



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:48 PM UTC

PDB ID : 8DKR / pdb_00008dkr
Title : Pseudomonas-phage E217 TerL nuclease domain
Authors : Cingolani, G.; Lokareddy, R.; Hou, D.
Deposited on : 2022-07-06
Resolution : 2.05 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

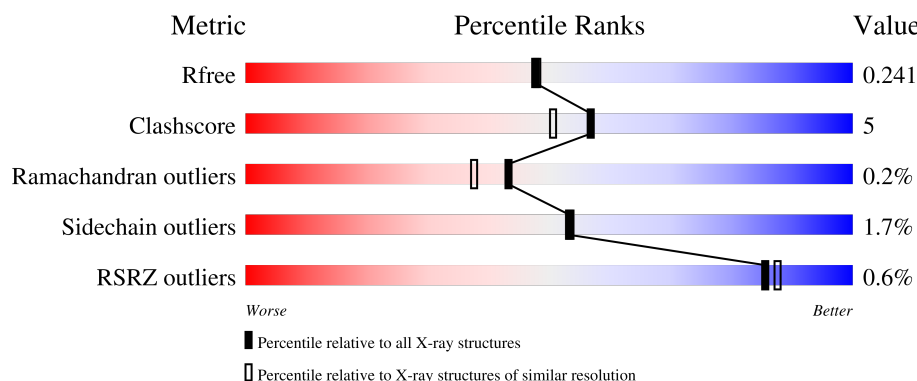
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	255	% 79% 14% 7%
1	B	255	86% 11% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4017 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 Large terminase protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	248	Total	C	N	O	S	0	0	0
			1942	1228	334	373	7			
1	A	238	Total	C	N	O	S	0	0	0
			1868	1182	319	360	7			

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	108	Total	O	0	0
			108	108		
3	A	96	Total	O	0	0
			96	96		

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.

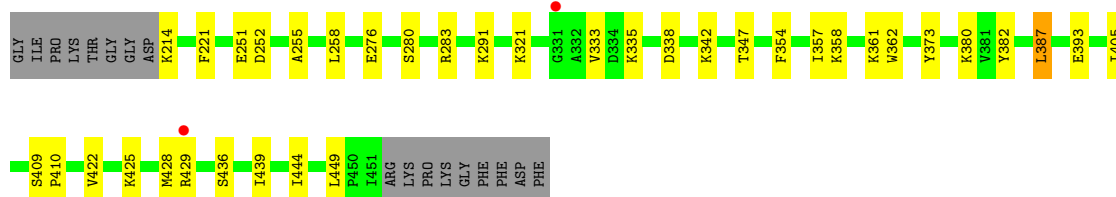
- Molecule 1: Large terminase protein

Chain B:  86% 11% .



- Molecule 1: Large terminase protein

Chain A:  79% 14% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.60Å 62.63Å 149.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.93 – 2.05 14.93 – 2.05	Depositor EDS
% Data completeness (in resolution range)	80.1 (14.93-2.05) 79.4 (14.93-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.20	Depositor
R, R_{free}	0.217 , 0.243 0.217 , 0.241	Depositor DCC
R_{free} test set	1451 reflections (4.04%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.946	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.032 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4017	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.17	0/1905	0.39	1/2568 (0.0%)
1	B	0.22	0/1980	0.43	0/2667
All	All	0.20	0/3885	0.41	1/5235 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	449	LEU	CB-CA-C	5.13	115.62	109.31

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	1868	0	1861	22	0
1	B	1942	0	1947	14	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	96	0	0	1	0
3	B	108	0	0	2	0
All	All	4017	0	3808	35	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 (35) 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:B:329:ALA:HB1	1:B:358:LYS:HD3	1.83	0.58
1:A:251:GLU:O	1:A:429:ARG:NH1	2.36	0.58
1:B:221:PHE:HB3	1:B:369:PHE:HB3	1.86	0.57
1:A:425:LYS:HA	1:A:428:MET:HE3	1.85	0.57
1:B:223:LEU:HB3	1:A:405:ILE:HD11	1.87	0.56
1:B:342:LYS:NZ	3:B:606:HOH:O	2.39	0.55
1:A:221:PHE:HA	1:A:373:TYR:HB2	1.91	0.53
1:A:255:ALA:HB1	1:A:439:ILE:HD13	1.90	0.52
1:A:361:LYS:NZ	3:A:605:HOH:O	2.43	0.51
1:B:213:ASP:HA	1:B:411:ARG:HD3	1.94	0.49
1:A:358:LYS:HE3	1:A:422:VAL:HB	1.94	0.49
1:A:357:ILE:HD11	1:A:361:LYS:HE2	1.93	0.49
1:A:333:VAL:HG11	1:A:354:PHE:HB2	1.94	0.48
1:B:258:LEU:HB3	1:B:266:GLU:HB2	1.96	0.47
1:A:429:ARG:NH1	1:A:436:SER:H	2.12	0.47
1:A:429:ARG:NH2	1:A:436:SER:OG	2.48	0.47
1:A:382:TYR:HB2	1:A:387:LEU:HD11	1.97	0.46
1:B:362:TRP:CE2	1:B:444:ILE:HG13	2.50	0.46
1:A:362:TRP:CE2	1:A:444:ILE:HG13	2.52	0.45
1:A:335:LYS:HD3	1:A:338:ASP:OD2	2.16	0.45
1:B:409:SER:HB2	1:B:410:PRO:HD3	1.99	0.44
1:A:321:LYS:HD3	1:A:321:LYS:HA	1.83	0.44
1:B:352:ASP:O	1:B:419:ARG:HG2	2.17	0.43
1:B:364:GLU:O	1:B:368:ARG:HG3	2.19	0.43
1:B:403:LEU:HD11	1:B:443:VAL:HG21	2.01	0.43
1:A:342:LYS:HG3	1:A:347:THR:HG22	2.00	0.43
1:A:409:SER:HB2	1:A:410:PRO:HD3	2.01	0.42
1:A:251:GLU:HB3	1:A:429:ARG:CZ	2.49	0.42
1:B:399:LYS:HA	1:B:399:LYS:HD3	1.88	0.41
1:B:240:LYS:NZ	3:B:603:HOH:O	2.31	0.41
1:A:258:LEU:HD22	1:A:291:LYS:HG3	2.01	0.41
1:A:214:LYS:HD2	1:A:214:LYS:HA	1.66	0.41
1:A:280:SER:O	1:A:283:ARG:HB3	2.21	0.41
1:B:280:SER:O	1:B:283:ARG:HB3	2.21	0.40
1:A:380:LYS:NZ	1:A:382:TYR:OH	2.47	0.40

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	236/255 (92%)	230 (98%)	6 (2%)	0	100	100
1	B	246/255 (96%)	239 (97%)	6 (2%)	1 (0%)	30	22
All	All	482/510 (94%)	469 (97%)	12 (2%)	1 (0%)	43	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	452	ARG

5.3.2 Protein sidechains [i](#)

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	204/218 (94%)	200 (98%)	4 (2%)	48	48
1	B	212/218 (97%)	209 (99%)	3 (1%)	59	60
All	All	416/436 (95%)	409 (98%)	7 (2%)	53	53

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	276	GLU
1	B	429	ARG
1	B	451	ILE
1	A	252	ASP
1	A	276	GLU

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Mol	Chain	Res	Type
1	A	387	LEU
1	A	393	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	B	345	HIS
1	A	286	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 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 ⓘ

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	238/255 (93%)	-0.09	2 (0%) 82 84	30, 40, 55, 67	0
1	B	248/255 (97%)	-0.11	1 (0%) 88 90	30, 39, 60, 78	0
All	All	486/510 (95%)	-0.10	3 (0%) 85 87	30, 39, 57, 78	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	429	ARG	2.7
1	B	453	LYS	2.5
1	A	331	GLY	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	MG	A	502	1/1	0.91	0.24	21,21,21,21	0
2	MG	B	501	1/1	0.94	0.08	37,37,37,37	0

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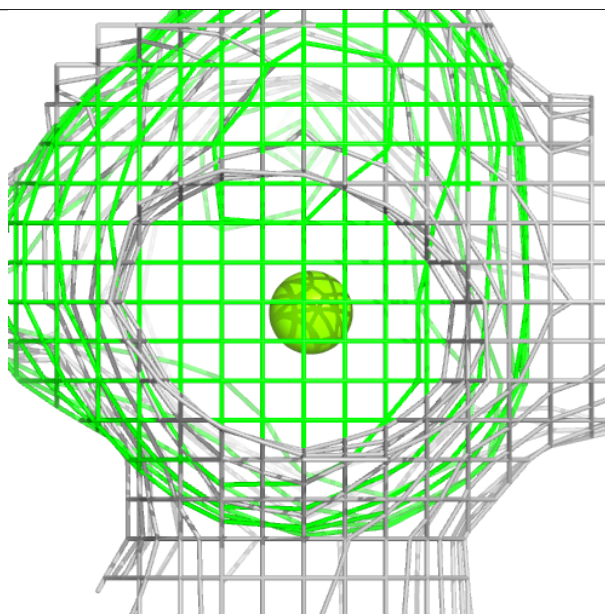
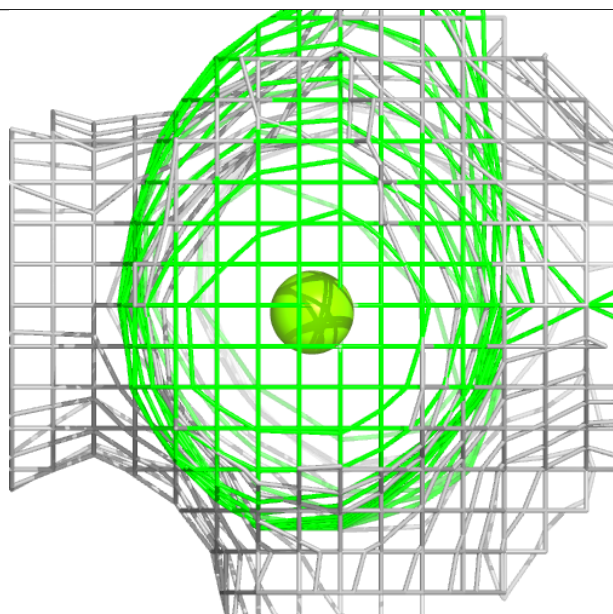
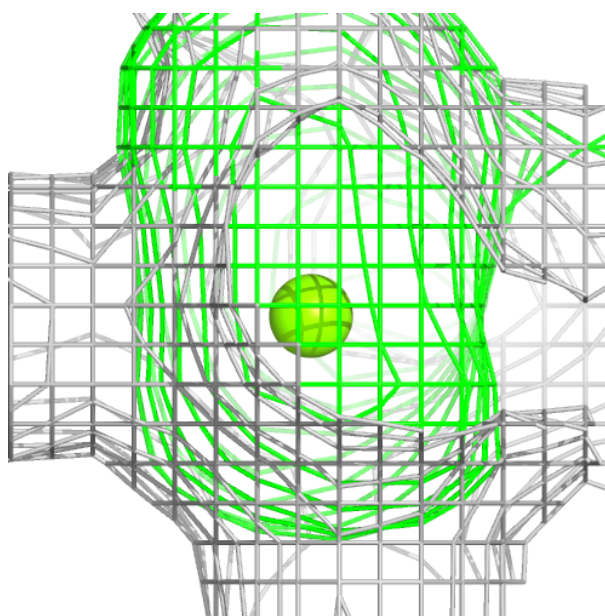
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	501	1/1	0.97	0.20	20,20,20,20	0

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.

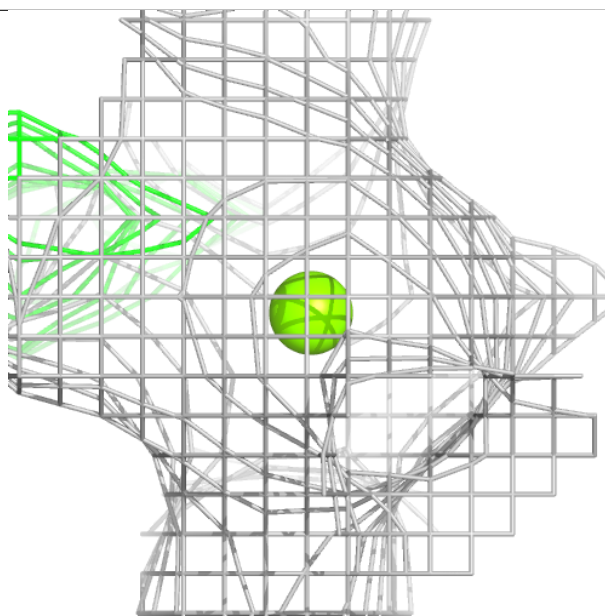
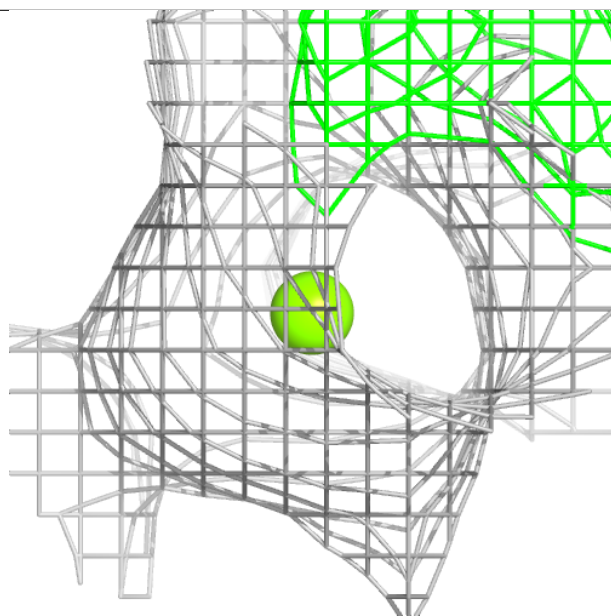
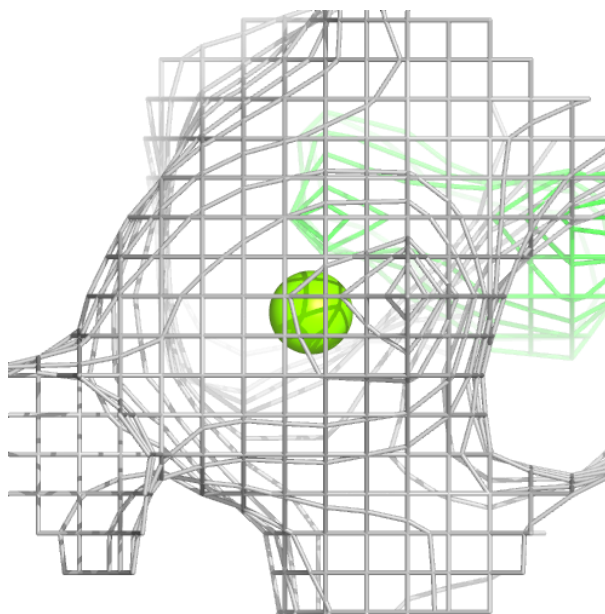
Electron density around MG A 502:

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



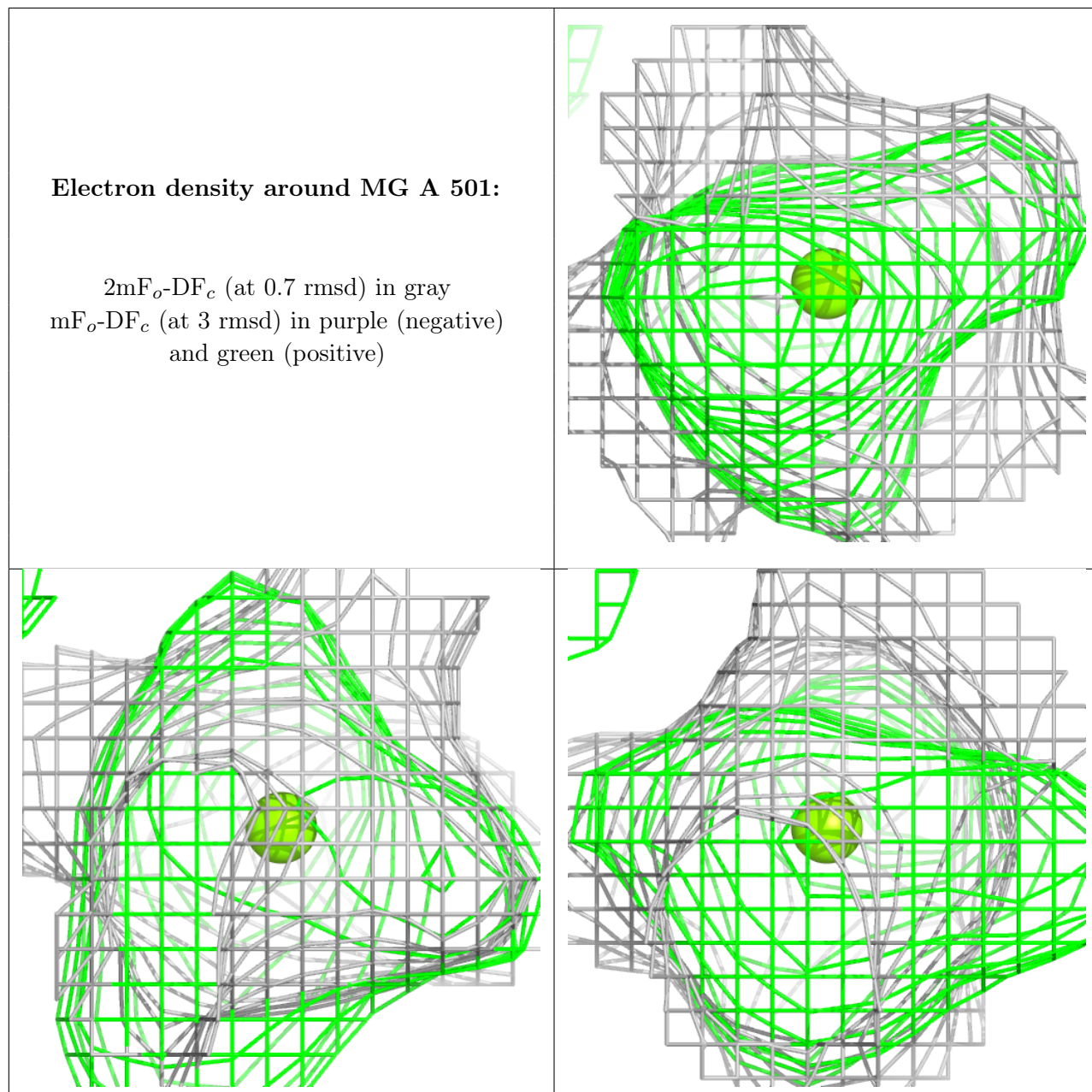
Electron density around MG B 501:

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



Electron density around MG A 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.