



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 22, 2025 – 04:08 PM JST

PDB ID : 9K6M / pdb_00009k6m
Title : Crystal structure of the Dictyostelium discoideum mitochondrial calcium uptake protein (DdMICU)
Authors : Jin, M.; Yang, J.; Park, J.; Kim, H.; Eom, S.H.
Deposited on : 2024-10-22
Resolution : 2.50 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

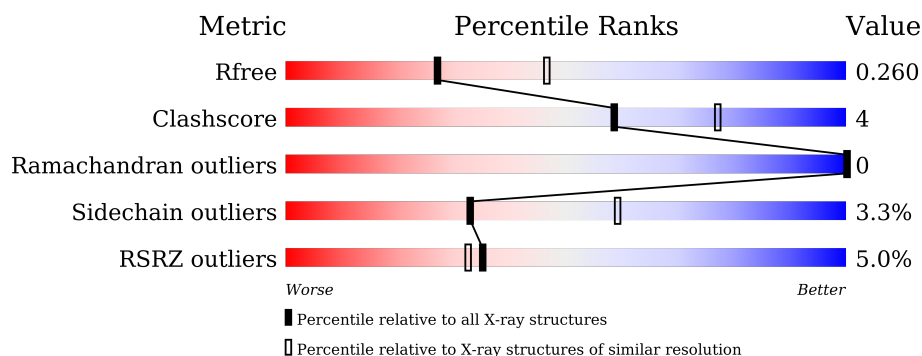
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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 ≥ 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	371	<div> <div>4%</div> <div> <div></div> <div>66%</div> <div>8%</div> <div>25%</div> </div> </div>
1	B	371	<div> <div>4%</div> <div> <div></div> <div>63%</div> <div>7%</div> <div>30%</div> </div> </div>

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Chain	Residue	Modelled	Actual	Comment	Reference
B	102	GLN	-	expression tag	UNP Q54JS1
B	103	ASP	-	expression tag	UNP Q54JS1
B	104	PRO	-	expression tag	UNP Q54JS1

- 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	3	Total Ca 3 3	0	0
2	B	3	Total Ca 3 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	30	Total O 30 30	0	0
3	B	48	Total O 48 48	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.94Å 103.94Å 297.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.11 – 2.50 49.11 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.0 (49.11-2.50) 98.0 (49.11-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.78 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0415, PHENIX 1.21	Depositor
R, R_{free}	0.221 , 0.260 0.221 , 0.260	Depositor DCC
R_{free} test set	1442 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4298	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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.

5.3 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	271/371 (73%)	263 (97%)	8 (3%)	0	100	100
1	B	252/371 (68%)	240 (95%)	12 (5%)	0	100	100
All	All	523/742 (70%)	503 (96%)	20 (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	231/338 (68%)	222 (96%)	9 (4%)	27	52
1	B	224/338 (66%)	217 (97%)	7 (3%)	35	62
All	All	455/676 (67%)	439 (96%)	16 (4%)	33	57

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	VAL
1	A	189	ILE
1	A	237	PHE
1	A	288[A]	LYS
1	A	288[B]	LYS
1	A	291	SER
1	A	304	PHE
1	A	340	SER

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Mol	Chain	Res	Type
1	A	420	ASP
1	B	132	THR
1	B	144	LYS
1	B	182	ASP
1	B	293	LEU
1	B	352	ILE
1	B	411	GLN
1	B	424	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	312	GLN
1	A	315	GLN
1	A	382	GLN
1	B	238	ASN
1	B	299	GLN
1	B	382	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	277/371 (74%)	0.30	14 (5%) 34 32	15, 48, 86, 121	2 (0%)
1	B	261/371 (70%)	0.06	13 (4%) 35 32	12, 35, 77, 111	1 (0%)
All	All	538/742 (72%)	0.18	27 (5%) 35 32	12, 41, 83, 121	3 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	272	LEU	4.9
1	A	166	LYS	4.5
1	A	177	SER	4.5
1	A	331	LEU	4.0
1	A	333	HIS	4.0
1	B	327	LYS	4.0
1	B	330	GLN	3.8
1	A	251	ALA	3.8
1	B	436	ARG	3.7
1	A	334	HIS	3.7
1	A	250	PHE	3.4
1	B	333	HIS	3.1
1	B	332	GLU	2.9
1	B	334	HIS	2.9
1	B	244	LEU	2.8
1	B	331	LEU	2.7
1	A	436	ARG	2.7
1	A	327	LYS	2.7
1	A	304	PHE	2.7
1	A	131	SER	2.6
1	B	181	LYS	2.5
1	B	435	TYR	2.5
1	A	271	HIS	2.3
1	B	430	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	336	LYS	2.3
1	A	268	PHE	2.1
1	B	247	GLN	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](#)

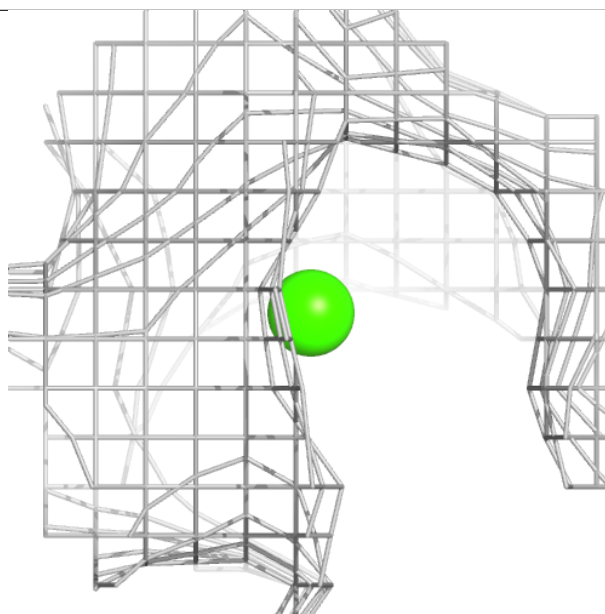
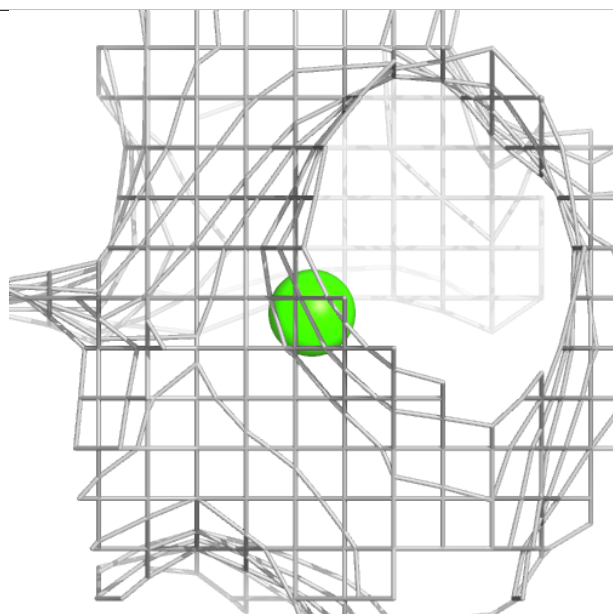
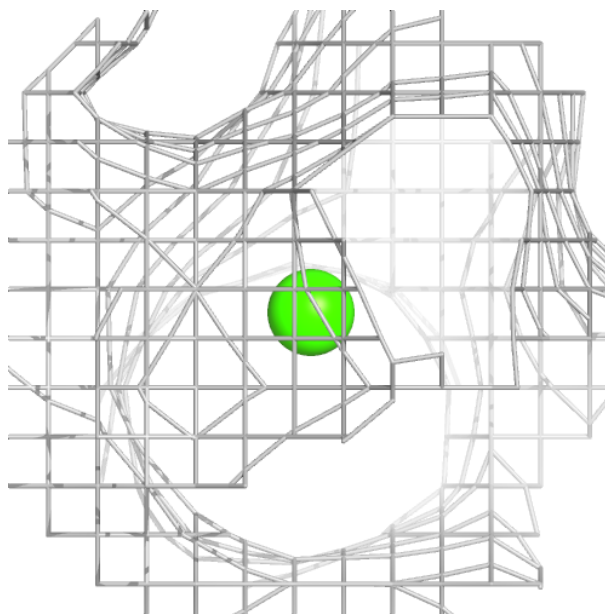
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	A	503	1/1	0.99	0.02	68,68,68,68	0
2	CA	B	502	1/1	0.99	0.03	31,31,31,31	0
2	CA	B	503	1/1	0.99	0.03	49,49,49,49	0
2	CA	B	501	1/1	1.00	0.01	26,26,26,26	0
2	CA	A	502	1/1	1.00	0.01	29,29,29,29	0
2	CA	A	501	1/1	1.00	0.03	35,35,35,35	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.

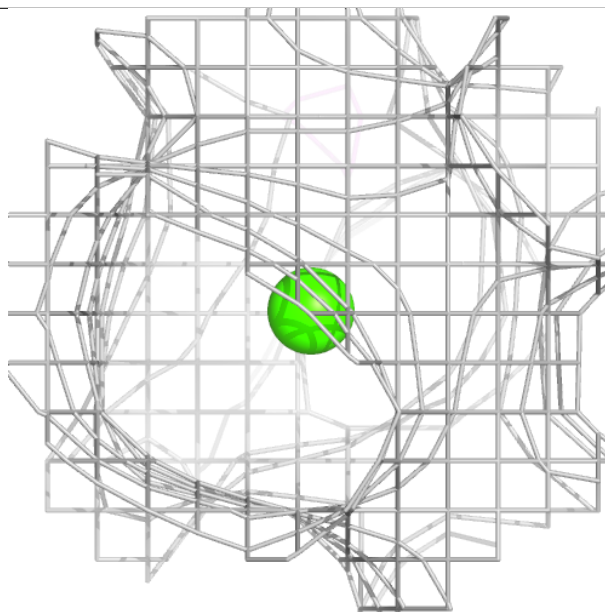
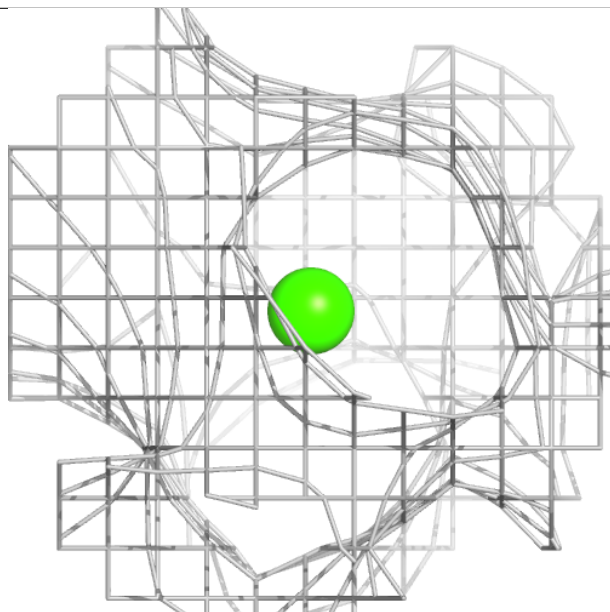
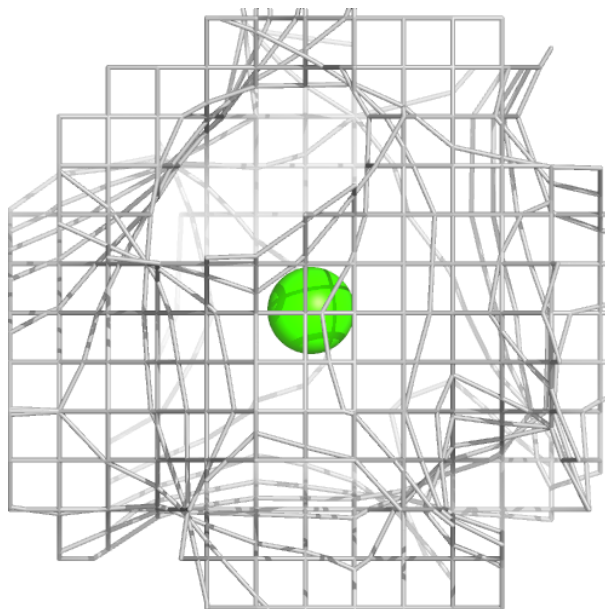
Electron density around CA A 503:

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



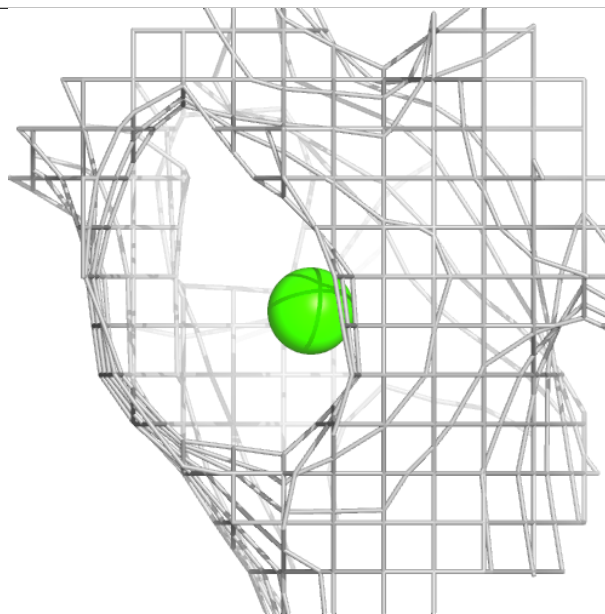
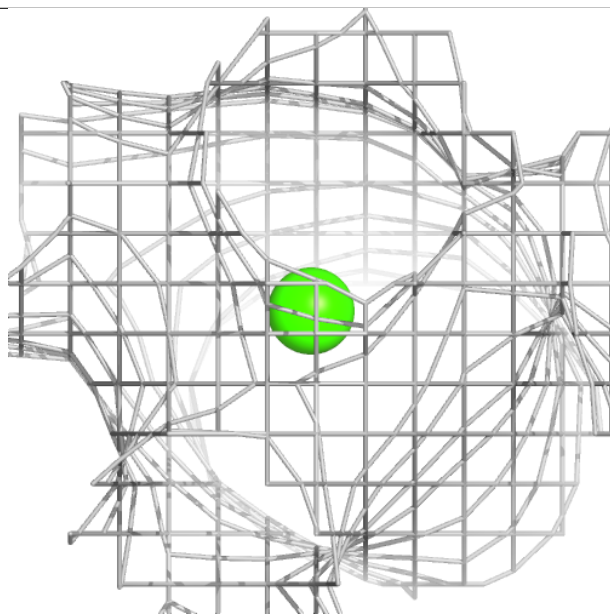
Electron density around CA B 502:

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



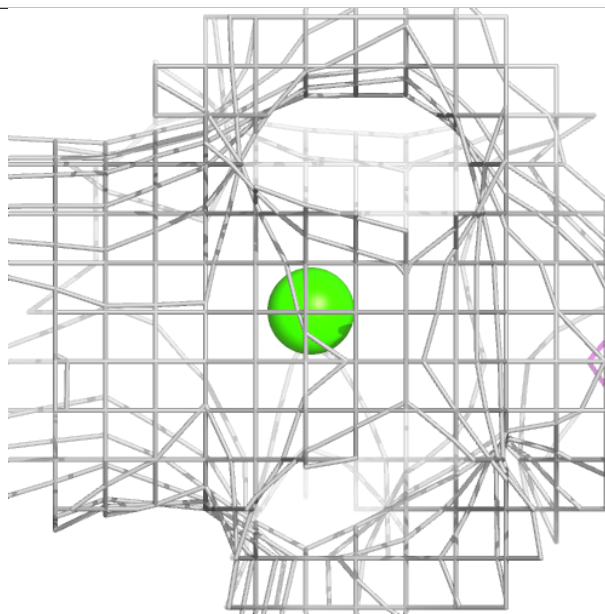
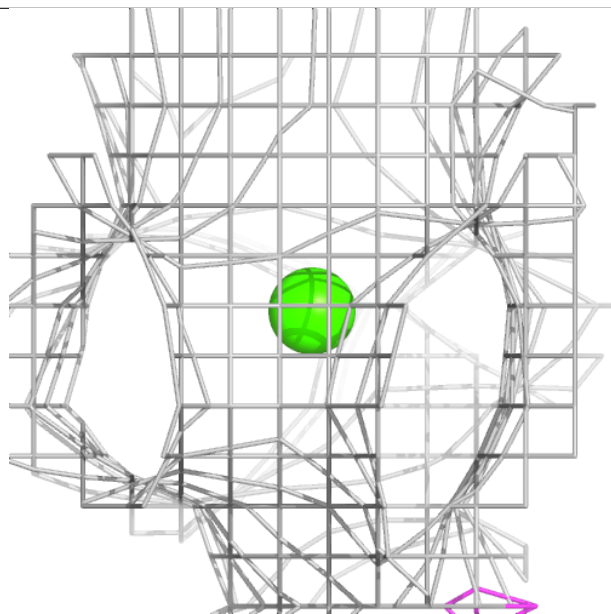
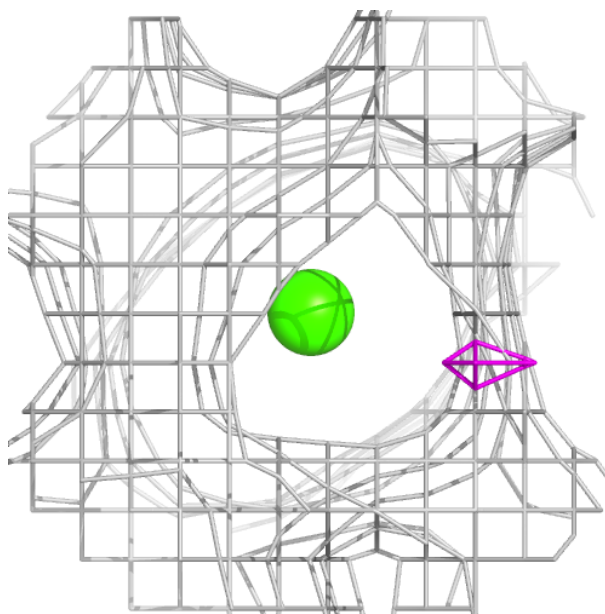
Electron density around CA B 503:

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



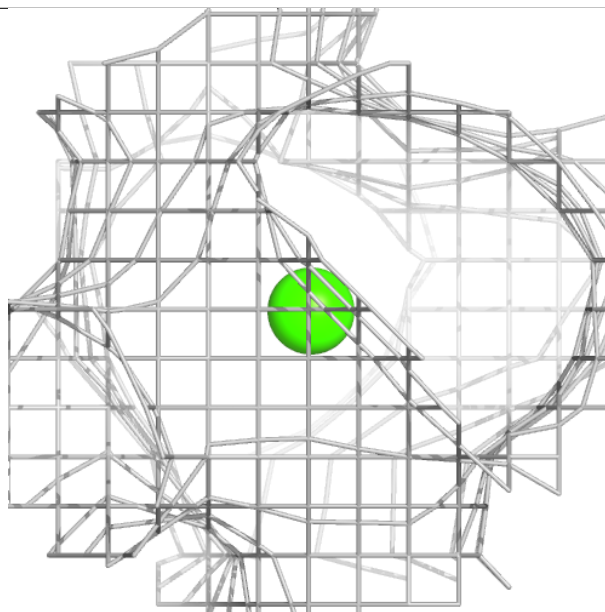
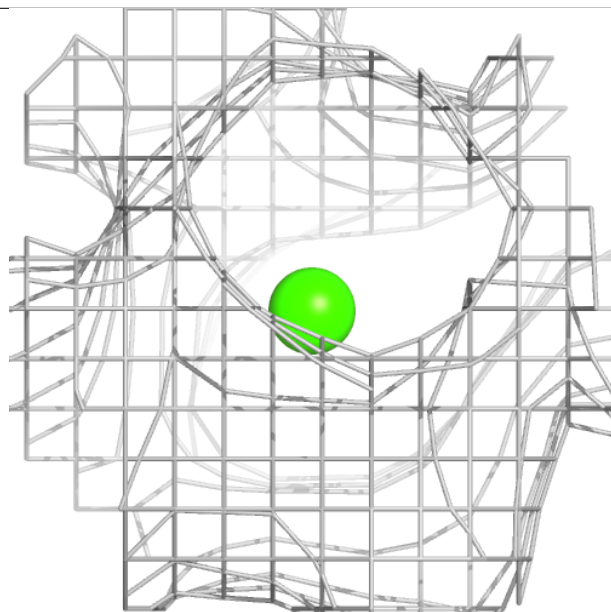
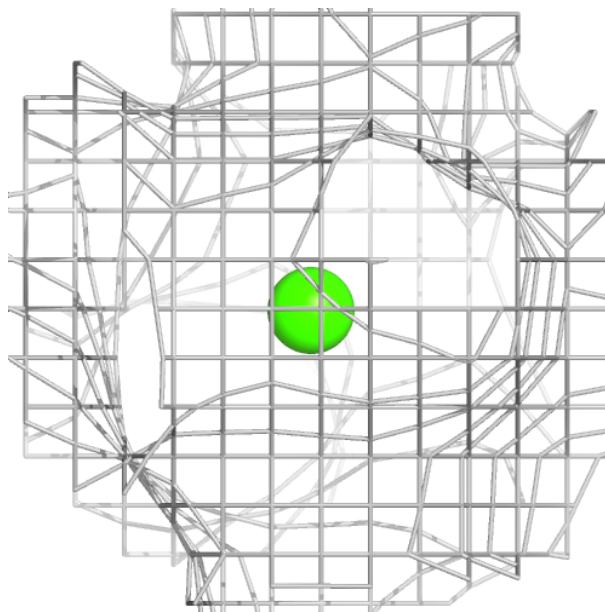
Electron density around CA B 501:

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



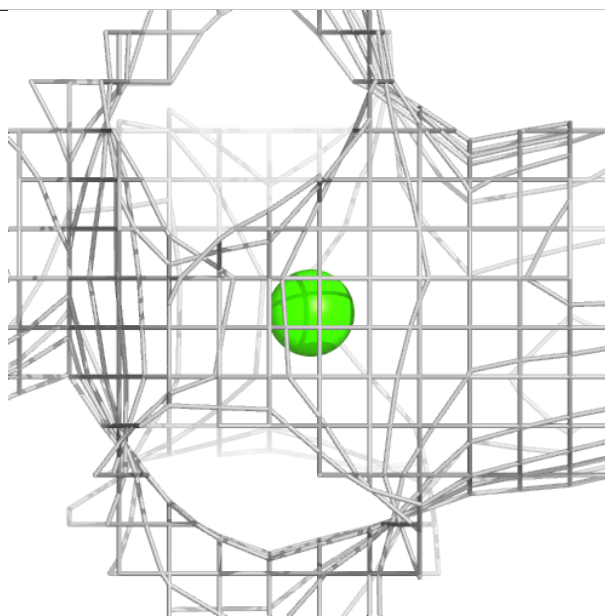
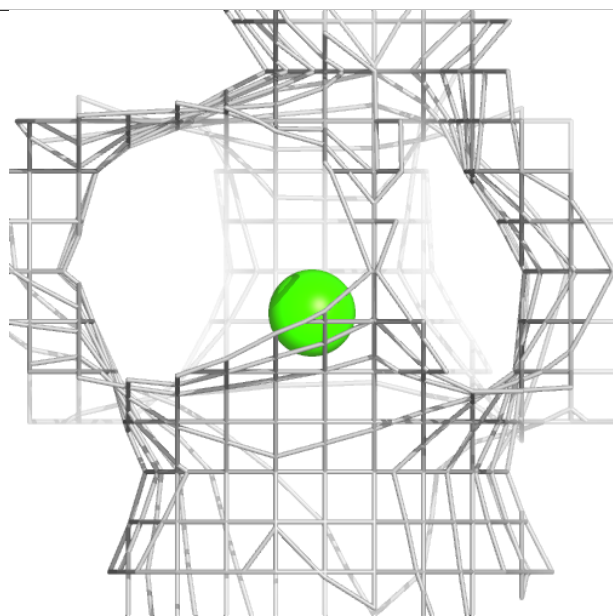
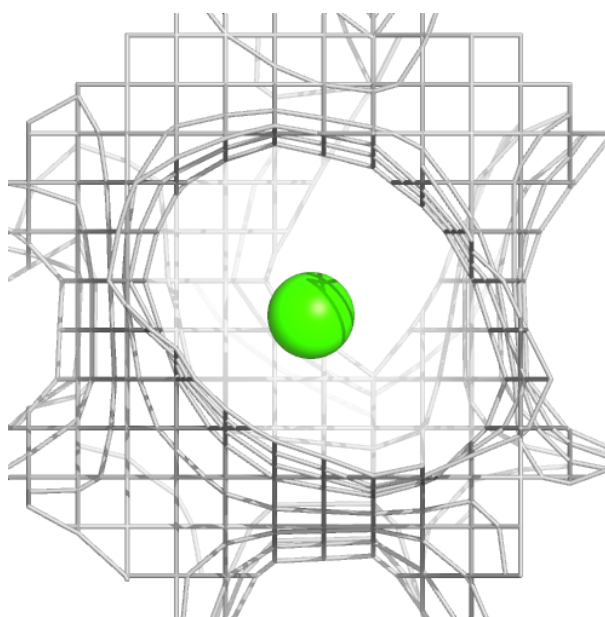
Electron density around CA A 502:

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



Electron density around CA A 501:

$2mF_o-DF_c$ (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.