



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 23, 2026 – 04:10 PM JST

PDB ID : 9X8F / pdb_00009x8f
Title : Crystal structure of the N-terminal of an alpha-amylase family glycosyl hydrolase from *Vibrio parahaemolyticus*
Authors : Cheng, Q.; Li, B.
Deposited on : 2025-10-19
Resolution : 1.96 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 Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

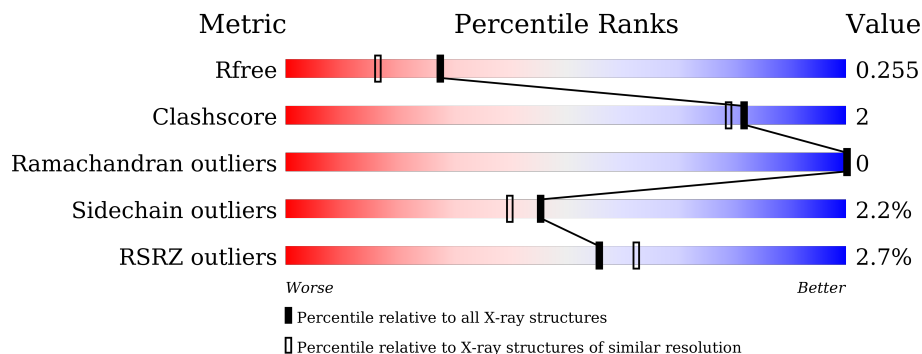
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	633	<div> <div>3%</div> <div>91%</div> <div>8%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5291 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 Alpha-amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	633	Total	C	N	O	S	0	0	0
			5014	3149	835	1004	26			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Mg	0	0
			3	3		

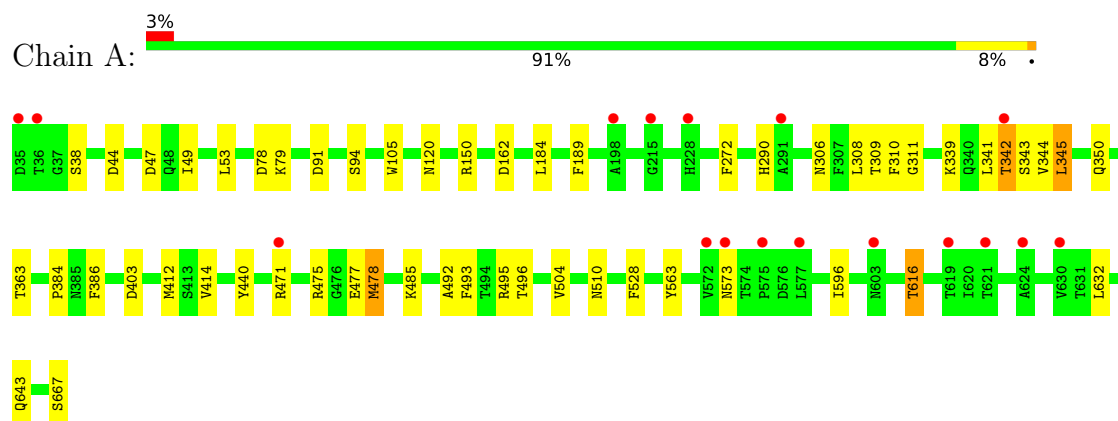
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	274	Total	O	0	0
			274	274		

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: Alpha-amylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	118.77Å 118.77Å 107.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.00 – 1.96 24.00 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.9 (24.00-1.96) 99.9 (24.00-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.96Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.199 , 0.246 0.208 , 0.255	Depositor DCC
R_{free} test set	2775 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5291	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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 Model quality

5.1 Standard geometry

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

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	0/5132	1.04	9/6971 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	363	THR	CA-CB-OG1	-6.04	100.55	109.60
1	A	478	MET	CG-SD-CE	-5.81	88.12	100.90
1	A	573	ASN	CB-CA-C	5.75	120.44	111.70
1	A	162	ASP	CA-CB-CG	5.61	118.21	112.60
1	A	91	ASP	CA-CB-CG	5.49	118.09	112.60
1	A	272	PHE	CA-CB-CG	5.49	119.29	113.80
1	A	403	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	189	PHE	CA-CB-CG	5.20	119.00	113.80
1	A	496	THR	CA-CB-OG1	-5.05	102.03	109.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	471	ARG	Sidechain

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	5014	0	4720	24	0
2	A	3	0	0	0	0
3	A	274	0	0	1	0
All	All	5291	0	4720	24	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 2.

All (24) 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:49:ILE:HD13	1:A:412:MET:HE1	1.76	0.67
1:A:414:VAL:HG12	1:A:478:MET:HE1	1.81	0.62
1:A:478:MET:HE3	1:A:493:PHE:CD1	2.37	0.60
1:A:79:LYS:HE3	1:A:120:ASN:O	2.04	0.58
1:A:414:VAL:HG12	1:A:478:MET:CE	2.35	0.56
1:A:53:LEU:C	1:A:53:LEU:HD12	2.31	0.55
1:A:309:THR:H	1:A:342:THR:HG23	1.74	0.53
1:A:311:GLY:HA3	1:A:341:LEU:HD22	1.94	0.49
1:A:478:MET:CE	1:A:493:PHE:CD1	2.97	0.47
1:A:485:LYS:HD2	1:A:643:GLN:HG2	1.96	0.47
1:A:477:GLU:O	1:A:495:ARG:HA	2.16	0.46
1:A:345:LEU:HD13	1:A:384:PRO:HB2	1.97	0.45
1:A:47:ASP:OD2	1:A:475:ARG:NH2	2.49	0.45
1:A:78:ASP:HB3	1:A:440:TYR:CZ	2.52	0.44
1:A:308:LEU:HD12	1:A:342:THR:OG1	2.17	0.44
1:A:310:PHE:HA	1:A:343:SER:O	2.17	0.44
1:A:311:GLY:CA	1:A:341:LEU:HD22	2.48	0.43
1:A:528:PHE:HB3	1:A:563:TYR:HB3	2.00	0.43
1:A:350:GLN:HG3	1:A:386:PHE:CE2	2.55	0.42
1:A:38:SER:HB2	1:A:150:ARG:HG2	2.01	0.42
1:A:616:THR:HG22	3:A:1066:HOH:O	2.19	0.42
1:A:290:HIS:CE1	1:A:339:LYS:HD2	2.56	0.41
1:A:632:LEU:C	1:A:632:LEU:HD23	2.46	0.41
1:A:492:ALA:HA	1:A:504:VAL:O	2.22	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	631/633 (100%)	614 (97%)	17 (3%)	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	549/549 (100%)	537 (98%)	12 (2%)	45	40

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ASP
1	A	94	SER
1	A	105	TRP
1	A	184	LEU
1	A	306	ASN
1	A	342	THR
1	A	344	VAL
1	A	345	LEU
1	A	510	ASN
1	A	596	ILE

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Mol	Chain	Res	Type
1	A	616	THR
1	A	667	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	452	GLN
1	A	530	GLN
1	A	550	HIS
1	A	570	GLN
1	A	580	GLN
1	A	607	ASN
1	A	627	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 3 ligands modelled in this entry, 3 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 [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, 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	633/633 (100%)	0.27	17 (2%) 56 62	19, 27, 45, 66	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	228	HIS	3.5
1	A	572	VAL	3.5
1	A	36	THR	3.1
1	A	621	THR	2.7
1	A	215	GLY	2.7
1	A	624	ALA	2.6
1	A	577	LEU	2.5
1	A	573	ASN	2.4
1	A	35	ASP	2.2
1	A	575	PRO	2.2
1	A	198	ALA	2.2
1	A	291	ALA	2.2
1	A	603	ASN	2.1
1	A	342	THR	2.1
1	A	630	VAL	2.1
1	A	619	THR	2.1
1	A	471	ARG	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 oligosaccharides in this entry.

6.4 Ligands

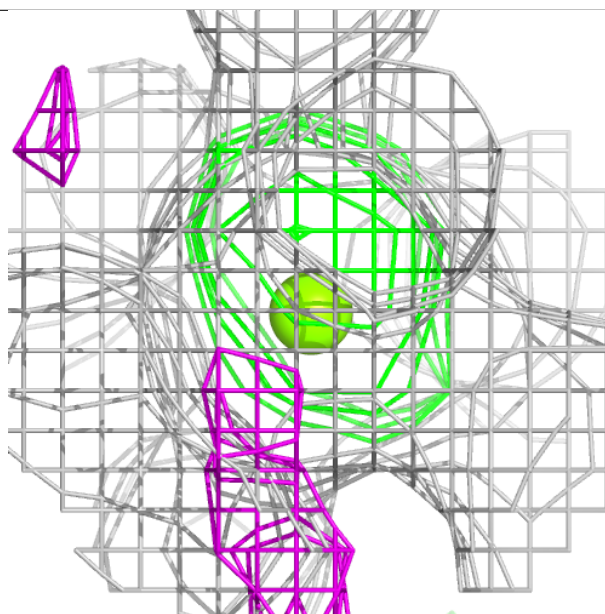
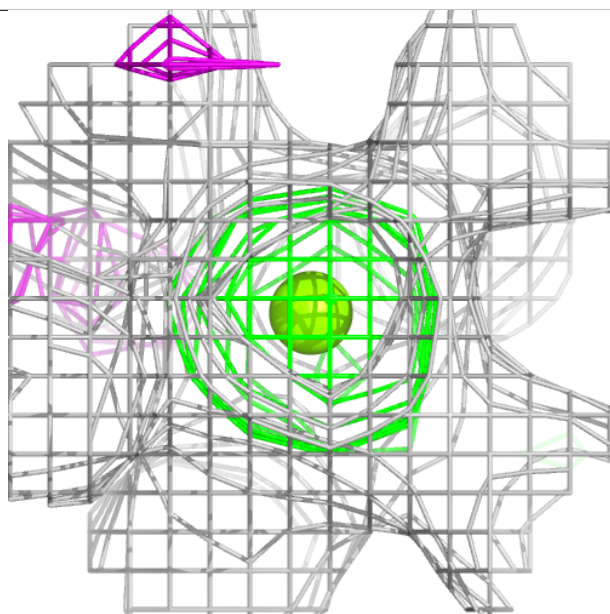
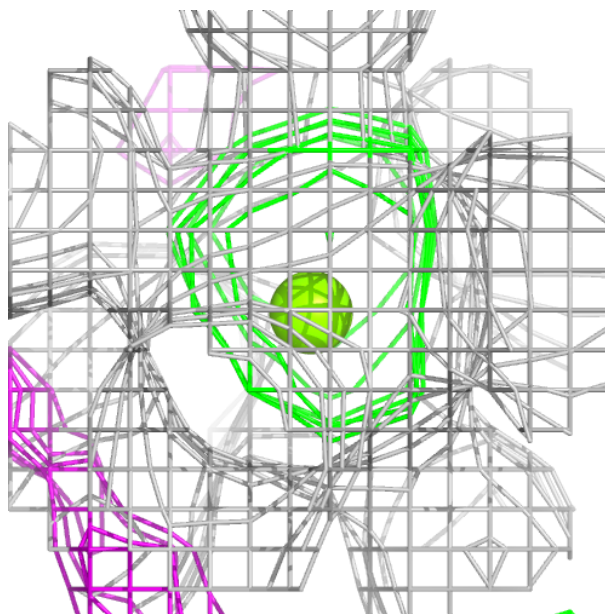
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	A	901	1/1	0.99	0.11	10,10,10,10	0
2	MG	A	902	1/1	0.99	0.08	10,10,10,10	0
2	MG	A	903	1/1	0.99	0.05	11,11,11,11	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.

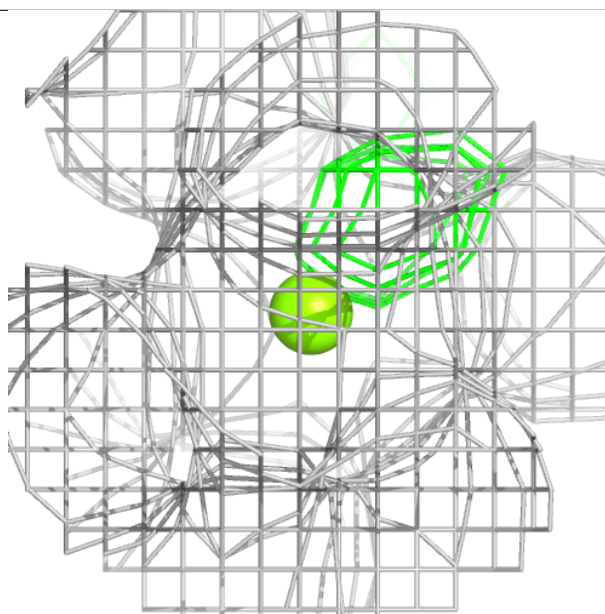
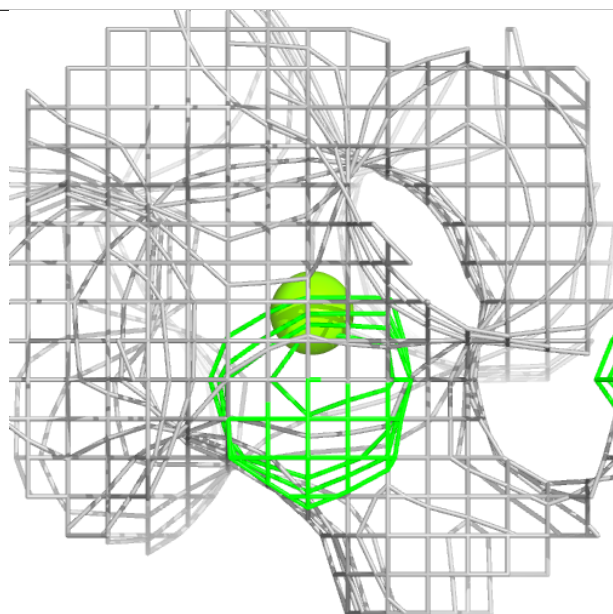
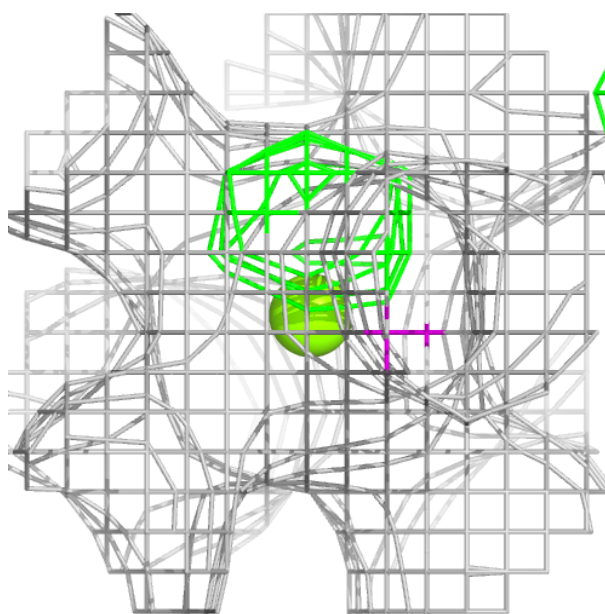
Electron density around MG A 901:

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



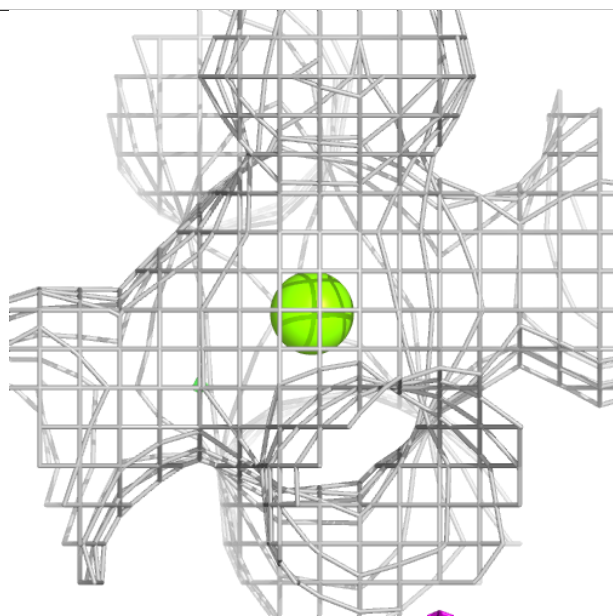
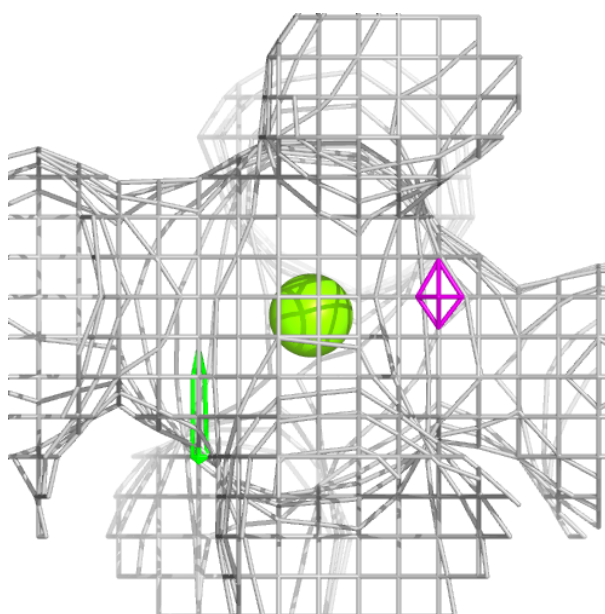
Electron density around MG A 902:

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



Electron density around MG A 903:

$2mF_o-DF_c$ (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.