Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2024 – 12:32 AM EST

PDB ID	:	6OWU
Title	:	THE PRP8 INTEIN OF CRYPTOCOCCUS NEOFORMANS in complex with Zn2+
Authors	:	Li, Z.; Li, H.
Deposited on	:	2019-05-11
Resolution	:	1.84 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:

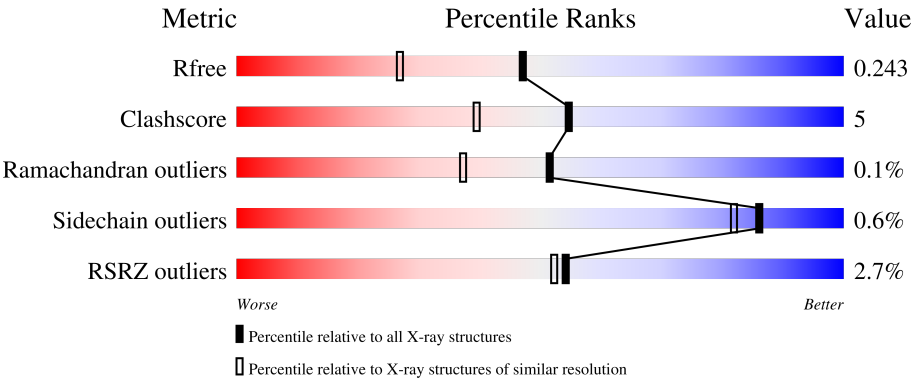
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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 <=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	184	2% 68% 9% • 22%
1	B	184	2% 67% 10% • 22%
1	C	184	3% 70% 8% 22%
1	D	184	2% 65% 12% • 22%
1	E	184	3% 71% 7% • 22%

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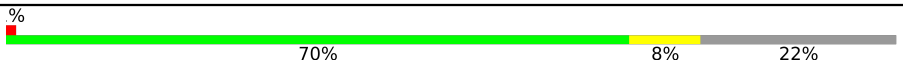
Mol	Chain	Length	Quality of chain
1	F	184	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7645 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 PRP8 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	0	1	0
			1178	732	209	234	3			
1	B	143	Total	C	N	O	S	0	1	0
			1178	732	209	234	3			
1	C	143	Total	C	N	O	S	0	1	0
			1178	732	209	234	3			
1	D	143	Total	C	N	O	S	0	1	0
			1178	732	209	234	3			
1	E	143	Total	C	N	O	S	0	2	0
			1184	735	210	236	3			
1	F	143	Total	C	N	O	S	0	1	0
			1178	732	209	234	3			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	initiating methionine	UNP Q6TER0
A	-2	GLY	-	expression tag	UNP Q6TER0
A	173	LEU	-	expression tag	UNP Q6TER0
A	174	GLU	-	expression tag	UNP Q6TER0
A	175	HIS	-	expression tag	UNP Q6TER0
A	176	HIS	-	expression tag	UNP Q6TER0
A	177	HIS	-	expression tag	UNP Q6TER0
A	178	HIS	-	expression tag	UNP Q6TER0
A	179	HIS	-	expression tag	UNP Q6TER0
A	180	HIS	-	expression tag	UNP Q6TER0
B	-3	MET	-	initiating methionine	UNP Q6TER0
B	-2	GLY	-	expression tag	UNP Q6TER0
B	173	LEU	-	expression tag	UNP Q6TER0
B	174	GLU	-	expression tag	UNP Q6TER0
B	175	HIS	-	expression tag	UNP Q6TER0
B	176	HIS	-	expression tag	UNP Q6TER0
B	177	HIS	-	expression tag	UNP Q6TER0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	178	HIS	-	expression tag	UNP Q6TER0
B	179	HIS	-	expression tag	UNP Q6TER0
B	180	HIS	-	expression tag	UNP Q6TER0
C	-3	MET	-	initiating methionine	UNP Q6TER0
C	-2	GLY	-	expression tag	UNP Q6TER0
C	173	LEU	-	expression tag	UNP Q6TER0
C	174	GLU	-	expression tag	UNP Q6TER0
C	175	HIS	-	expression tag	UNP Q6TER0
C	176	HIS	-	expression tag	UNP Q6TER0
C	177	HIS	-	expression tag	UNP Q6TER0
C	178	HIS	-	expression tag	UNP Q6TER0
C	179	HIS	-	expression tag	UNP Q6TER0
C	180	HIS	-	expression tag	UNP Q6TER0
D	-3	MET	-	initiating methionine	UNP Q6TER0
D	-2	GLY	-	expression tag	UNP Q6TER0
D	173	LEU	-	expression tag	UNP Q6TER0
D	174	GLU	-	expression tag	UNP Q6TER0
D	175	HIS	-	expression tag	UNP Q6TER0
D	176	HIS	-	expression tag	UNP Q6TER0
D	177	HIS	-	expression tag	UNP Q6TER0
D	178	HIS	-	expression tag	UNP Q6TER0
D	179	HIS	-	expression tag	UNP Q6TER0
D	180	HIS	-	expression tag	UNP Q6TER0
E	-3	MET	-	initiating methionine	UNP Q6TER0
E	-2	GLY	-	expression tag	UNP Q6TER0
E	173	LEU	-	expression tag	UNP Q6TER0
E	174	GLU	-	expression tag	UNP Q6TER0
E	175	HIS	-	expression tag	UNP Q6TER0
E	176	HIS	-	expression tag	UNP Q6TER0
E	177	HIS	-	expression tag	UNP Q6TER0
E	178	HIS	-	expression tag	UNP Q6TER0
E	179	HIS	-	expression tag	UNP Q6TER0
E	180	HIS	-	expression tag	UNP Q6TER0
F	-3	MET	-	initiating methionine	UNP Q6TER0
F	-2	GLY	-	expression tag	UNP Q6TER0
F	173	LEU	-	expression tag	UNP Q6TER0
F	174	GLU	-	expression tag	UNP Q6TER0
F	175	HIS	-	expression tag	UNP Q6TER0
F	176	HIS	-	expression tag	UNP Q6TER0
F	177	HIS	-	expression tag	UNP Q6TER0
F	178	HIS	-	expression tag	UNP Q6TER0
F	179	HIS	-	expression tag	UNP Q6TER0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	180	HIS	-	expression tag	UNP Q6TER0

- 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	2	Total Zn 2 2	0	0
2	C	1	Total Zn 1 1	0	0
2	D	2	Total Zn 2 2	0	0
2	E	1	Total Zn 1 1	0	0
2	F	2	Total Zn 2 2	0	0

- Molecule 3 is water.

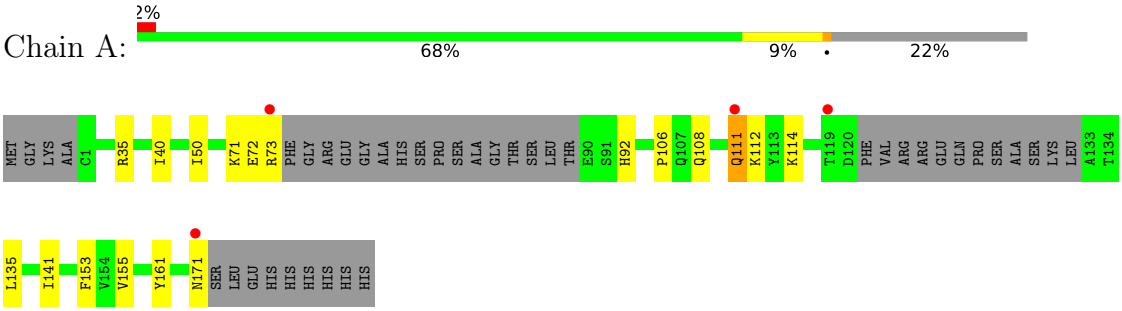
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	98	Total O 98 98	0	0
3	B	88	Total O 88 88	0	0
3	C	85	Total O 85 85	0	0
3	D	92	Total O 92 92	0	0
3	E	95	Total O 95 95	0	0
3	F	104	Total O 104 104	0	0

3 Residue-property plots

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.

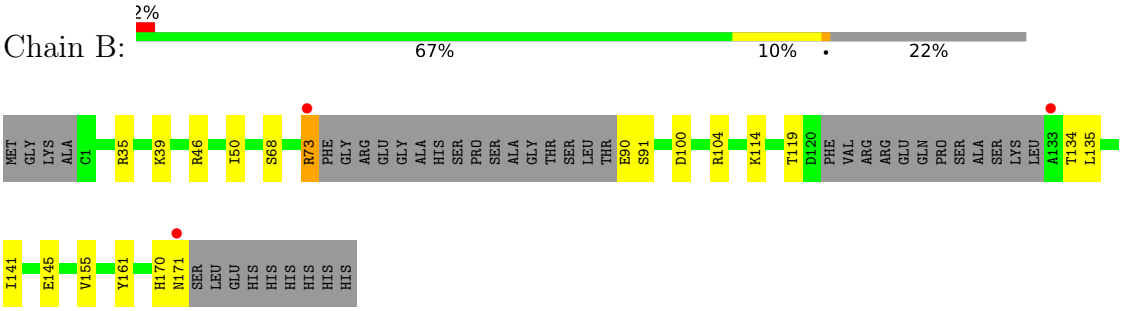
• Molecule 1: PRP8 protein

Chain A:



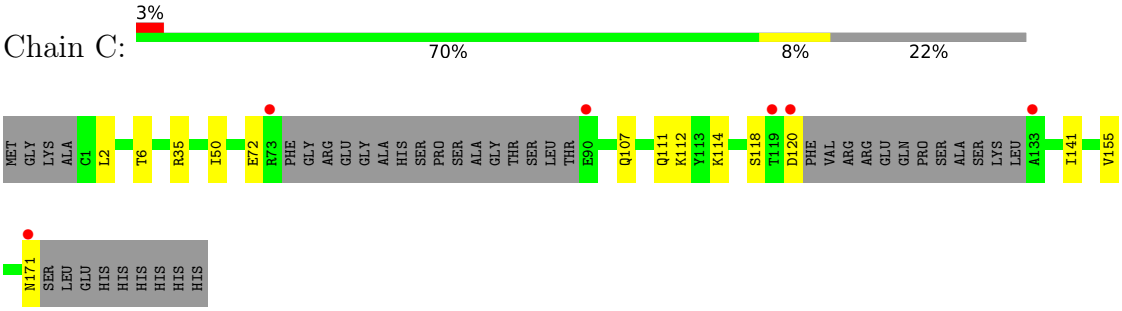
• Molecule 1: PRP8 protein

Chain B:



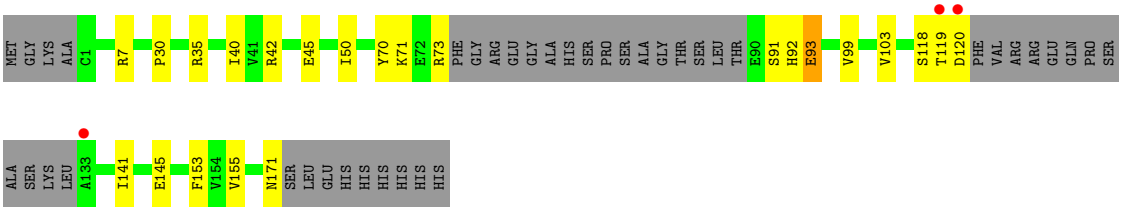
• Molecule 1: PRP8 protein

Chain C:



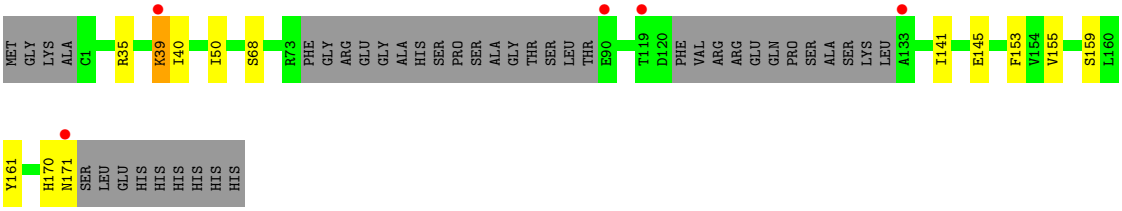
• Molecule 1: PRP8 protein

Chain D:



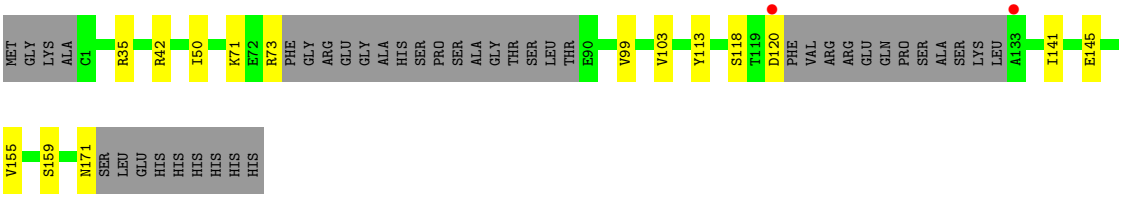
• Molecule 1: PRP8 protein

Chain E:



• Molecule 1: PRP8 protein

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	63.09Å 63.04Å 78.64Å 94.86° 103.13° 117.44°	Depositor
Resolution (Å)	40.09 – 1.84 40.09 – 1.84	Depositor EDS
% Data completeness (in resolution range)	80.4 (40.09-1.84) 80.4 (40.09-1.84)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.55 (at 1.84Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R, R_{free}	0.199 , 0.243 0.199 , 0.243	Depositor DCC
R_{free} test set	2011 reflections (2.82%)	wwPDB-VP
Wilson B-factor (Å^2)	20.6	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 55.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7645	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN

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	0.32	0/1194	0.63	3/1608 (0.2%)
1	B	0.32	0/1194	0.53	0/1608
1	C	0.31	0/1194	0.52	0/1608
1	D	0.32	0/1194	0.61	3/1608 (0.2%)
1	E	0.40	1/1200 (0.1%)	0.63	3/1616 (0.2%)
1	F	0.31	0/1194	0.53	0/1608
All	All	0.33	1/7170 (0.0%)	0.58	9/9656 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	39	LYS	CB-CG	5.20	1.66	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	111	GLN	CB-CA-C	-10.75	88.90	110.40
1	E	39	LYS	N-CA-CB	8.87	126.57	110.60
1	D	93	GLU	CA-CB-CG	8.03	131.06	113.40
1	E	39	LYS	CB-CA-C	-7.40	95.60	110.40
1	A	111	GLN	CA-CB-CG	7.04	128.89	113.40
1	D	93	GLU	CB-CA-C	-6.83	96.74	110.40
1	D	93	GLU	N-CA-CB	6.44	122.20	110.60
1	E	39	LYS	CG-CD-CE	5.75	129.15	111.90
1	A	111	GLN	N-CA-CB	5.36	120.25	110.60

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	1178	0	1150	16	0
1	B	1178	0	1149	15	0
1	C	1178	0	1150	9	0
1	D	1178	0	1149	17	0
1	E	1184	0	1154	9	0
1	F	1178	0	1149	10	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
3	A	98	0	0	1	0
3	B	88	0	0	1	0
3	C	85	0	0	0	0
3	D	92	0	0	4	0
3	E	95	0	0	1	0
3	F	104	0	0	2	0
All	All	7645	0	6901	73	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 (73) 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:D:155:VAL:H	1:D:171[A]:ASN:HD22	1.18	0.90
1:B:155:VAL:HB	1:B:171[B]:ASN:HD21	1.48	0.78
1:C:155:VAL:H	1:C:171[A]:ASN:HD21	1.30	0.78
1:D:155:VAL:H	1:D:171[B]:ASN:HD22	1.42	0.67
1:A:108:GLN:O	1:A:111:GLN:NE2	2.29	0.66
1:D:70:TYR:HA	1:D:93:GLU:O	1.98	0.64
1:C:107:GLN:O	1:C:111:GLN:HG2	1.97	0.63
1:A:155:VAL:H	1:A:171[B]:ASN:HD21	1.45	0.63
1:D:42:ARG:NH2	3:D:305:HOH:O	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:155:VAL:H	1:C:171[A]:ASN:ND2	2.00	0.60
1:D:73:ARG:N	1:D:91:SER:O	2.34	0.60
1:D:118:SER:O	1:D:120:ASP:N	2.38	0.56
1:B:155:VAL:HB	1:B:171[B]:ASN:ND2	2.20	0.55
1:A:108:GLN:O	1:A:111:GLN:HG2	2.07	0.55
1:F:42:ARG:NH2	3:F:303:HOH:O	2.38	0.55
1:E:35:ARG:HB3	1:E:155:VAL:HG13	1.88	0.55
1:A:35:ARG:HB3	1:A:155:VAL:HG13	1.90	0.54
1:B:35:ARG:HB3	1:B:155:VAL:HG13	1.90	0.54
1:D:40:ILE:HD13	1:D:153:PHE:HB3	1.91	0.53
1:E:68:SER:OG	1:E:170:HIS:HB2	2.09	0.52
1:D:155:VAL:N	1:D:171[A]:ASN:HD22	1.99	0.52
1:B:73:ARG:N	1:B:91:SER:O	2.35	0.52
1:D:50:ILE:HG12	1:D:141:ILE:HD12	1.92	0.52
1:D:99:VAL:O	1:D:103:VAL:HG13	2.10	0.52
1:E:155:VAL:H	1:E:171[A]:ASN:ND2	2.07	0.52
1:E:145:GLU:HG3	1:F:145:GLU:OE1	2.10	0.51
1:C:50:ILE:HG12	1:C:141:ILE:HD12	1.93	0.51
1:F:73:ARG:NH1	3:F:304:HOH:O	2.44	0.51
1:B:90:GLU:HG2	1:B:91:SER:H	1.76	0.50
1:E:161:TYR:OH	3:E:301:HOH:O	2.09	0.50
1:A:108:GLN:HG2	1:A:111:GLN:HE22	1.75	0.50
1:A:40:ILE:HD13	1:A:153:PHE:HB3	1.94	0.50
1:A:108:GLN:HA	1:A:111:GLN:NE2	2.27	0.50
1:A:155:VAL:H	1:A:171[A]:ASN:ND2	2.10	0.50
1:D:7:ARG:NH1	3:D:307:HOH:O	2.36	0.50
1:F:50:ILE:HG12	1:F:141:ILE:HD12	1.94	0.50
1:C:118:SER:O	1:C:120:ASP:N	2.46	0.49
1:D:35:ARG:HB3	1:D:155:VAL:HG13	1.95	0.49
1:B:161:TYR:OH	3:B:301:HOH:O	2.12	0.49
1:E:155:VAL:HB	1:E:171[A]:ASN:OD1	2.13	0.48
1:F:35:ARG:HB3	1:F:155:VAL:HG13	1.95	0.48
1:B:114:LYS:HD3	1:B:135:LEU:HD13	1.94	0.48
1:A:71:LYS:HA	1:A:112:LYS:O	2.13	0.47
1:A:155:VAL:H	1:A:171[B]:ASN:ND2	2.10	0.47
1:C:72:GLU:OE2	1:C:112:LYS:HA	2.14	0.46
1:B:90:GLU:HG2	1:B:91:SER:N	2.30	0.46
1:C:2:LEU:HD13	1:C:6:THR:HG21	1.97	0.46
1:D:45:GLU:OE2	3:D:301:HOH:O	2.20	0.46
1:A:161:TYR:OH	3:A:301:HOH:O	2.17	0.46
1:C:35:ARG:HB3	1:C:155:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ASP:HB3	1:B:104:ARG:NH2	2.31	0.45
1:D:155:VAL:H	1:D:171[A]:ASN:ND2	1.97	0.45
1:F:71:LYS:HD2	1:F:113:TYR:CZ	2.50	0.45
1:B:50:ILE:HG12	1:B:141:ILE:HD12	1.99	0.45
1:F:99:VAL:O	1:F:103:VAL:HG13	2.16	0.45
1:A:114:LYS:HD3	1:A:135:LEU:HD13	1.99	0.45
1:E:40:ILE:HD13	1:E:153:PHE:HB3	1.99	0.44
1:B:68:SER:OG	1:B:170:HIS:HB2	2.17	0.44
1:A:106:PRO:HA	1:B:46:ARG:HD2	1.99	0.44
1:F:159:SER:HB3	1:F:171[A]:ASN:OD1	2.17	0.44
1:F:118:SER:O	1:F:120:ASP:N	2.43	0.44
1:A:155:VAL:HB	1:A:171[A]:ASN:OD1	2.18	0.44
1:B:145:GLU:HG3	1:D:145:GLU:OE1	2.17	0.43
1:D:30:PRO:HG2	3:D:353:HOH:O	2.20	0.42
1:F:171[B]:ASN:C	1:F:171[B]:ASN:HD22	2.23	0.42
1:E:50:ILE:HG12	1:E:141:ILE:HD12	2.02	0.42
1:C:155:VAL:HB	1:C:171[B]:ASN:OD1	2.20	0.41
1:D:71:LYS:O	1:D:92:HIS:HA	2.20	0.41
1:A:72:GLU:HG3	1:A:92:HIS:NE2	2.35	0.41
1:A:50:ILE:HG12	1:A:141:ILE:HD12	2.02	0.41
1:E:159:SER:HB3	1:E:171[A]:ASN:ND2	2.35	0.41
1:B:119:THR:HG22	1:B:134:THR:HG21	2.01	0.41
1:B:171[A]:ASN:HD22	1:B:171[A]:ASN:HA	1.70	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	137/184 (74%)	134 (98%)	3 (2%)	0	100	100
1	B	137/184 (74%)	134 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	137/184 (74%)	134 (98%)	3 (2%)	0	100 100
1	D	137/184 (74%)	133 (97%)	3 (2%)	1 (1%)	22 9
1	E	138/184 (75%)	135 (98%)	3 (2%)	0	100 100
1	F	137/184 (74%)	134 (98%)	3 (2%)	0	100 100
All	All	823/1104 (74%)	804 (98%)	18 (2%)	1 (0%)	51 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	119	THR

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	133/165 (81%)	132 (99%)	1 (1%)	81 75
1	B	133/165 (81%)	131 (98%)	2 (2%)	65 52
1	C	133/165 (81%)	132 (99%)	1 (1%)	81 75
1	D	133/165 (81%)	133 (100%)	0	100 100
1	E	134/165 (81%)	133 (99%)	1 (1%)	84 78
1	F	133/165 (81%)	133 (100%)	0	100 100
All	All	799/990 (81%)	794 (99%)	5 (1%)	86 82

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

Mol	Chain	Res	Type
1	A	73	ARG
1	B	39	LYS
1	B	73	ARG
1	C	114	LYS
1	E	39	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	22	GLN
1	D	108	GLN
1	D	111	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 9 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, 95^{th} 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	143/184 (77%)	0.02	4 (2%)	53	51	15, 23, 34, 62	0
1	B	143/184 (77%)	-0.06	3 (2%)	63	62	16, 23, 35, 53	0
1	C	143/184 (77%)	0.03	6 (4%)	36	33	14, 23, 36, 59	0
1	D	143/184 (77%)	-0.03	3 (2%)	63	62	15, 23, 34, 59	0
1	E	143/184 (77%)	-0.09	5 (3%)	44	40	16, 22, 34, 57	0
1	F	143/184 (77%)	-0.06	2 (1%)	75	75	15, 23, 34, 55	0
All	All	858/1104 (77%)	-0.03	23 (2%)	54	52	14, 23, 36, 62	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	133	ALA	5.6
1	C	133	ALA	5.2
1	E	133	ALA	4.3
1	A	111	GLN	4.0
1	A	119	THR	4.0
1	A	73	ARG	3.9
1	F	133	ALA	3.7
1	D	120	ASP	3.5
1	C	73	ARG	3.4
1	E	90	GLU	3.2
1	E	171[A]	ASN	3.1
1	E	39	LYS	3.0
1	D	119	THR	3.0
1	B	73	ARG	2.6
1	C	90	GLU	2.6
1	C	120	ASP	2.5
1	C	119	THR	2.3
1	C	171[A]	ASN	2.3
1	B	171[A]	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	171[A]	ASN	2.2
1	F	120	ASP	2.2
1	B	133	ALA	2.2
1	E	119	THR	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)

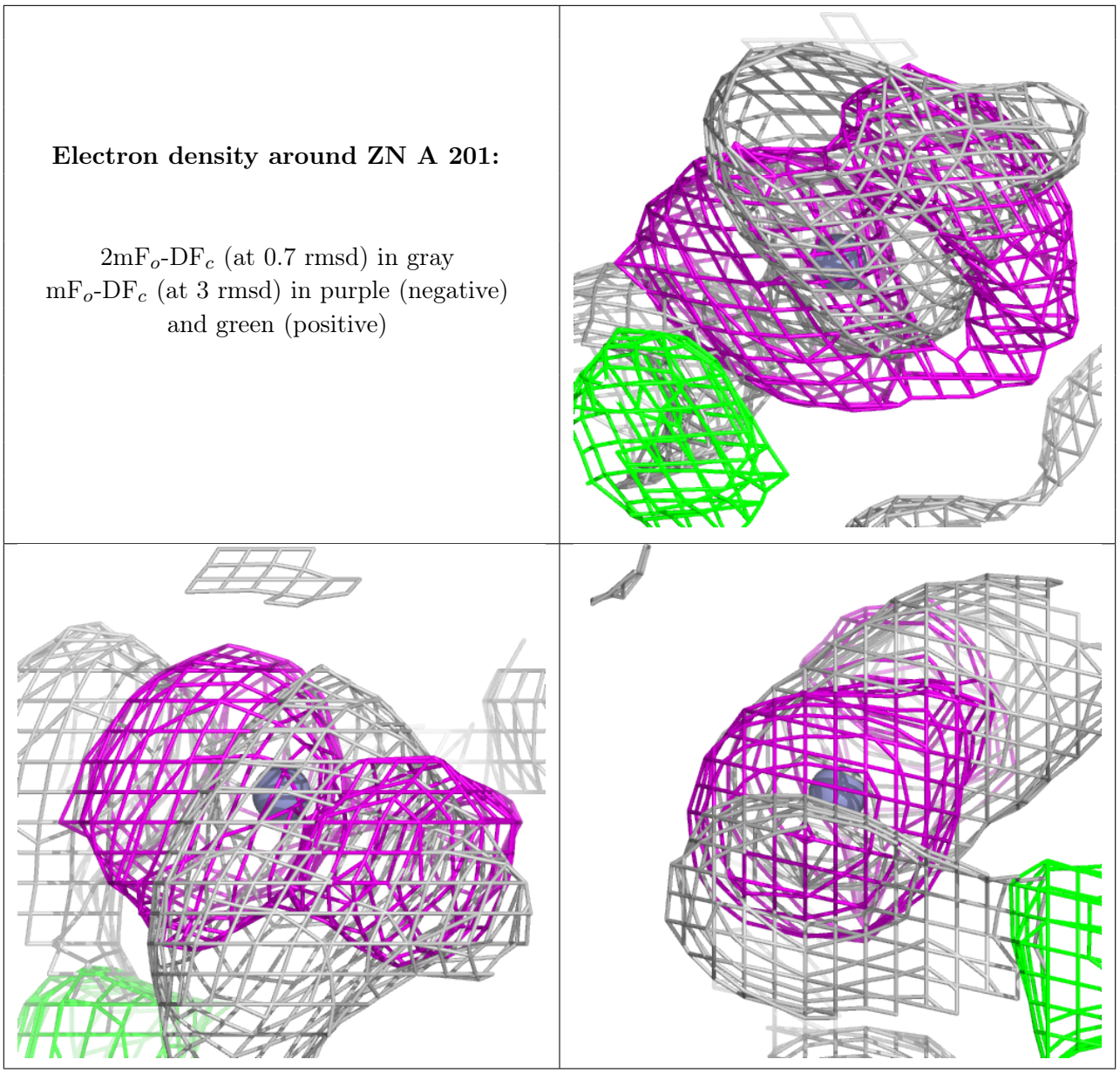
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	ZN	A	201	1/1	0.82	0.24	85,85,85,85	0
2	ZN	C	201	1/1	0.82	0.16	66,66,66,66	0
2	ZN	D	202	1/1	0.82	0.12	70,70,70,70	0
2	ZN	B	201	1/1	0.88	0.24	79,79,79,79	0
2	ZN	F	202	1/1	0.90	0.15	87,87,87,87	0
2	ZN	B	202	1/1	0.92	0.17	82,82,82,82	0
2	ZN	F	201	1/1	0.94	0.09	65,65,65,65	0
2	ZN	D	201	1/1	0.96	0.15	68,68,68,68	0
2	ZN	E	201	1/1	0.96	0.20	75,75,75,75	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.

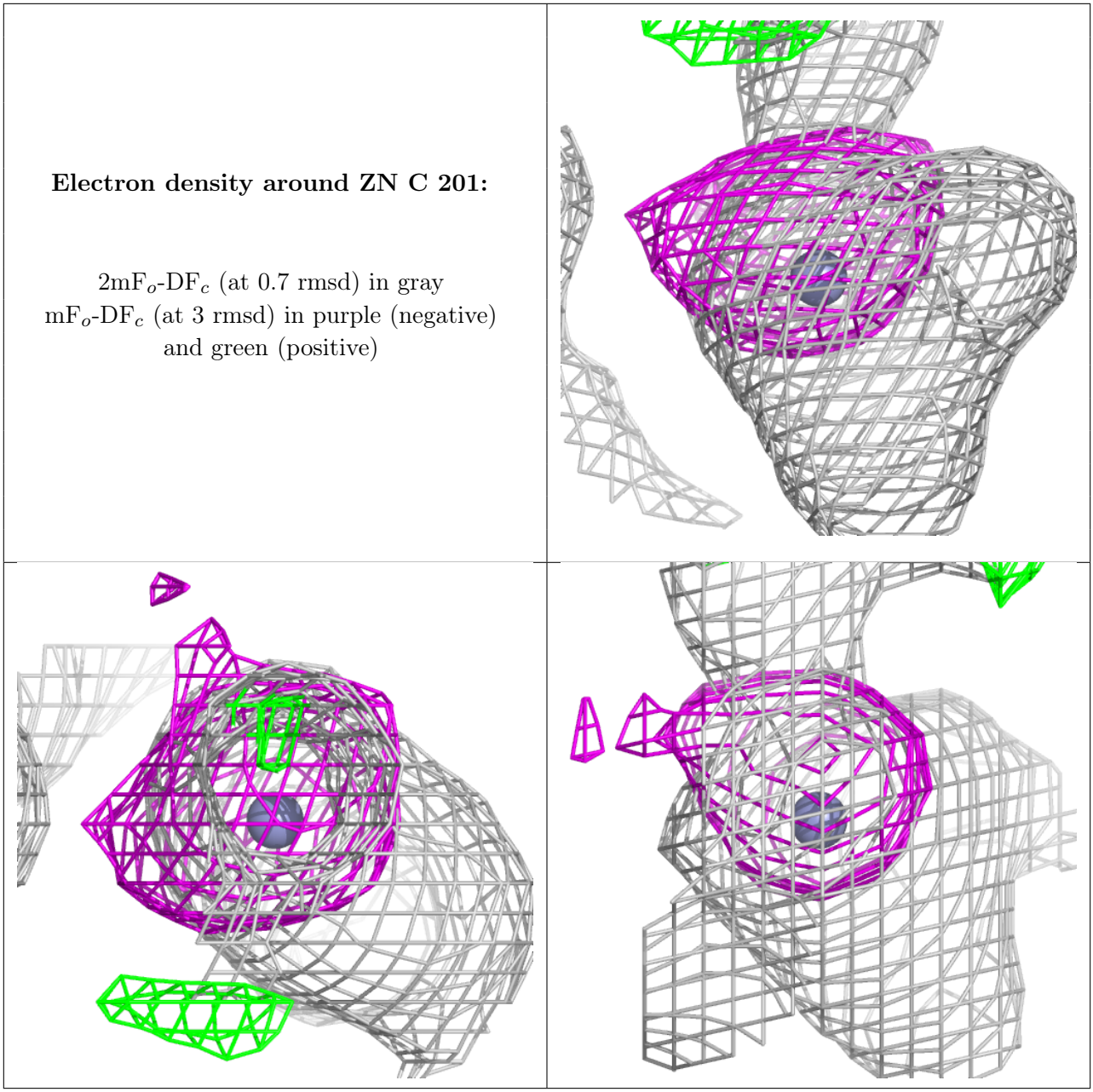
Electron density around ZN A 201:

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



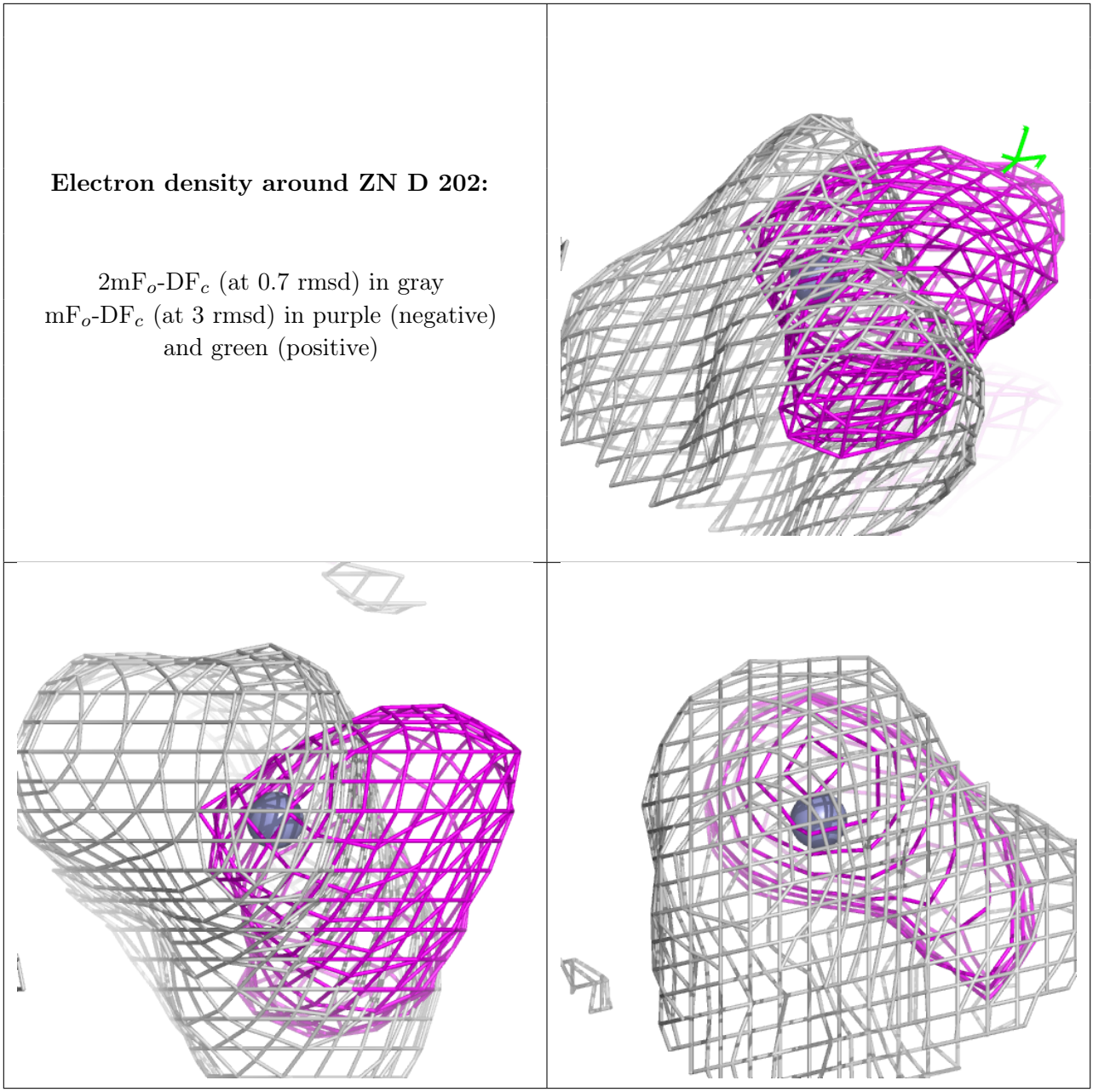
Electron density around ZN C 201:

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



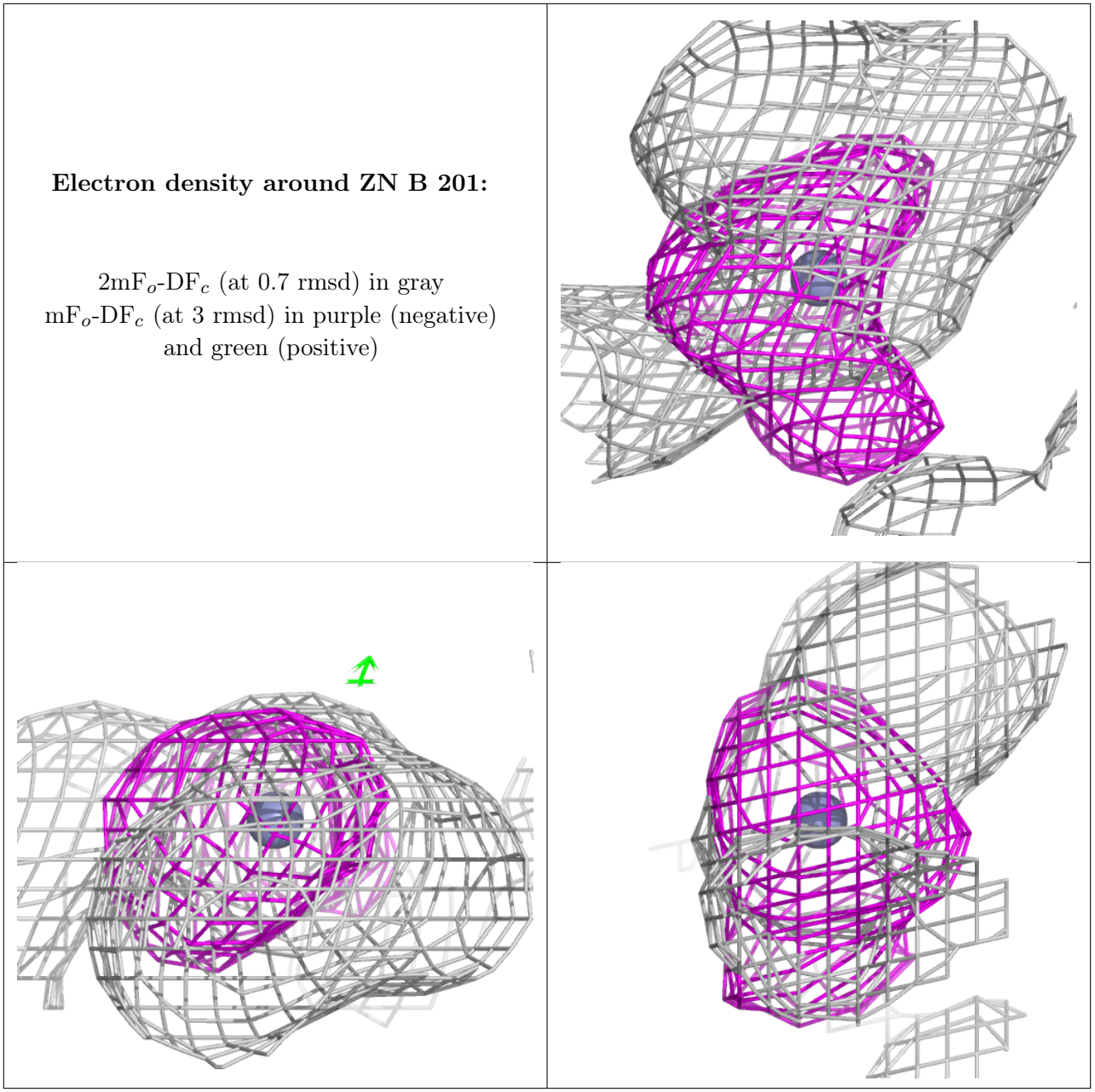
Electron density around ZN D 202:

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



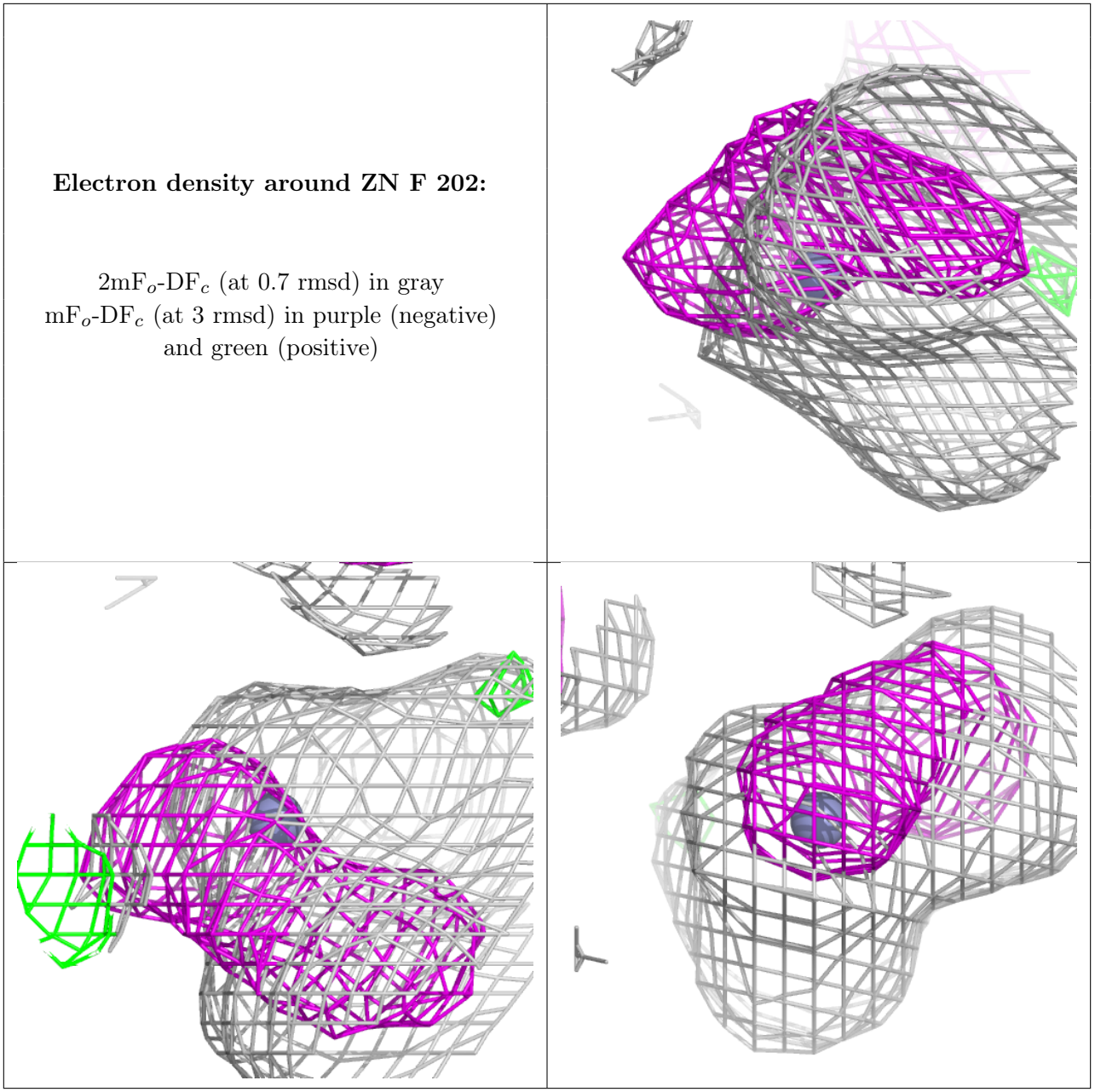
Electron density around ZN B 201:

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



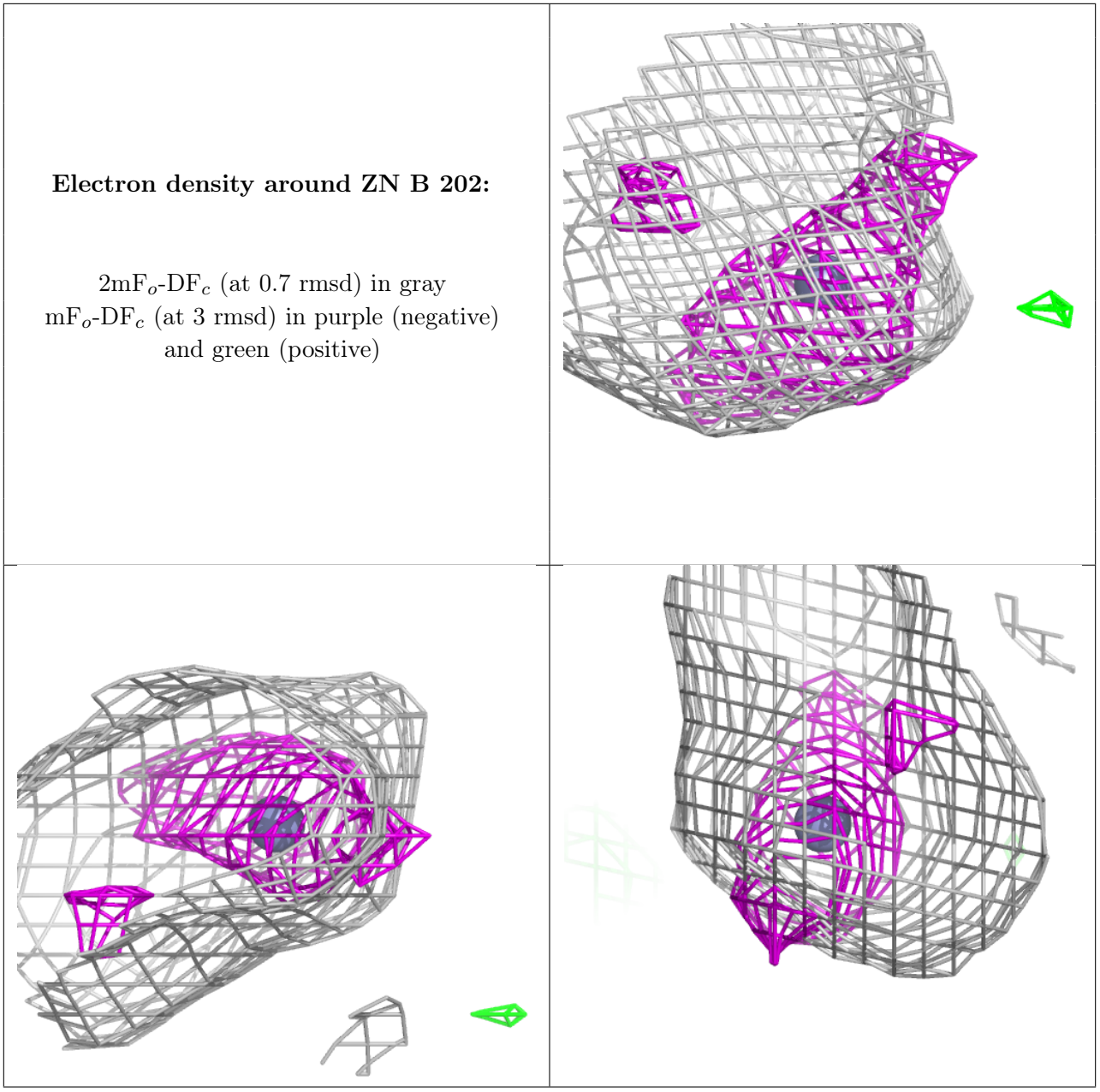
Electron density around ZN F 202:

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



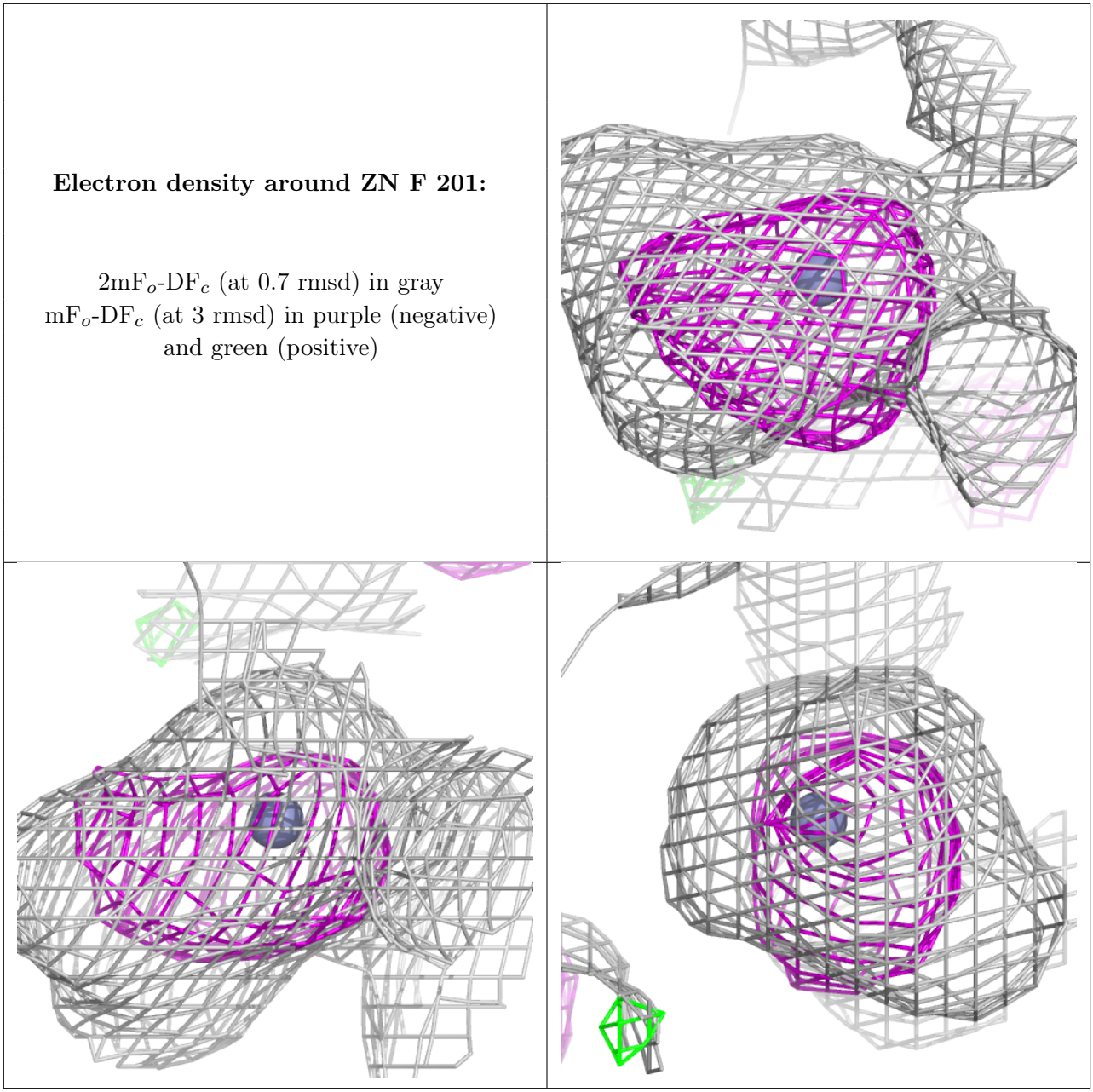
Electron density around ZN B 202:

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



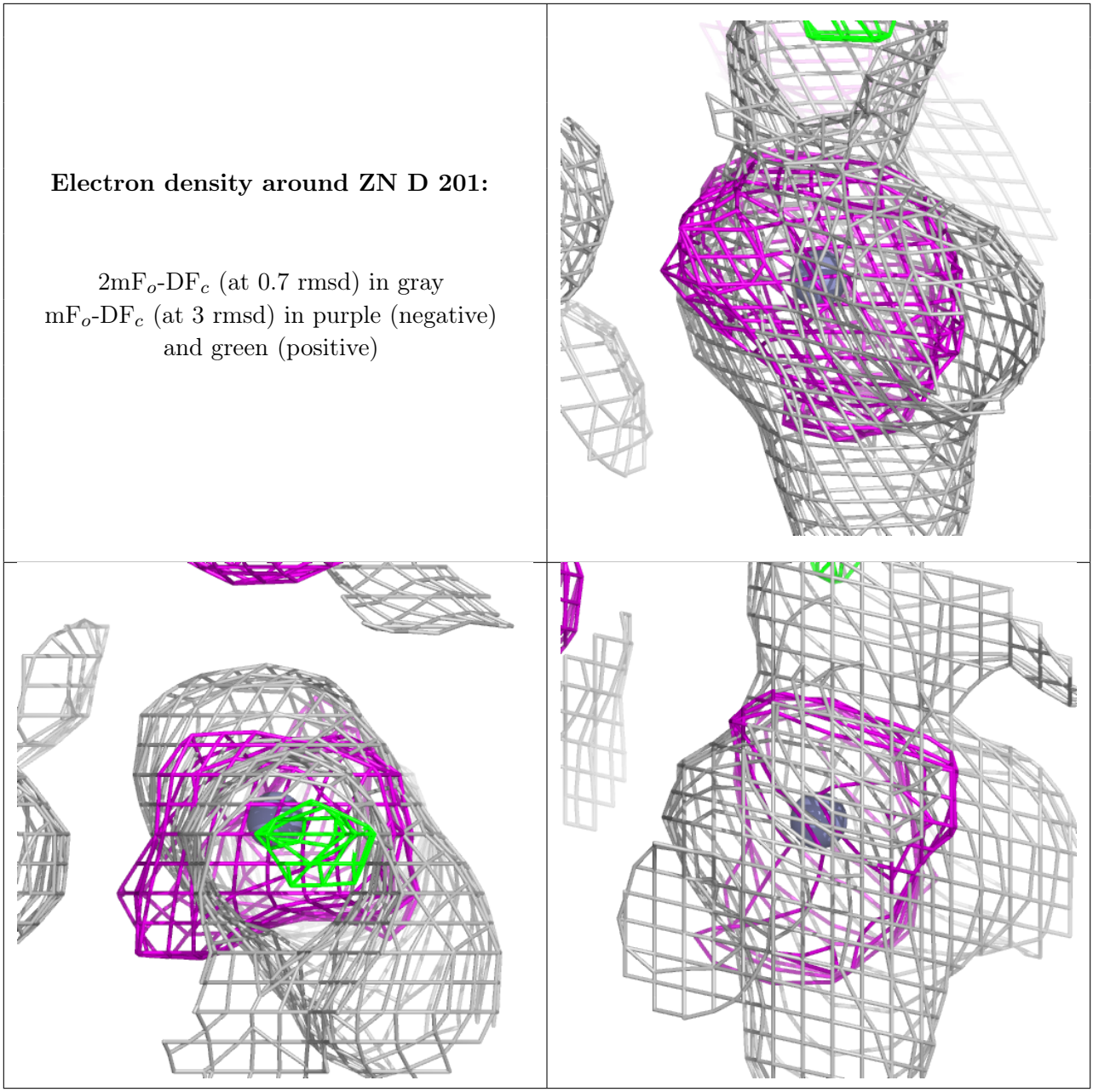
Electron density around ZN F 201:

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



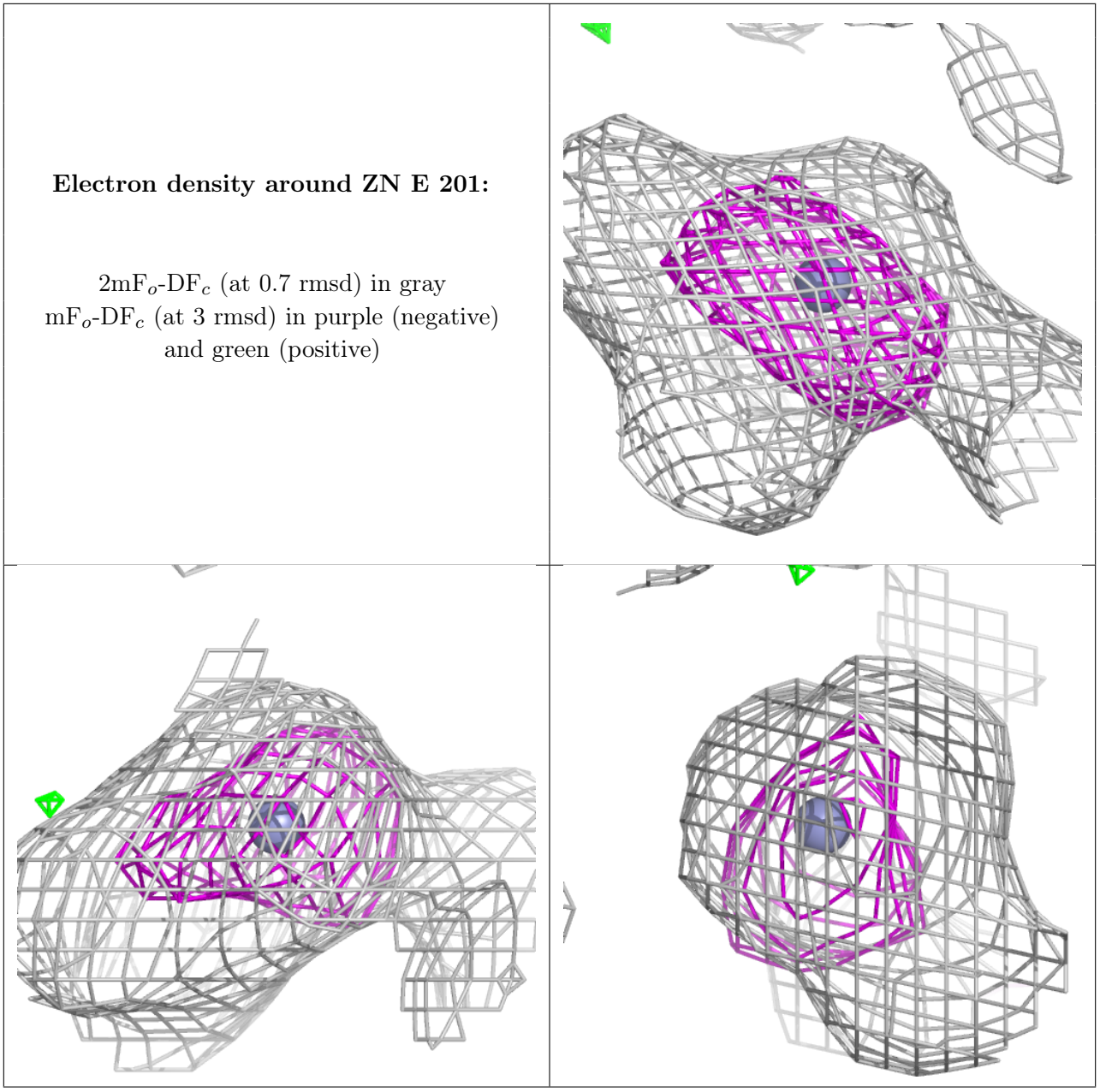
Electron density around ZN D 201:

$2mF_o$-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 E 201:

$2mF_o$-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.