:LEU:HD11	1:B:541:VAL:HG23	1.99	0.44
1:B:563:SER:HB3	1:B:566:ARG:HH21	1.82	0.44
1:B:377:MET:HE1	1:B:453:LEU:HD23	2.00	0.43
1:B:456:ASN:HB2	5:B:750:HOH:O	2.19	0.42
1:B:485:ALA:CA	4:B:602:HGB:HC3	2.50	0.41
1:A:417:PRO:HG3	1:A:423:PHE:CD2	2.56	0.41
1:A:377:MET:HE2	1:A:454:PRO:HD3	2.02	0.41
1:A:395:GLU:H	1:A:395:GLU:CD	2.23	0.41
1:A:391:GLU:HB2	1:A:399:GLU:HB3	2.03	0.40
1:B:415:ARG:NH2	1:B:418:THR:HG23	2.34	0.40
1:A:393:ARG:HB3	1:A:395:GLU:OE1	2.21	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	197/249 (79%)	194 (98%)	3 (2%)	0	100	100
1	B	197/249 (79%)	190 (96%)	7 (4%)	0	100	100
All	All	394/498 (79%)	384 (98%)	10 (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	A	176/215 (82%)	174 (99%)	2 (1%)	73	73
1	B	176/215 (82%)	173 (98%)	3 (2%)	60	57
All	All	352/430 (82%)	347 (99%)	5 (1%)	67	65

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

Mol	Chain	Res	Type
1	A	556	ARG
1	A	557	ASP
1	B	393	ARG
1	B	461	CYS
1	B	561	ARG

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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z  > 2$
4	HGB	B	602	5,1	5,10,11	1.47	1 (20%)	8,13,14	2.07	4 (50%)

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
4	HGB	B	602	5,1	-	0/0/4/6	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	602	HGB	C2-C1	3.05	1.50	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	602	HGB	C3-C5-C7	-3.05	115.61	121.56
4	B	602	HGB	C6-C4-C2	-2.87	117.01	121.13
4	B	602	HGB	C4-C2-C3	2.79	123.15	117.59
4	B	602	HGB	C3-C2-C1	-2.14	117.50	120.37

There are no chirality outliers.

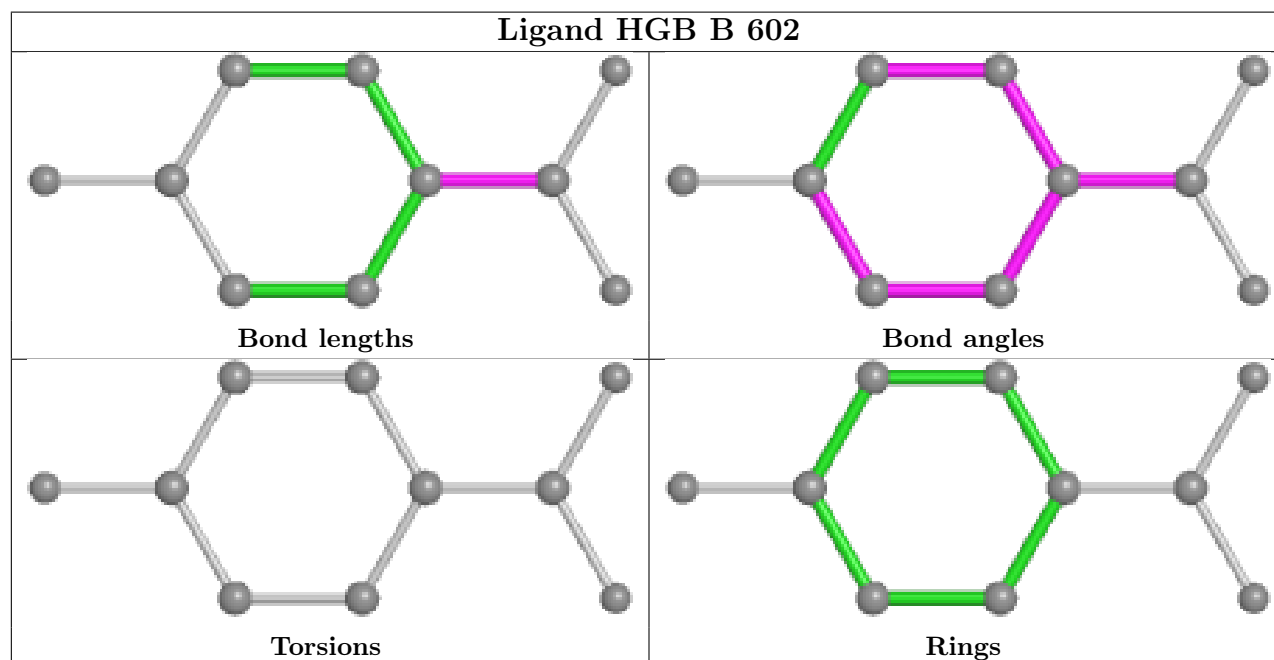
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	602	HGB	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	201/249 (80%)	0.44	20 (9%) <b>7</b> <b>8</b>	23, 41, 77, 113	0
1	B	201/249 (80%)	0.53	24 (11%) <b>4</b> <b>5</b>	21, 40, 81, 111	0
All	All	402/498 (80%)	0.49	44 (10%) <b>5</b> <b>6</b>	21, 40, 81, 113	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	564	THR	9.3
1	B	563	SER	8.7
1	B	562	THR	8.6
1	A	564	THR	8.3
1	A	565	PRO	7.0
1	B	363	ALA	6.3
1	A	563	SER	6.2
1	B	463	GLY	6.0
1	A	363	ALA	5.8
1	B	367	TYR	5.2
1	B	516	LYS	5.1
1	A	516	LYS	4.7
1	A	367	TYR	4.6
1	B	547	THR	3.9
1	A	523	GLU	3.9
1	A	567	VAL	3.8
1	B	561	ARG	3.8
1	A	566	ARG	3.7
1	B	485	ALA	3.7
1	B	523	GLU	3.4
1	A	400	ILE	3.4
1	A	562	THR	3.4
1	B	400	ILE	3.2
1	B	565	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	547	THR	2.9
1	B	411	ILE	2.6
1	B	530	ALA	2.5
1	B	566	ARG	2.5
1	A	429	TYR	2.4
1	B	402	LEU	2.4
1	B	429	TYR	2.4
1	B	401	ALA	2.3
1	A	413	PHE	2.2
1	A	530	ALA	2.2
1	B	414	PHE	2.2
1	A	402	LEU	2.2
1	A	485	ALA	2.2
1	A	411	ILE	2.1
1	A	393	ARG	2.1
1	B	413	PHE	2.1
1	B	543	GLY	2.1
1	A	514	VAL	2.1
1	B	515	GLU	2.0
1	B	531	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	B	603	1/1	0.87	0.07	41,41,41,41	0
3	MG	A	602	1/1	0.89	0.08	46,46,46,46	0
4	HGB	B	602	10/11	0.99	0.13	36,40,44,44	10

*Continued on next page...*



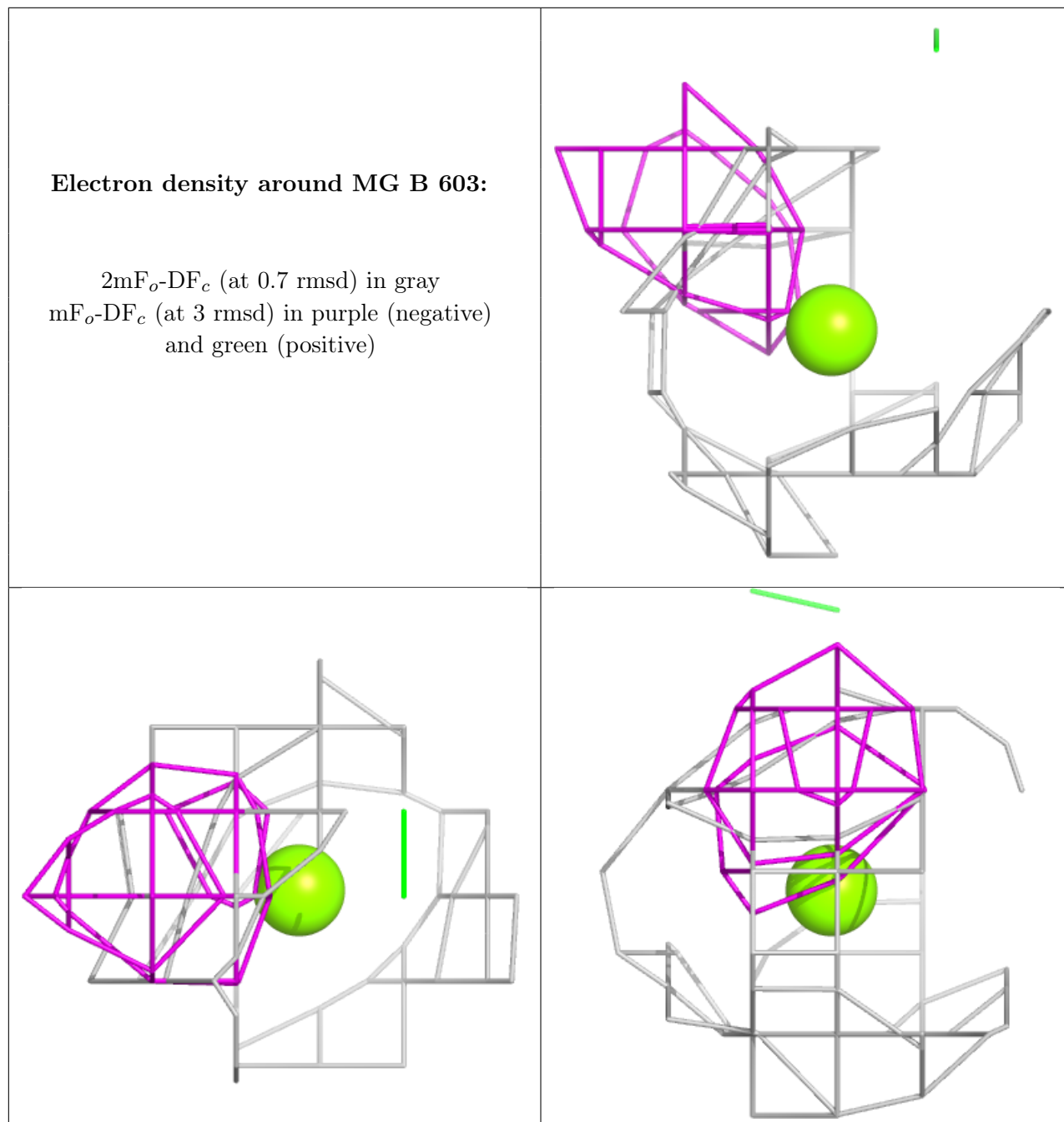
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	601	1/1	1.00	0.10	25,25,25,25	0
2	ZN	A	601	1/1	1.00	0.09	28,28,28,28	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.

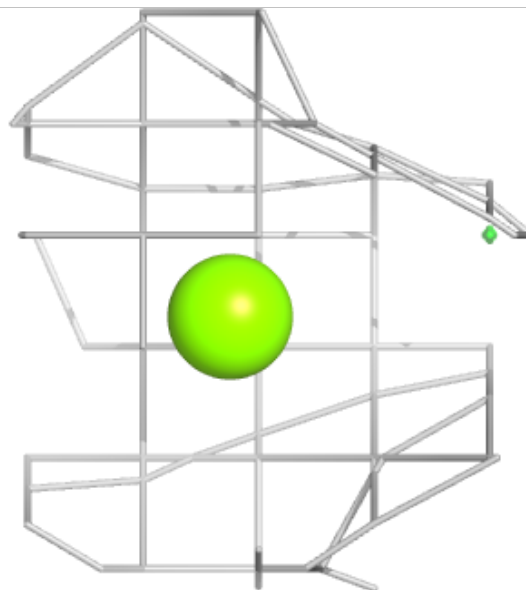
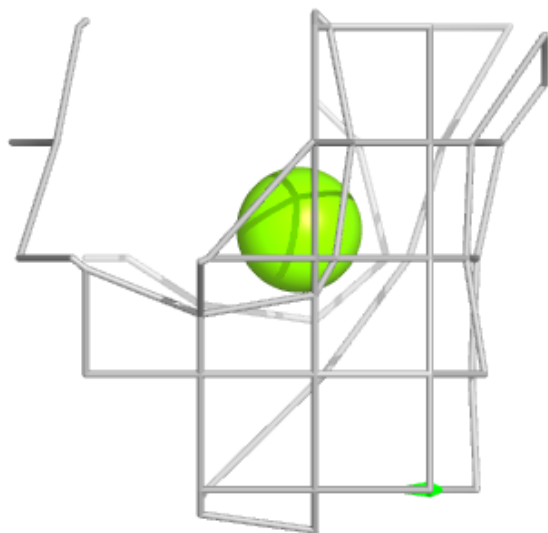
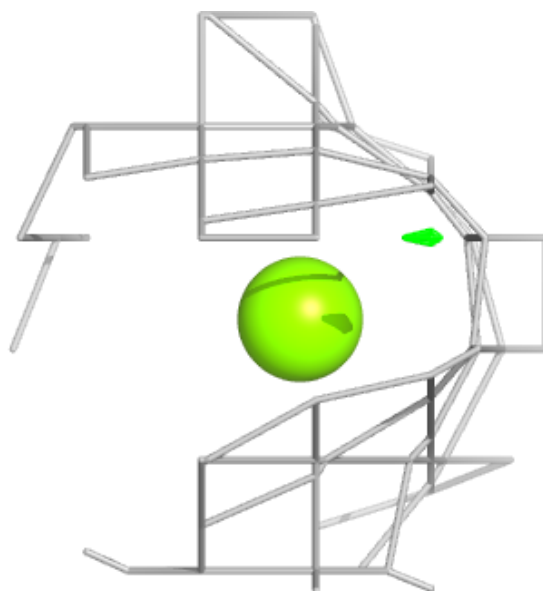
**Electron density around MG B 603:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



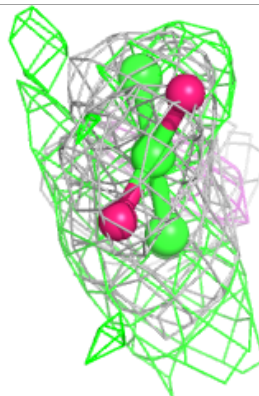
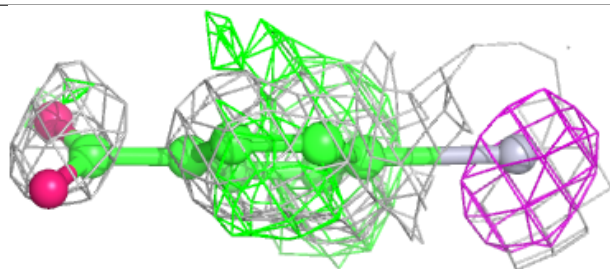
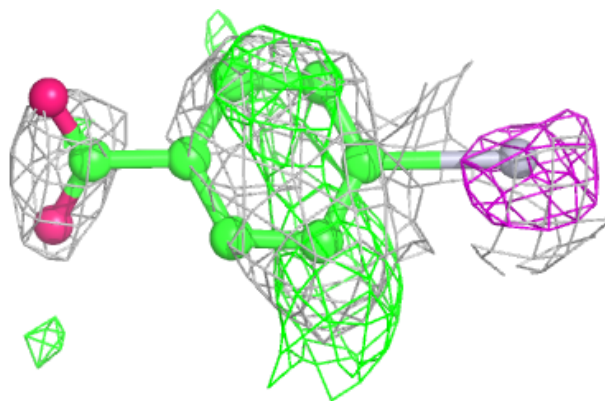
**Electron density around MG A 602:**

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



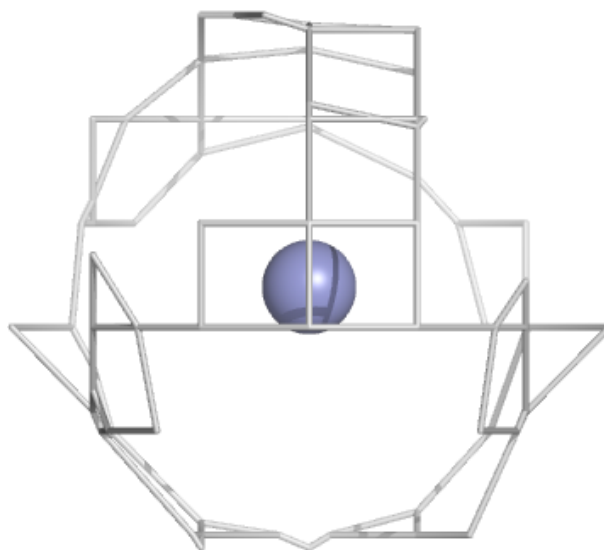
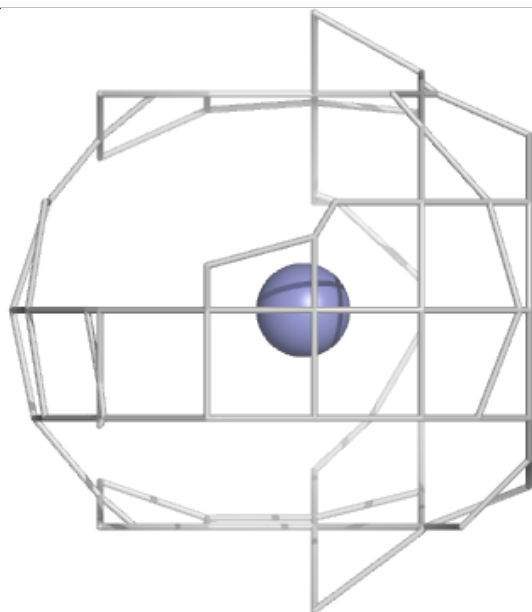
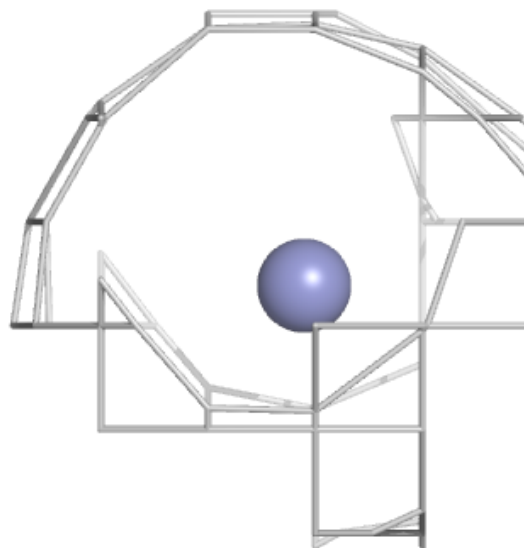
**Electron density around HGB B 602:**

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



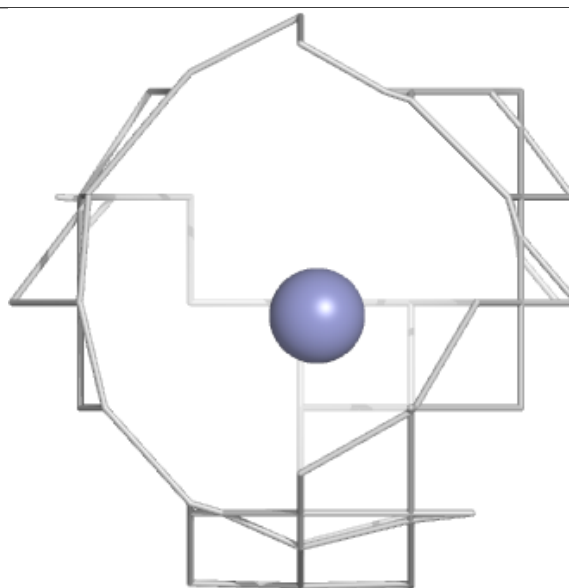
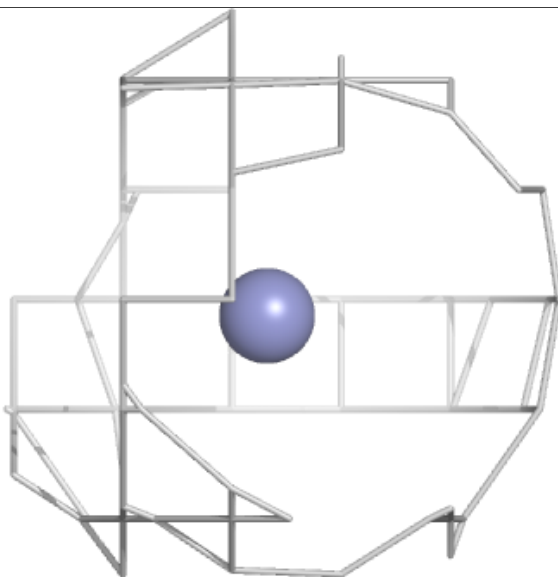
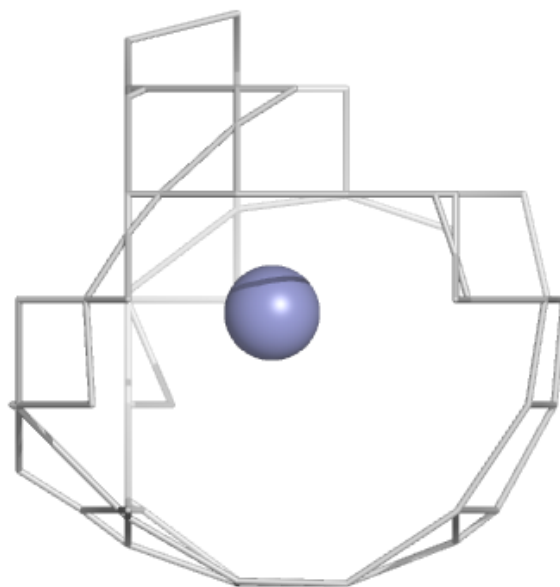
**Electron density around ZN B 601:**

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



**Electron density around ZN 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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.