



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 20, 2025 – 02:41 AM JST

PDB ID : 9K7X / pdb\_00009k7x  
Title : Crystal structure of designed calcium-induced homotrimer C3-Ca1-DN\*3-20  
Authors : Qu, Y.N.; Cao, L.X.  
Deposited on : 2024-10-24  
Resolution : 2.00 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

i

## X-RAY DIFFRACTION


A.

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 <sub>free</sub>	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	112	 <div>72%6%21%</div>
1	B	112	 <div>%63%16%21%</div>
1	C	112	 <div>68%12%21%</div>
1	D	112	 <div>%77%.20%</div>
1	E	112	 <div>%62%16%21%</div>
1	F	112	 <div>62%16%22%</div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4473 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 C3-Ca1-DN\*3-20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	88	Total	C	N	O	S	0	0	0
			686	430	107	148	1			
1	B	89	Total	C	N	O	S	0	0	0
			696	436	109	150	1			
1	C	89	Total	C	N	O	S	0	0	0
			696	436	109	150	1			
1	D	90	Total	C	N	O	S	0	0	0
			700	438	110	151	1			
1	E	88	Total	C	N	O	S	0	0	0
			682	428	107	146	1			
1	F	87	Total	C	N	O	S	0	0	0
			682	428	107	146	1			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		
2	C	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is water.

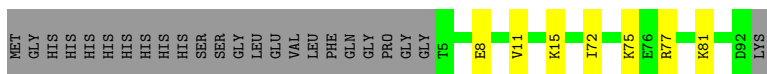
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total	O	0	0
			62	62		
4	B	68	Total	O	0	0
			68	68		
4	C	68	Total	O	0	0
			68	68		
4	D	52	Total	O	0	0
			52	52		
4	E	35	Total	O	0	0
			35	35		
4	F	35	Total	O	0	0
			35	35		

### 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.

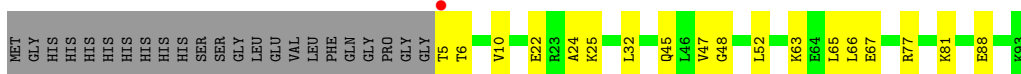
- Molecule 1: C3-Ca1-DN\*3-20

Chain A: 



- Molecule 1: C3-Ca1-DN\*3-20

Chain B: 




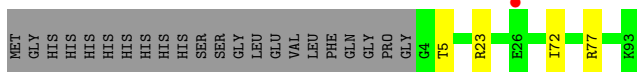
- Molecule 1: C3-Ca1-DN\*3-20

Chain C: 



- Molecule 1: C3-Ca1-DN\*3-20

Chain D: 



- Molecule 1: C3-Ca1-DN\*3-20

Chain E: 



- Molecule 1: C3-Ca1-DN\*3-20

Chain F: 

MET	GLY	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	SER	SER	GLY	LEU	GLU	VAL	LEU	PHE	GLN	GLY	PRO	GLY	GLY	THR	THR	E7	E8	V11	K12	K16	L18	R23	A24	K25	D29	D42	K57	L65	L66	E67	E68	S69	D70	E71	I72	K75	K93
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	34.61Å 77.56Å 82.81Å 90.00° 92.46° 90.00°	Depositor
Resolution (Å)	27.11 – 2.00 27.11 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (27.11-2.00) 97.5 (27.11-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.46 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.172 , 0.227 0.172 , 0.227	Depositor DCC
$R_{free}$ test set	1966 reflections (6.63%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 48.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4473	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.96% 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 [i](#)

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

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

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	0.29	0/686	0.42	0/921
1	B	0.31	0/696	0.46	0/932
1	C	0.29	0/696	0.44	0/932
1	D	0.28	0/700	0.39	0/937
1	E	0.25	0/682	0.39	0/915
1	F	0.25	0/682	0.42	0/912
All	All	0.28	0/4142	0.42	0/5549

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	A	686	0	709	8	0
1	B	696	0	722	13	0
1	C	696	0	722	13	0
1	D	700	0	725	3	0
1	E	682	0	708	13	0
1	F	682	0	708	16	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
3	D	8	0	12	0	0
4	A	62	0	0	3	0
4	B	68	0	0	2	0
4	C	68	0	0	5	0
4	D	52	0	0	1	0
4	E	35	0	0	3	0
4	F	35	0	0	5	0
All	All	4473	0	4306	62	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.

The worst 5 of 62 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:E:25:LYS:HE3	1:E:64:GLU:HB2	1.65	0.78
1:F:11:VAL:HG22	1:F:15:LYS:HE2	1.69	0.74
1:B:63:LYS:NZ	1:B:88:GLU:OE1	2.21	0.70
1:B:48:GLY:HA2	1:B:52:LEU:CD2	2.23	0.69
1:E:25:LYS:NZ	4:E:104:HOH:O	2.31	0.64

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	86/112 (77%)	86 (100%)	0	0	100	100
1	B	87/112 (78%)	87 (100%)	0	0	100	100
1	C	87/112 (78%)	85 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	88/112 (79%)	88 (100%)	0	0	100	100
1	E	86/112 (77%)	85 (99%)	0	1 (1%)	11	6
1	F	85/112 (76%)	85 (100%)	0	0	100	100
All	All	519/672 (77%)	516 (99%)	2 (0%)	1 (0%)	44	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	70	ASP

### 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	77/96 (80%)	77 (100%)	0	100	100
1	B	78/96 (81%)	76 (97%)	2 (3%)	41	44
1	C	78/96 (81%)	78 (100%)	0	100	100
1	D	78/96 (81%)	78 (100%)	0	100	100
1	E	76/96 (79%)	75 (99%)	1 (1%)	65	71
1	F	76/96 (79%)	76 (100%)	0	100	100
All	All	463/576 (80%)	460 (99%)	3 (1%)	84	88

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	5	THR
1	B	6	THR
1	E	31	GLU

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

Mol	Chain	Res	Type
1	A	79	GLN
1	F	38	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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	$\# Z  > 2$
3	TRS	D	101	-	7,7,7	0.27	0	9,9,9	0.31	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
3	TRS	D	101	-	-	0/9/9/9	-

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.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	88/112 (78%)	-0.50	0 <b>100</b> <b>100</b>	9, 17, 36, 40	0
1	B	89/112 (79%)	-0.56	1 (1%) 77 76	8, 16, 32, 49	0
1	C	89/112 (79%)	-0.49	0 <b>100</b> <b>100</b>	10, 19, 35, 51	0
1	D	90/112 (80%)	-0.32	1 (1%) 77 76	8, 21, 41, 50	0
1	E	88/112 (78%)	-0.22	1 (1%) 77 76	11, 23, 42, 54	0
1	F	87/112 (77%)	-0.19	0 <b>100</b> <b>100</b>	11, 22, 40, 49	0
All	All	531/672 (79%)	-0.38	3 (0%) 85 85	8, 20, 40, 54	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	5	THR	3.2
1	D	26	GLU	2.6
1	E	69	SER	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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

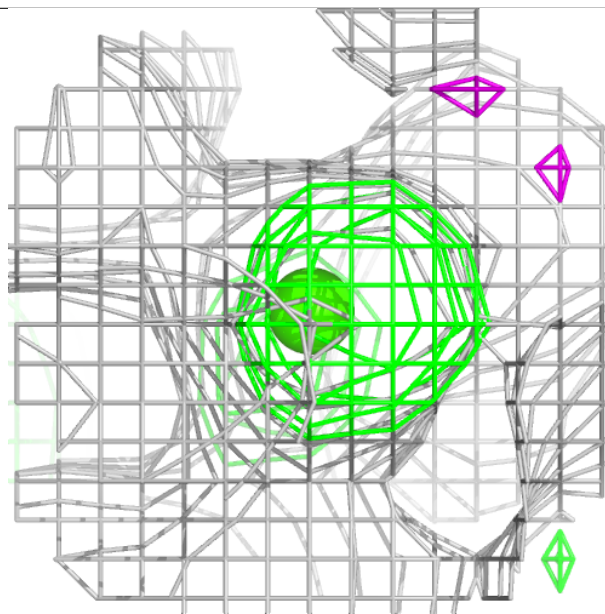
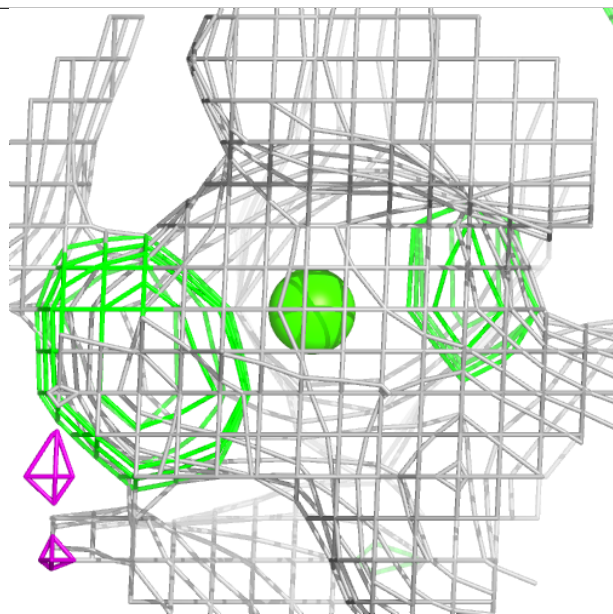
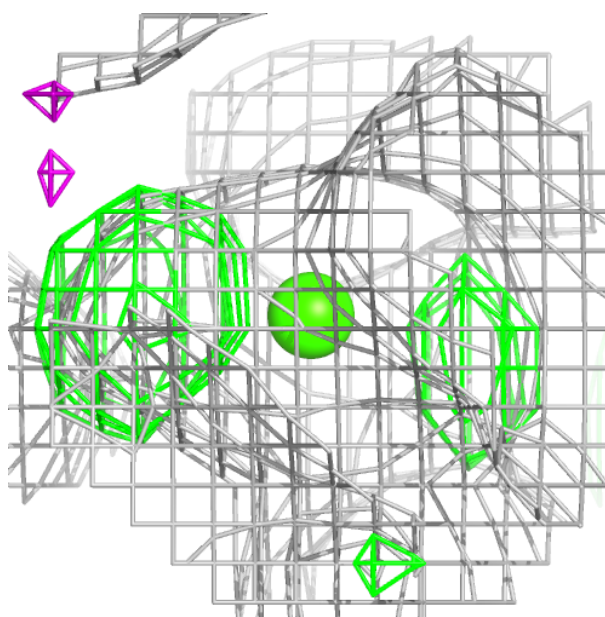
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	CA	A	101	1/1	0.87	0.07	24,24,24,24	0
3	TRS	D	101	8/8	0.94	0.05	22,27,31,31	0
2	CA	C	101	1/1	0.96	0.06	20,20,20,20	0
2	CA	A	102	1/1	0.99	0.05	14,14,14,14	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.

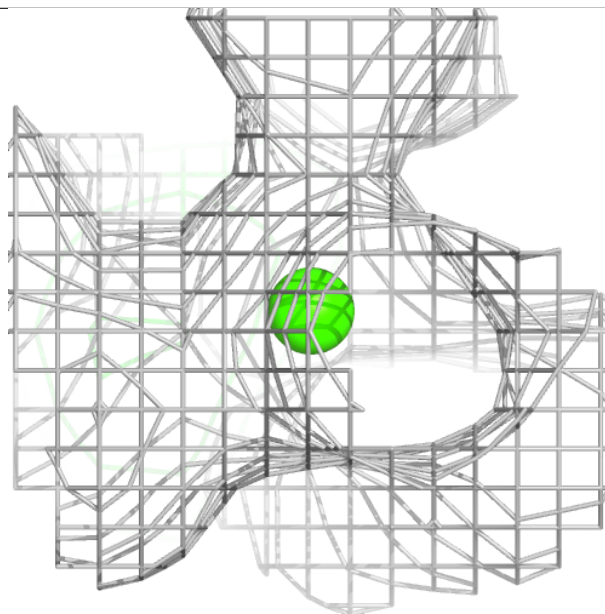
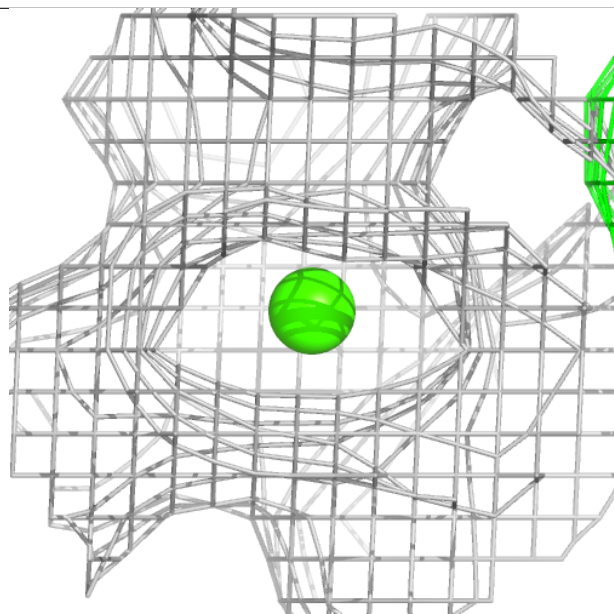
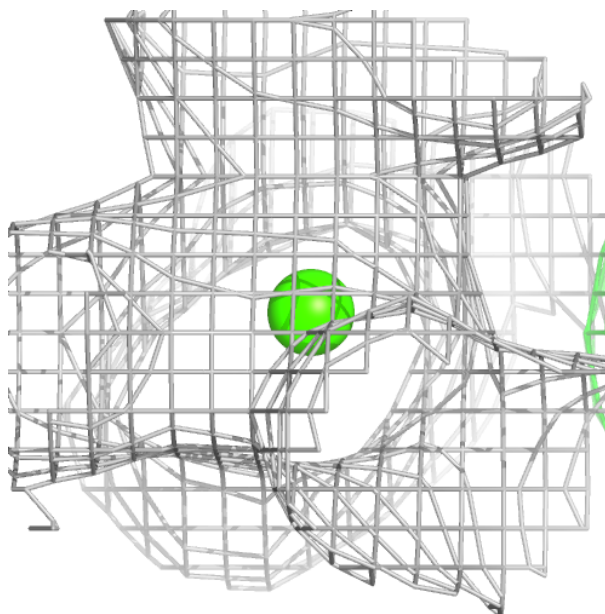
**Electron density around CA A 101:**

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



**Electron density around CA C 101:**

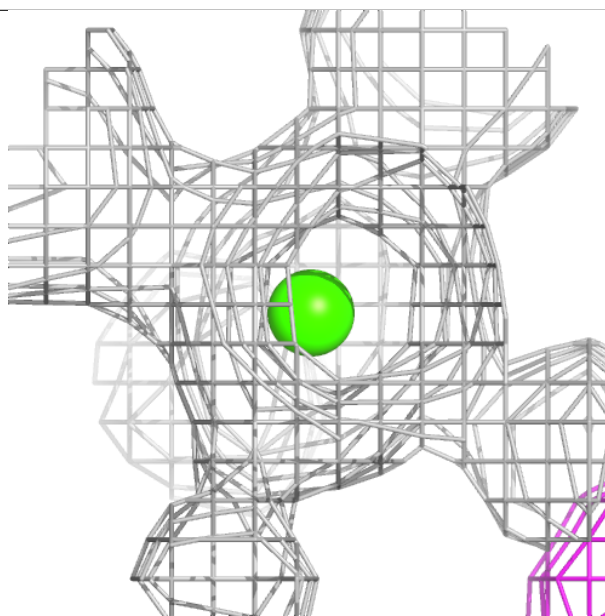
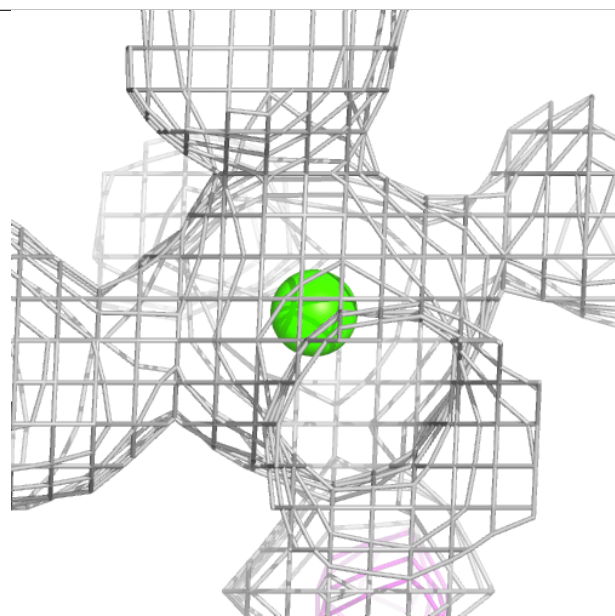
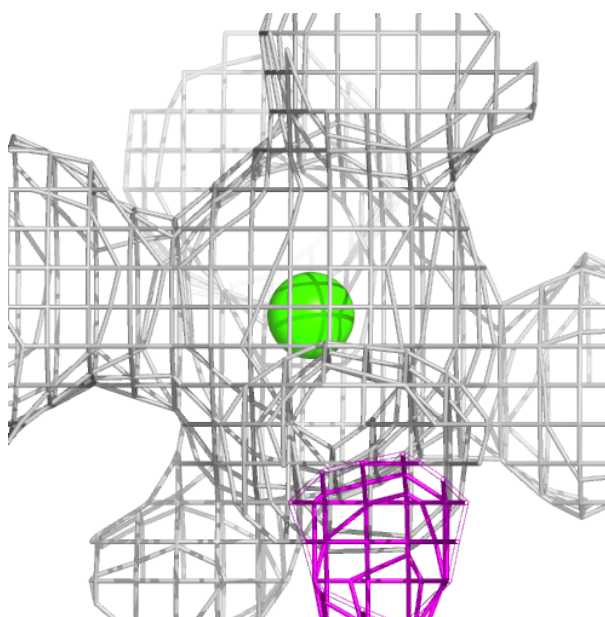
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around CA A 102:**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.