



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:08 AM UTC

PDB ID : 7C06 / pdb_00007c06
Title : Crystal structure of yeast U2AF1 complex bound to 3' splice site RNA, 5'-UAGGU.
Authors : Yoshida, H.; Park, S.Y.; Urano, T.; Obayashi, E.
Deposited on : 2020-04-30
Resolution : 3.02 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

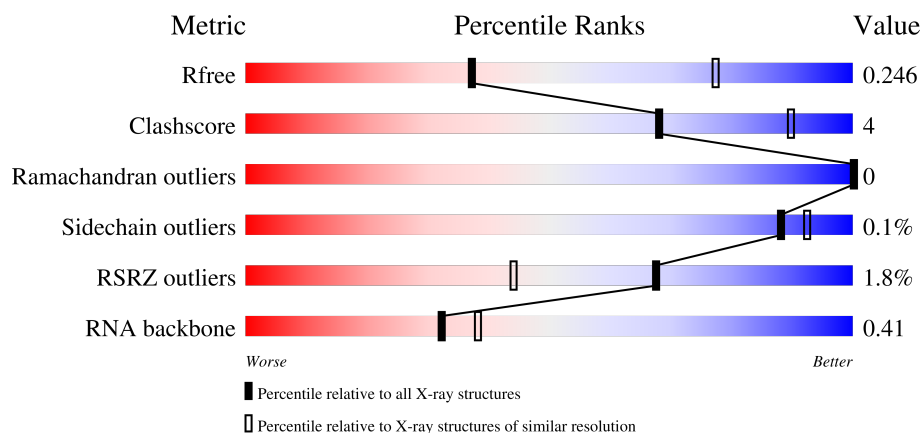
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.02 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)
RNA backbone	3983	1139 (3.24-2.80)

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	216	 78% 12% 11%
1	D	216	 81% 6% 13%
1	G	216	 80% 8% 11%
1	J	216	 83% 6% 11%

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Mol	Chain	Length	Quality of chain
1	M	216	
1	P	216	
1	S	216	
1	V	216	
1	Y	216	
2	B	69	
2	E	69	
2	H	69	
2	K	69	
2	N	69	
2	Q	69	
2	T	69	
2	W	69	
2	Z	69	
3	1	6	
3	C	6	
3	F	6	
3	I	6	
3	L	6	
3	O	6	
3	R	6	
3	U	6	
3	X	6	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18418 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 Splicing factor U2AF 23 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	0	0
			1567	981	278	295	13			
1	D	187	Total	C	N	O	S	0	0	0
			1524	955	270	286	13			
1	G	192	Total	C	N	O	S	0	0	0
			1558	976	277	292	13			
1	J	193	Total	C	N	O	S	0	0	0
			1567	981	278	295	13			
1	M	178	Total	C	N	O	S	0	0	0
			1452	911	259	269	13			
1	P	192	Total	C	N	O	S	0	0	0
			1558	976	277	292	13			
1	S	186	Total	C	N	O	S	0	1	0
			1524	955	271	285	13			
1	V	174	Total	C	N	O	S	0	0	0
			1419	892	254	260	13			
1	Y	179	Total	C	N	O	S	0	0	0
			1461	916	260	272	13			

- Molecule 2 is a protein called Splicing factor U2AF 59 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	56	Total	C	N	O	S	0	0	0
			455	288	82	84	1			
2	E	51	Total	C	N	O	S	0	0	0
			417	266	74	76	1			
2	H	53	Total	C	N	O	S	0	0	0
			430	274	76	79	1			
2	K	54	Total	C	N	O	S	0	0	0
			435	277	77	80	1			
2	N	53	Total	C	N	O	S	0	0	0
			430	274	76	79	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	53	Total	C	N	O	S	0	0	0
			430	274	76	79	1			
2	T	50	Total	C	N	O	S	0	0	0
			406	260	70	75	1			
2	W	53	Total	C	N	O	S	0	0	0
			430	274	76	79	1			
2	Z	48	Total	C	N	O	S	0	0	0
			392	251	68	72	1			

- Molecule 3 is a RNA chain called RNA (5'-R(*U*UP*AP*GP*GP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	F	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	I	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	L	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	O	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	R	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	U	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	X	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			
3	1	5	Total	C	N	O	P	0	0	0
			105	48	19	34	4			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Zn	0	0
			2	2		
4	D	2	Total	Zn	0	0
			2	2		
4	G	2	Total	Zn	0	0
			2	2		
4	J	2	Total	Zn	0	0
			2	2		

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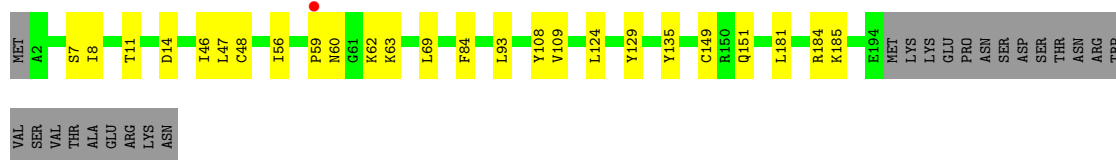
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	2	Total 2	Zn 2	0	0
4	P	2	Total 2	Zn 2	0	0
4	S	2	Total 2	Zn 2	0	0
4	V	2	Total 2	Zn 2	0	0
4	Y	2	Total 2	Zn 2	0	0

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: Splicing factor U2AF 23 kDa subunit

Chain A: 



- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain D: 



- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain G: 



- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain J: 



- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain M: 



SER
THR
ASN
ARG
TRP
VAL
SER
THR
GLU
ALA
ARG
LYS
ASN

- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain P:  85% 11%

MET
A2
I46
N54
P55
I56
D79
F84
V109
L124
R150
E193
GLU
MET
LYS
LYS
GLU
PRO
ASN
SER
SER
ASP
THR
ASN
ARG
TRP
VAL
SER
VAL
THR
ALA
GLU
ARG
LYS
ASN

- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain S:  80% 6% 14%

MET
ALA
SER
HIS
LEU
A6
S7
I8
M41
F42
L47
F48
F49
H57
E58
PRO
ASN
G61
K62
E83
K86
V95
V107
S139
R184
E193
GLU
MET
LYS
LYS
GLU
PRO
ASN
SER
ASP
SER
THR
ASN
ARG
TRP
VAL
SER
VAL
THR
ALA
GLU
ARG
LYS
ASN

- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain V:  75% 6% 19%

MET
ALA
SER
HIS
LEU
ALA
SER
ILE
TYR
GLY
THR
GLN
ASP
LYS
V16
S19
I46
N54
P55
I56
H57
GLU
PRO
ASN
G81
T65
E68
C82
V90
V109
I121
C149
H152
F165
H166
H167
A192
GLU
GLU
MET
LYS
LYS
GLU
PRO
ASN
SER

ASP
SER
THR
ASN
ARG
VAL
SER
VAL
THR
ALA
GLU
ARG
LYS
ASN

- Molecule 1: Splicing factor U2AF 23 kDa subunit

Chain Y:  78% 5% 17%

MET
ALA
SER
HIS
LEU
ALA
SER
ILE
TYR
GLY
THR
GLN
ASP
LYS
V16
S19
K23
M51
N60
K63
M80
D101
Q131
K185
L189
E194
MET
LYS
LYS
GLU
PRO
ASN
SER
ASP
SER
THR
ASN
ARG
TRP
VAL
SER
VAL
THR
ALA
GLU
ARG
LYS
ASN

- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain B:  74% 7% 19%

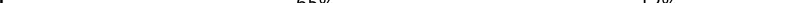
SER
SER
VAL
GLY
ARG
SER
ARG
SER
PRO
PRO
PRO
SER
ARG
E106
E115
Q118
P124
L134
I137
A161

- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain E:  59% 14% 26%

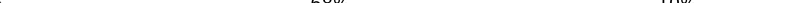
SER
SER
VAL
ARG
SER
ARG
SER
PRO
PRO
PRO
SER
ARG
GLU
ARG
VAL
R110
L116
R130
K131
W135
P139
Y142
A150
S153
G154
V155
F156
G160
ALA

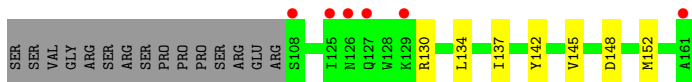
- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain H: 

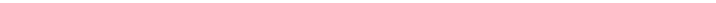


- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain K: 

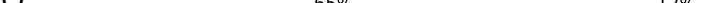


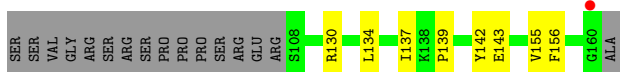
- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain N:  %

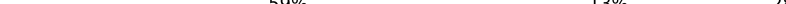


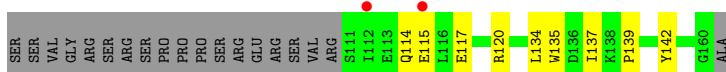
- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain Q:  %



- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain T: 

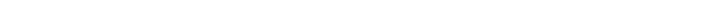


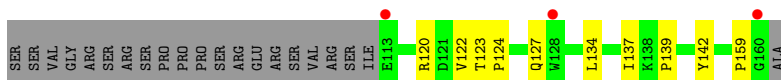
- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain W: 4% 67% 10% 23%

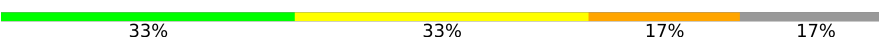


- Molecule 2: Splicing factor U2AF 59 kDa subunit

Chain Z: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain C: 



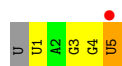
- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain F: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain I: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain L: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain O: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain R: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain U: 



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain X:  67% 17% 17%



- Molecule 3: RNA (5'-R(*U*UP*AP*GP*GP*U)-3')

Chain 1:  50% 17% 17% 17%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.82Å 255.10Å 94.11Å 90.00° 101.12° 90.00°	Depositor
Resolution (Å)	38.41 – 3.02 38.41 – 3.02	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.41-3.02) 99.9 (38.41-3.02)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.215 , 0.249 0.216 , 0.246	Depositor DCC
R_{free} test set	4117 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	68.1	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18418	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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:
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	0.10	0/1604	0.31	0/2163
1	D	0.10	0/1560	0.31	0/2103
1	G	0.11	0/1595	0.33	0/2151
1	J	0.09	0/1604	0.28	0/2163
1	M	0.10	0/1487	0.31	0/2005
1	P	0.10	0/1595	0.29	0/2151
1	S	0.09	0/1559	0.31	0/2099
1	V	0.09	0/1452	0.28	0/1955
1	Y	0.11	0/1496	0.31	0/2017
2	B	0.11	0/465	0.37	0/629
2	E	0.12	0/427	0.35	0/578
2	H	0.12	0/440	0.37	0/596
2	K	0.12	0/445	0.36	0/603
2	N	0.10	0/440	0.34	0/596
2	Q	0.11	0/440	0.34	0/596
2	T	0.10	0/416	0.32	0/564
2	W	0.11	0/440	0.37	0/596
2	Z	0.13	0/402	0.42	0/545
3	1	0.05	0/117	0.15	0/181
3	C	0.13	0/117	0.26	0/181
3	F	0.07	0/117	0.16	0/181
3	I	0.10	0/117	0.19	0/181
3	L	0.10	0/117	0.22	0/181
3	O	0.06	0/117	0.21	0/181
3	R	0.07	0/117	0.18	0/181
3	U	0.07	0/117	0.19	0/181
3	X	0.08	0/117	0.24	0/181
All	All	0.10	0/18920	0.31	0/25739

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

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	1567	0	1487	16	0
1	D	1524	0	1448	11	0
1	G	1558	0	1481	14	0
1	J	1567	0	1487	10	0
1	M	1452	0	1382	8	0
1	P	1558	0	1481	5	0
1	S	1524	0	1445	12	0
1	V	1419	0	1356	9	0
1	Y	1461	0	1388	9	0
2	B	455	0	460	5	0
2	E	417	0	422	9	0
2	H	430	0	436	6	0
2	K	435	0	441	6	0
2	N	430	0	436	3	0
2	Q	430	0	436	5	0
2	T	406	0	409	6	0
2	W	430	0	436	4	0
2	Z	392	0	393	9	0
3	1	105	0	55	2	0
3	C	105	0	55	3	0
3	F	105	0	55	0	0
3	I	105	0	55	6	0
3	L	105	0	55	0	0
3	O	105	0	55	1	0
3	R	105	0	55	1	0
3	U	105	0	55	0	0
3	X	105	0	55	0	0
4	A	2	0	0	0	0
4	D	2	0	0	0	0
4	G	2	0	0	0	0
4	J	2	0	0	0	0
4	M	2	0	0	0	0
4	P	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	S	2	0	0	0	0
4	V	2	0	0	0	0
4	Y	2	0	0	0	0
All	All	18418	0	17319	128	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 4.

All (128) 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:J:59:PRO:O	1:J:60:ASN:ND2	2.26	0.69
1:A:59:PRO:O	1:A:60:ASN:ND2	2.27	0.67
1:D:155:SER:HA	1:J:59:PRO:HB3	1.78	0.66
1:A:11:THR:HB	3:C:5:U:H5'	1.81	0.62
1:Y:185:LYS:NZ	2:Z:122:VAL:O	2.35	0.60
1:Y:23:LYS:NZ	3:1:4:G:O2'	2.35	0.59
2:K:152:MET:HG3	1:S:8:ILE:HB	1.85	0.59
2:E:131:LYS:HD3	2:E:131:LYS:H	1.66	0.59
1:G:35:ARG:NH1	3:I:1:U:O2'	2.35	0.59
1:S:184:ARG:NH2	2:T:115:GLU:OE2	2.24	0.58
1:V:149:CYS:HB3	1:V:165:PHE:HB2	1.86	0.58
1:G:150:ARG:NH1	3:I:5:U:O4	2.35	0.56
2:T:117:GLU:HA	2:T:120:ARG:HG3	1.87	0.56
1:J:58:GLU:HG3	1:J:59:PRO:HD2	1.87	0.56
1:Y:60:ASN:O	1:Y:63:LYS:HG3	2.05	0.56
1:G:154:THR:HB	1:G:156:GLU:HG2	1.87	0.55
1:G:159:ARG:HD2	1:G:163:CYS:HA	1.88	0.55
2:B:115:GLU:HA	2:B:118:GLN:HE21	1.73	0.54
1:J:50:ASN:OD1	1:J:132:ARG:NH2	2.41	0.54
1:G:172:SER:OG	1:G:174:GLN:OE1	2.26	0.54
2:Q:139:PRO:HG2	2:Q:142:TYR:CG	2.44	0.53
1:M:102:HIS:CD2	1:M:103:LEU:HD23	2.43	0.53
1:D:82:CYS:HB2	2:E:130:ARG:HH11	1.75	0.52
2:H:114:GLN:O	2:H:118:GLN:HG2	2.09	0.52
1:D:50:ASN:OD1	1:D:132:ARG:NH2	2.42	0.52
2:Z:120:ARG:O	2:Z:122:VAL:HG23	2.10	0.52
1:A:181:LEU:HD23	1:A:184:ARG:HH21	1.75	0.51
1:V:65:THR:HG23	1:V:68:GLU:H	1.75	0.51
2:E:139:PRO:HG2	2:E:142:TYR:CG	2.46	0.51
2:Z:139:PRO:HG2	2:Z:142:TYR:CD1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:139:PRO:HG2	2:Z:142:TYR:CG	2.46	0.50
1:M:83:GLU:HB2	2:N:130:ARG:HH12	1.75	0.50
1:V:149:CYS:SG	1:V:167:HIS:CD2	3.05	0.50
1:S:47:LEU:HB2	1:S:139:SER:HB2	1.93	0.50
1:G:149:CYS:SG	1:G:151:GLN:HG2	2.53	0.49
1:M:60:ASN:HB3	1:M:64:PHE:HE2	1.78	0.49
2:K:134:LEU:HA	2:K:137:ILE:HD12	1.95	0.49
2:N:139:PRO:HG2	2:N:142:TYR:CG	2.47	0.49
2:K:142:TYR:CD2	2:K:145:VAL:HG21	2.47	0.49
1:M:56:ILE:HD11	1:M:69:LEU:HD13	1.95	0.49
1:A:93:LEU:HD13	1:A:109:VAL:HG22	1.95	0.49
1:G:150:ARG:HD3	3:I:4:G:N1	2.27	0.49
1:A:62:LYS:H	1:A:62:LYS:HD2	1.78	0.49
1:V:46:ILE:HG22	1:V:109:VAL:HG13	1.95	0.48
1:S:95:VAL:HG22	1:S:107:VAL:HG22	1.95	0.48
1:A:185:LYS:HG2	2:B:124:PRO:HG3	1.94	0.48
1:V:149:CYS:SG	1:V:152:HIS:HB2	2.54	0.48
1:J:147:ALA:HB1	1:J:166:MET:HE3	1.96	0.48
2:K:148:ASP:OD2	1:S:8:ILE:HG13	2.13	0.48
1:A:129:TYR:CE1	2:B:134:LEU:HB2	2.49	0.47
1:G:35:ARG:HH12	3:I:1:U:HO2'	1.60	0.47
2:K:142:TYR:HD2	2:K:145:VAL:HG21	1.78	0.47
1:D:83:GLU:OE1	2:E:130:ARG:NH2	2.39	0.47
2:Z:124:PRO:HD2	2:Z:127:GLN:HG3	1.95	0.47
2:Q:143:GLU:HB2	1:S:57:HIS:HB3	1.97	0.47
2:H:120:ARG:O	2:H:122:VAL:HG23	2.15	0.47
2:N:117:GLU:OE2	2:N:120:ARG:NH1	2.47	0.47
1:S:47:LEU:HD22	1:S:49:PRO:HG3	1.95	0.47
2:W:134:LEU:HA	2:W:137:ILE:HD12	1.97	0.47
2:H:139:PRO:HG2	2:H:142:TYR:CD1	2.50	0.47
1:P:79:ASP:HA	2:Q:130:ARG:HD2	1.96	0.46
3:C:3:G:O2'	3:C:4:G:H2'	2.16	0.46
2:T:139:PRO:HG2	2:T:142:TYR:CG	2.50	0.46
1:Y:19:SER:HB2	3:1:5:U:H2'	1.96	0.46
1:S:83:GLU:O	1:S:86:LYS:HG2	2.16	0.46
1:D:95:VAL:HG22	1:D:107:VAL:HG22	1.98	0.46
2:W:139:PRO:HG2	2:W:142:TYR:CG	2.51	0.46
1:S:62:LYS:HD2	1:S:62:LYS:HA	1.86	0.45
1:P:46:ILE:HG12	1:P:109:VAL:HB	1.98	0.45
1:V:82:CYS:HB2	2:W:130:ARG:HD3	1.98	0.45
1:V:90:VAL:HG13	1:V:109:VAL:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:134:LEU:HA	2:Z:137:ILE:HD12	1.97	0.45
2:Q:134:LEU:HA	2:Q:137:ILE:HD12	1.97	0.45
2:T:134:LEU:HA	2:T:137:ILE:HD12	1.97	0.45
1:J:33:CYS:O	1:S:41:ASN:ND2	2.49	0.45
1:M:95:VAL:HG22	1:M:107:VAL:HG22	1.98	0.45
1:G:80:MET:HB3	1:G:93:LEU:HD11	1.98	0.45
1:J:36:LYS:HD3	1:S:42:PHE:CD2	2.52	0.45
1:M:23:LYS:NZ	3:O:4:G:O2'	2.50	0.45
1:D:83:GLU:O	1:D:86:LYS:HG2	2.17	0.45
1:Y:185:LYS:HE2	1:Y:189:LEU:HD11	1.99	0.45
2:B:134:LEU:HA	2:B:137:ILE:HD12	2.00	0.44
2:H:139:PRO:HG2	2:H:142:TYR:CG	2.52	0.44
1:J:83:GLU:HB2	2:K:130:ARG:HH12	1.82	0.44
1:M:159:ARG:HG2	1:M:163:CYS:HA	1.98	0.44
1:G:59:PRO:C	1:G:61:GLY:H	2.26	0.44
1:J:47:LEU:HD13	1:J:108:TYR:CE2	2.53	0.44
1:Y:131:GLN:HA	2:Z:139:PRO:HD3	1.99	0.44
1:A:84:PHE:HE1	1:A:124:LEU:HD11	1.82	0.43
2:W:149:GLN:HA	2:W:152:MET:HG2	2.00	0.43
1:D:189:LEU:HD22	2:E:116:LEU:HD11	2.00	0.43
2:Q:155:VAL:HG23	2:Q:156:PHE:CD2	2.53	0.43
1:D:83:GLU:HG2	2:E:135:TRP:CE2	2.53	0.43
1:A:63:LYS:O	1:A:63:LYS:HG2	2.19	0.43
1:S:83:GLU:HG2	2:T:135:TRP:CE2	2.53	0.43
1:A:149:CYS:SG	1:A:151:GLN:HG2	2.58	0.43
1:P:54:ASN:OD1	1:P:56:ILE:HG12	2.19	0.43
1:Y:101:ASP:O	2:Z:159:PRO:HB2	2.19	0.43
1:A:46:ILE:HG12	1:A:109:VAL:HB	2.00	0.43
1:D:56:ILE:HD11	1:D:69:LEU:CD1	2.49	0.42
2:H:150:ALA:HB1	2:H:156:PHE:CD2	2.54	0.42
1:V:46:ILE:HD11	1:V:121:ILE:HG22	2.01	0.42
1:A:8:ILE:O	1:A:14:ASP:HB2	2.18	0.42
1:A:56:ILE:HD11	1:A:69:LEU:HD11	2.01	0.42
1:G:34:SER:O	1:Y:63:LYS:HD2	2.20	0.42
1:V:54:ASN:CG	1:V:56:ILE:HG12	2.45	0.42
1:D:56:ILE:HD11	1:D:69:LEU:HD11	2.02	0.42
2:T:114:GLN:N	2:T:114:GLN:OE1	2.52	0.42
2:Z:123:THR:HG22	2:Z:127:GLN:HB2	2.01	0.41
1:A:48:CYS:HA	1:A:135:TYR:O	2.20	0.41
3:C:3:G:HO2'	3:C:4:G:H2'	1.84	0.41
2:E:155:VAL:HG23	2:E:156:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:62:LYS:HB2	1:G:62:LYS:HE3	1.87	0.41
2:B:118:GLN:H	2:B:118:GLN:HG2	1.68	0.41
3:I:3:G:HO2'	3:I:4:G:H2'	1.86	0.41
1:J:14:ASP:O	1:J:35:ARG:NH2	2.40	0.41
1:A:7:SER:HB3	2:H:122:VAL:HG22	2.03	0.41
1:P:150:ARG:HG2	3:R:4:G:O6	2.21	0.41
1:Y:51:MET:HE3	1:Y:80:MET:HE1	2.02	0.41
2:E:150:ALA:HB1	2:E:156:PHE:CD2	2.56	0.41
2:E:153:SER:OG	2:E:155:VAL:HG22	2.21	0.41
1:G:181:LEU:HD23	1:G:184:ARG:HH21	1.86	0.40
3:I:3:G:O2'	3:I:4:G:H2'	2.21	0.40
1:A:47:LEU:HD13	1:A:108:TYR:CE2	2.56	0.40
1:D:47:LEU:HD13	1:D:108:TYR:CE2	2.57	0.40
1:G:61:GLY:C	1:G:63:LYS:H	2.29	0.40
1:M:47:LEU:HD13	1:M:108:TYR:CE2	2.56	0.40
1:P:84:PHE:HE1	1:P:124:LEU:HD11	1.85	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	191/216 (88%)	183 (96%)	8 (4%)	0	100	100
1	D	185/216 (86%)	180 (97%)	5 (3%)	0	100	100
1	G	190/216 (88%)	184 (97%)	6 (3%)	0	100	100
1	J	191/216 (88%)	185 (97%)	6 (3%)	0	100	100
1	M	176/216 (82%)	172 (98%)	4 (2%)	0	100	100
1	P	190/216 (88%)	185 (97%)	5 (3%)	0	100	100
1	S	183/216 (85%)	177 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	V	170/216 (79%)	167 (98%)	3 (2%)	0	100	100
1	Y	177/216 (82%)	172 (97%)	5 (3%)	0	100	100
2	B	54/69 (78%)	51 (94%)	3 (6%)	0	100	100
2	E	49/69 (71%)	45 (92%)	4 (8%)	0	100	100
2	H	51/69 (74%)	49 (96%)	2 (4%)	0	100	100
2	K	52/69 (75%)	51 (98%)	1 (2%)	0	100	100
2	N	51/69 (74%)	48 (94%)	3 (6%)	0	100	100
2	Q	51/69 (74%)	48 (94%)	3 (6%)	0	100	100
2	T	48/69 (70%)	46 (96%)	2 (4%)	0	100	100
2	W	51/69 (74%)	48 (94%)	3 (6%)	0	100	100
2	Z	46/69 (67%)	40 (87%)	6 (13%)	0	100	100
All	All	2106/2565 (82%)	2031 (96%)	75 (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	170/192 (88%)	170 (100%)	0	100	100
1	D	166/192 (86%)	166 (100%)	0	100	100
1	G	169/192 (88%)	168 (99%)	1 (1%)	78	87
1	J	170/192 (88%)	170 (100%)	0	100	100
1	M	158/192 (82%)	158 (100%)	0	100	100
1	P	169/192 (88%)	169 (100%)	0	100	100
1	S	165/192 (86%)	165 (100%)	0	100	100
1	V	154/192 (80%)	153 (99%)	1 (1%)	78	87
1	Y	159/192 (83%)	159 (100%)	0	100	100
2	B	50/62 (81%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	46/62 (74%)	46 (100%)	0	100	100
2	H	48/62 (77%)	48 (100%)	0	100	100
2	K	48/62 (77%)	48 (100%)	0	100	100
2	N	48/62 (77%)	48 (100%)	0	100	100
2	Q	48/62 (77%)	48 (100%)	0	100	100
2	T	45/62 (73%)	45 (100%)	0	100	100
2	W	48/62 (77%)	48 (100%)	0	100	100
2	Z	43/62 (69%)	43 (100%)	0	100	100
All	All	1904/2286 (83%)	1902 (100%)	2 (0%)	88	92

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	151	GLN
1	V	109	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	HIS
1	A	164	ASN
1	D	17	ASN
1	D	57	HIS
1	G	41	ASN
1	G	118	GLN
1	G	164	ASN
1	J	44	GLN
1	M	164	ASN
1	P	102	HIS
1	P	164	ASN
1	S	17	ASN
1	S	164	ASN
1	V	164	ASN
2	W	118	GLN
1	Y	17	ASN
1	Y	57	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	1	4/6 (66%)	1 (25%)	0
3	C	4/6 (66%)	1 (25%)	0
3	F	4/6 (66%)	0	0
3	I	4/6 (66%)	1 (25%)	0
3	L	4/6 (66%)	1 (25%)	0
3	O	4/6 (66%)	1 (25%)	0
3	R	4/6 (66%)	1 (25%)	0
3	U	4/6 (66%)	1 (25%)	0
3	X	4/6 (66%)	1 (25%)	0
All	All	36/54 (66%)	8 (22%)	0

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	5	U
3	I	5	U
3	L	5	U
3	O	5	U
3	R	5	U
3	U	5	U
3	X	5	U
3	1	5	U

There are no RNA pucker outliers to report.

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 18 ligands modelled in this entry, 18 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	193/216 (89%)	-0.11	1 (0%) 87 72	38, 57, 99, 115	0
1	D	187/216 (86%)	-0.18	3 (1%) 70 47	36, 53, 96, 114	0
1	G	192/216 (88%)	-0.20	0 100 100	31, 50, 89, 107	0
1	J	193/216 (89%)	0.27	1 (0%) 87 72	45, 68, 104, 118	0
1	M	178/216 (82%)	0.06	7 (3%) 43 24	38, 67, 108, 121	0
1	P	192/216 (88%)	0.16	0 100 100	41, 64, 93, 112	0
1	S	186/216 (86%)	0.24	3 (1%) 70 47	27, 74, 118, 136	1 (0%)
1	V	174/216 (80%)	0.30	3 (1%) 69 46	57, 82, 107, 119	0
1	Y	179/216 (82%)	0.23	1 (0%) 85 69	44, 83, 118, 132	0
2	B	56/69 (81%)	-0.05	0 100 100	44, 65, 107, 126	0
2	E	51/69 (73%)	0.11	1 (1%) 65 41	40, 66, 135, 138	0
2	H	53/69 (76%)	-0.02	1 (1%) 66 43	30, 52, 100, 123	0
2	K	54/69 (78%)	0.42	6 (11%) 10 6	40, 68, 112, 143	0
2	N	53/69 (76%)	0.11	1 (1%) 66 43	42, 71, 133, 143	0
2	Q	53/69 (76%)	0.36	1 (1%) 66 43	56, 72, 118, 146	0
2	T	50/69 (72%)	0.45	2 (4%) 42 23	63, 84, 153, 164	0
2	W	53/69 (76%)	0.50	3 (5%) 29 15	66, 86, 135, 140	0
2	Z	48/69 (69%)	0.27	3 (6%) 26 13	44, 72, 146, 152	0
3	I	5/6 (83%)	0.49	0 100 100	96, 105, 109, 128	0
3	C	5/6 (83%)	-0.30	0 100 100	51, 52, 68, 84	0
3	F	5/6 (83%)	-0.50	0 100 100	51, 52, 89, 115	0
3	I	5/6 (83%)	0.01	1 (20%) 3 2	49, 59, 89, 89	0
3	L	5/6 (83%)	0.48	1 (20%) 3 2	66, 71, 80, 113	0
3	O	5/6 (83%)	0.28	0 100 100	90, 94, 103, 121	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
3	R	5/6 (83%)	-0.13	0 100 100	55, 56, 72, 90	0
3	U	5/6 (83%)	-0.15	0 100 100	65, 65, 92, 130	0
3	X	5/6 (83%)	-0.01	0 100 100	89, 90, 100, 112	0
All	All	2190/2619 (83%)	0.11	39 (1%) 67 44	27, 68, 117, 164	1 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	V	16	VAL	4.3
1	M	16	VAL	4.1
2	K	161	ALA	3.8
1	J	8	ILE	3.7
1	S	61	GLY	3.5
1	Y	16	VAL	3.5
3	L	5	U	3.5
2	Q	160	GLY	3.2
2	W	119	LEU	3.0
2	Z	160	GLY	3.0
1	V	19	SER	3.0
1	D	154	THR	3.0
2	Z	113	GLU	2.9
1	D	155	SER	2.9
1	S	58	GLU	2.8
1	V	61	GLY	2.8
2	W	120	ARG	2.7
2	W	113	GLU	2.7
2	K	126	ASN	2.5
1	M	193	GLU	2.5
1	M	34	SER	2.5
1	M	155	SER	2.5
2	T	115	GLU	2.5
1	M	38	VAL	2.4
2	K	129	LYS	2.4
2	E	160	GLY	2.3
2	H	160	GLY	2.3
1	D	192	ALA	2.3
2	K	127	GLN	2.3
3	I	5	U	2.3
1	M	102	HIS	2.2
2	K	108	SER	2.2
2	Z	128	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	59	PRO	2.2
1	S	6	ALA	2.1
2	N	160	GLY	2.1
2	T	112	ILE	2.1
1	M	17	ASN	2.1
2	K	125	ILE	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 [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
4	ZN	A	302	1/1	0.99	0.05	50,50,50,50	0
4	ZN	D	302	1/1	0.99	0.03	46,46,46,46	0
4	ZN	J	301	1/1	0.99	0.03	55,55,55,55	0
4	ZN	M	302	1/1	0.99	0.02	54,54,54,54	0
4	ZN	S	302	1/1	0.99	0.04	67,67,67,67	0
4	ZN	V	302	1/1	0.99	0.02	67,67,67,67	0
4	ZN	Y	301	1/1	0.99	0.02	83,83,83,83	0
4	ZN	Y	302	1/1	0.99	0.02	73,73,73,73	0
4	ZN	M	301	1/1	1.00	0.02	78,78,78,78	0
4	ZN	A	301	1/1	1.00	0.03	51,51,51,51	0
4	ZN	P	301	1/1	1.00	0.03	51,51,51,51	0
4	ZN	P	302	1/1	1.00	0.02	49,49,49,49	0
4	ZN	S	301	1/1	1.00	0.05	51,51,51,51	0
4	ZN	G	301	1/1	1.00	0.01	44,44,44,44	0
4	ZN	V	301	1/1	1.00	0.03	65,65,65,65	0
4	ZN	G	302	1/1	1.00	0.01	41,41,41,41	0
4	ZN	D	301	1/1	1.00	0.02	44,44,44,44	0

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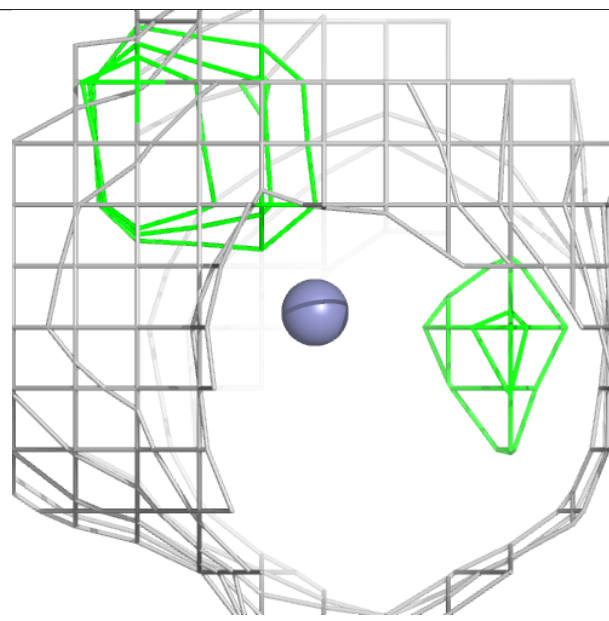
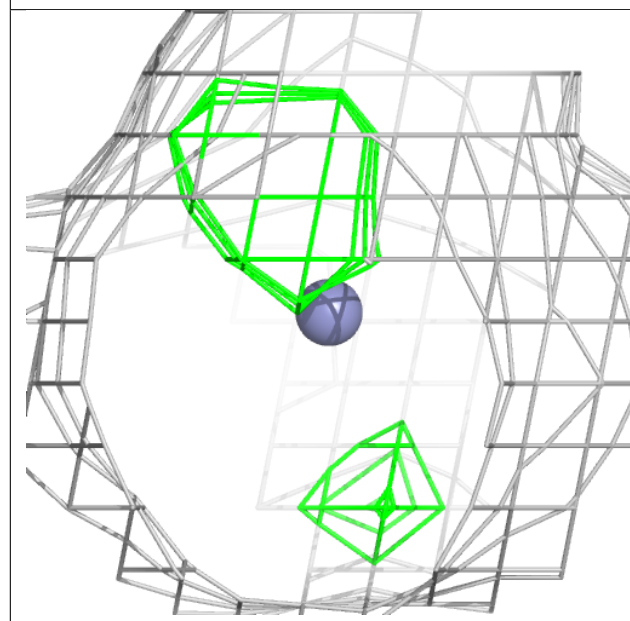
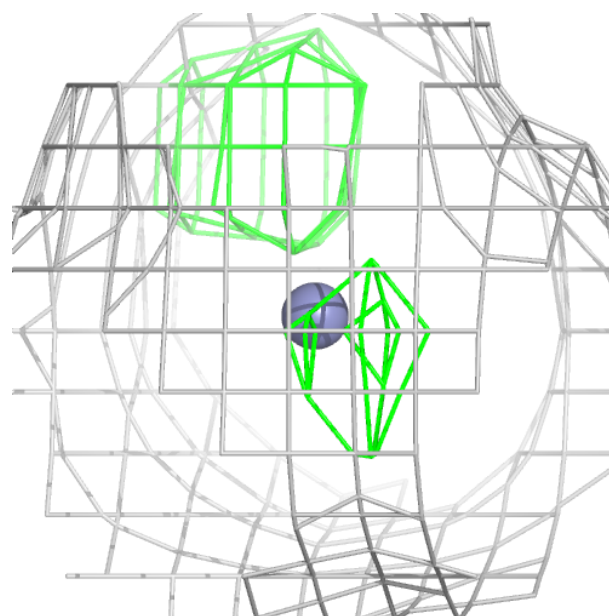
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	J	302	1/1	1.00	0.02	62,62,62,62	0

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.

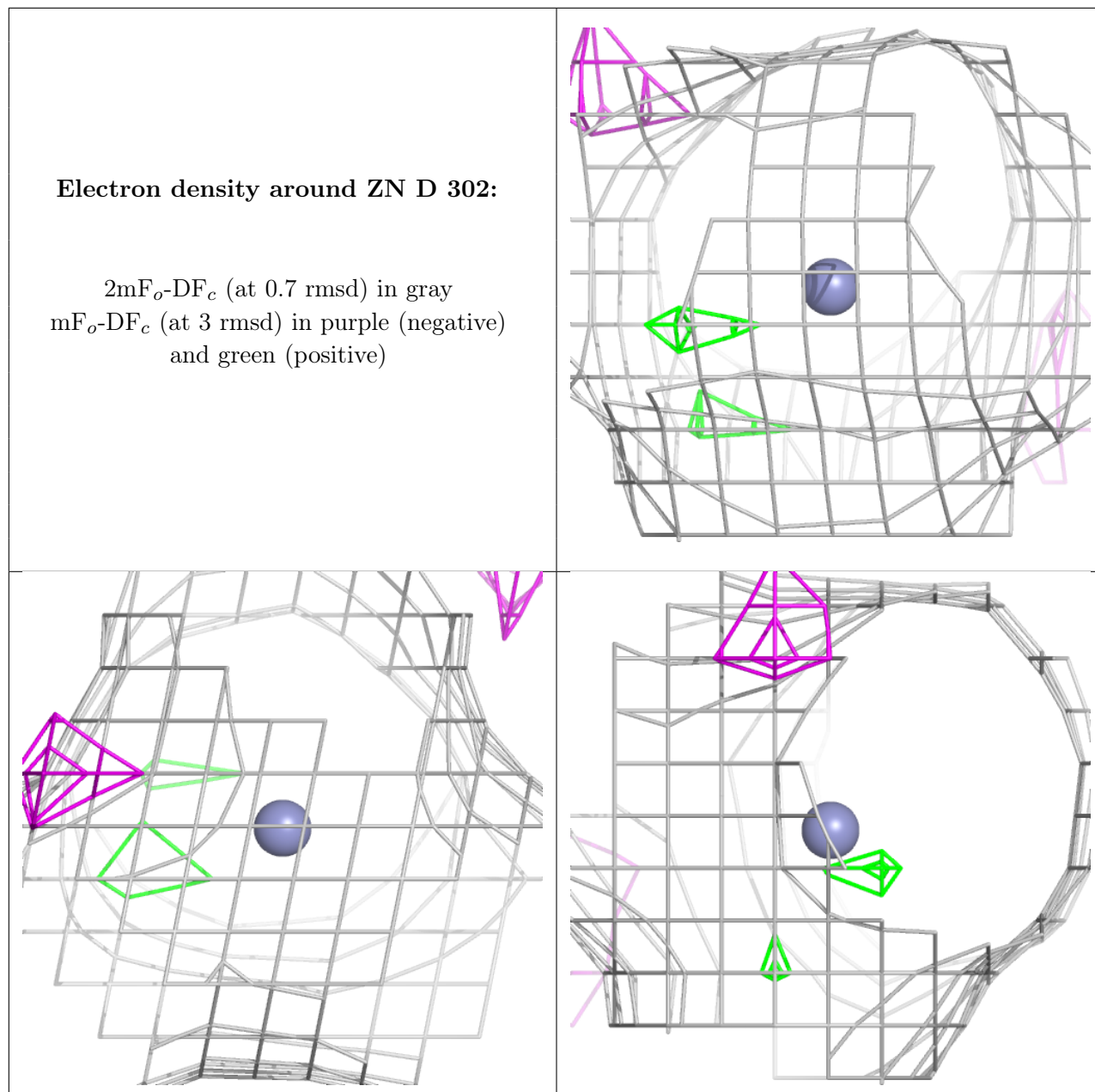
Electron density around ZN A 302:

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



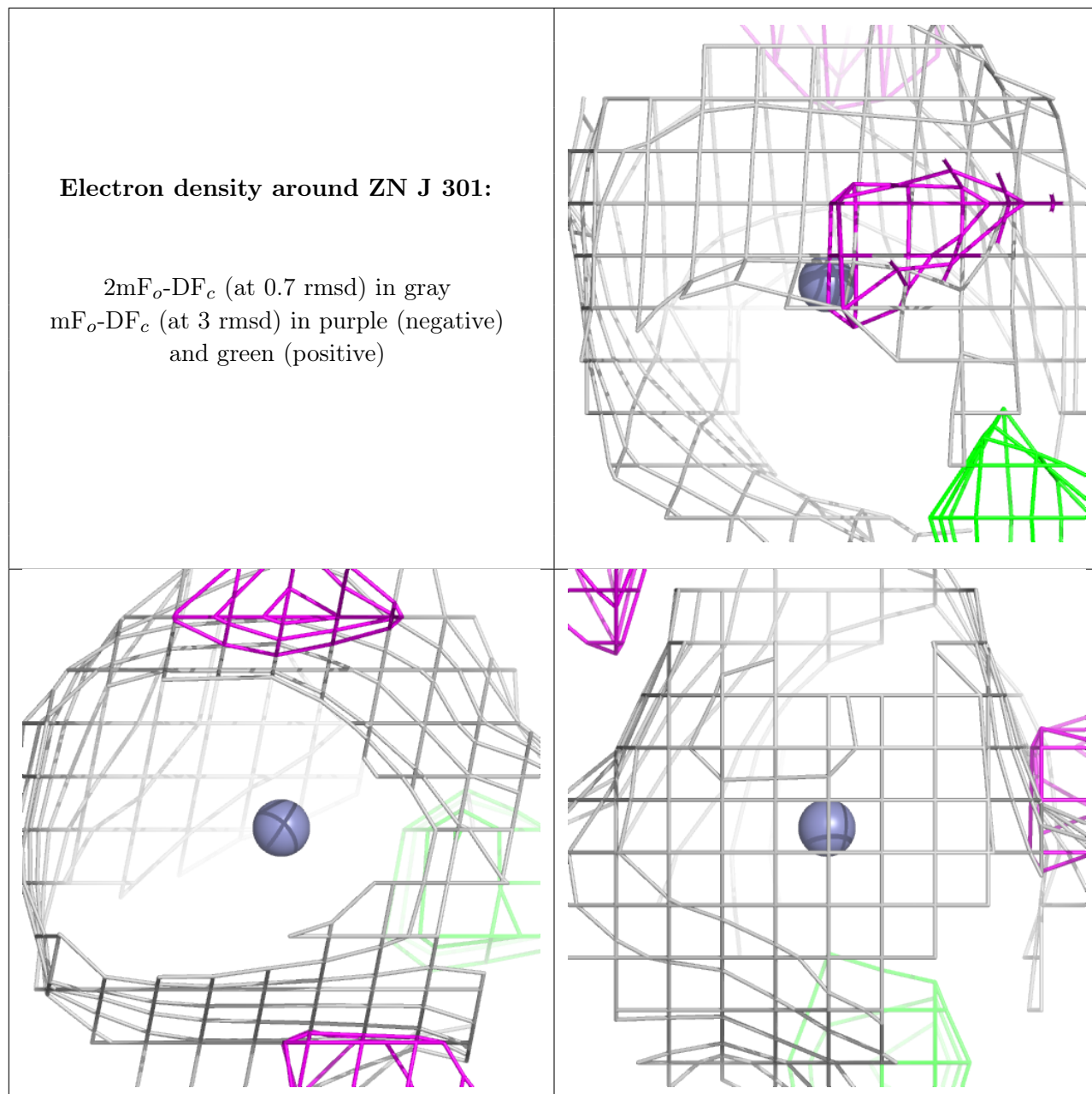
Electron density around ZN D 302:

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



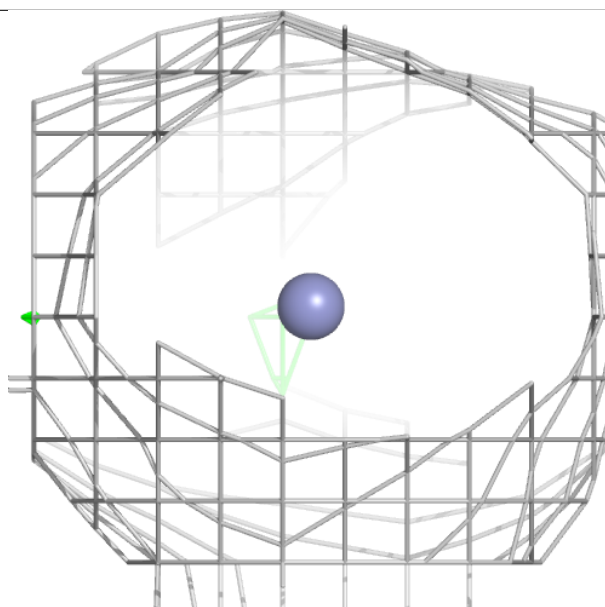
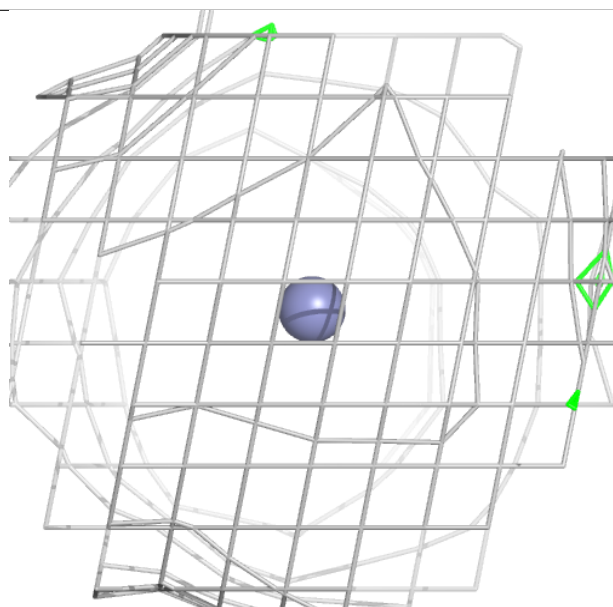
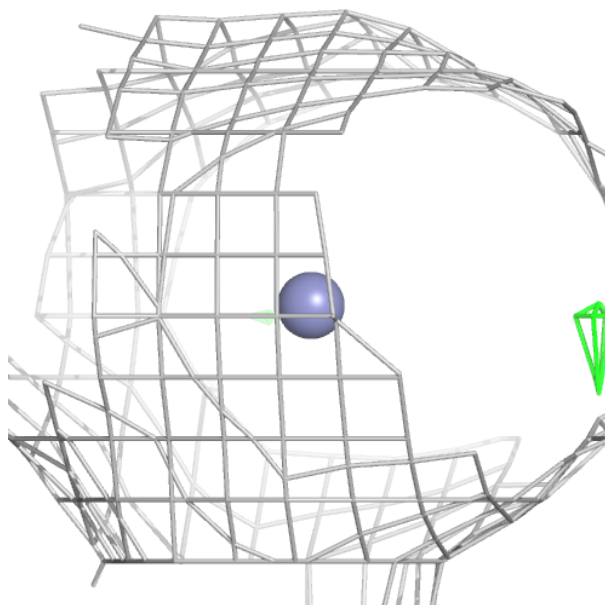
Electron density around ZN J 301:

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and green (positive)



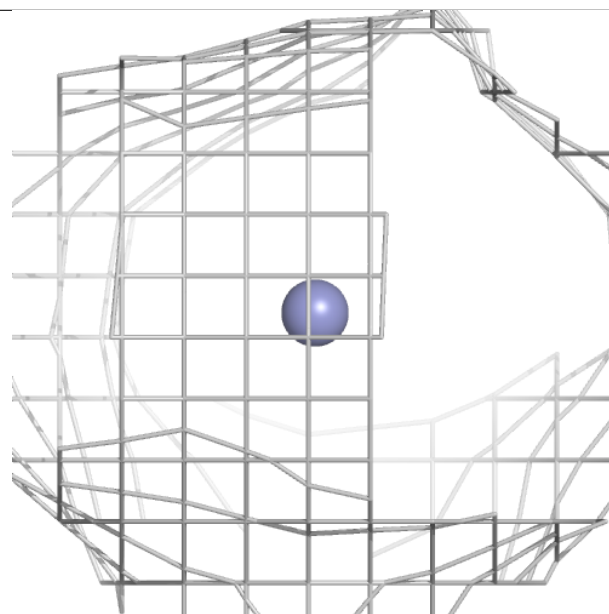
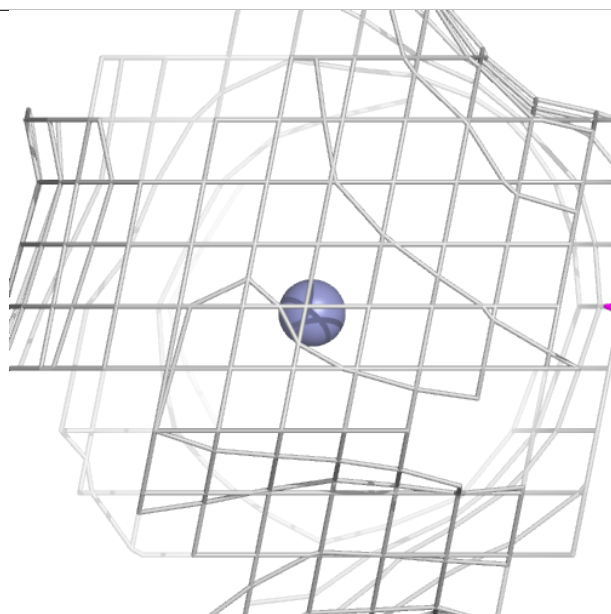
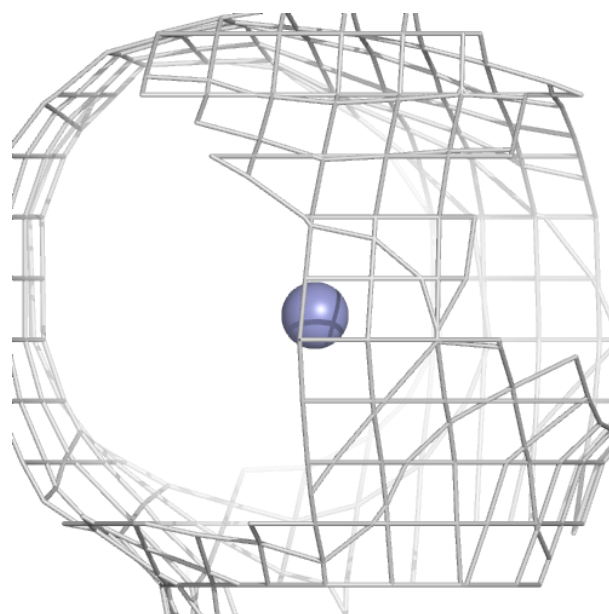
Electron density around ZN M 302:

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



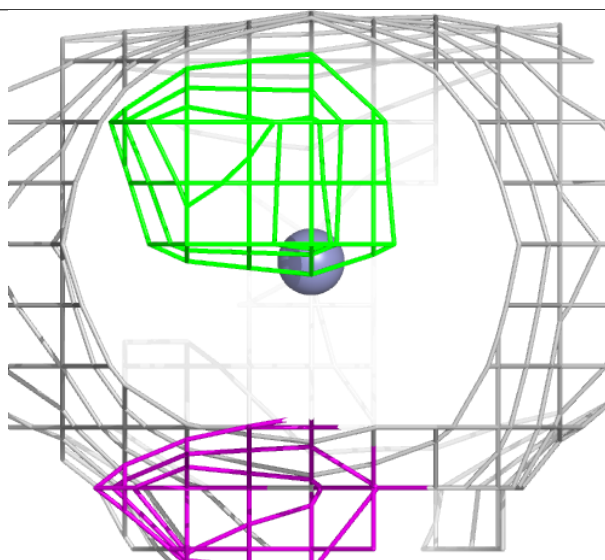
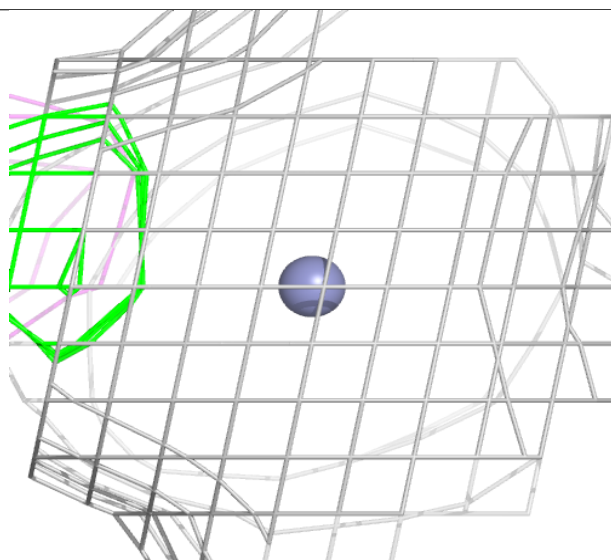
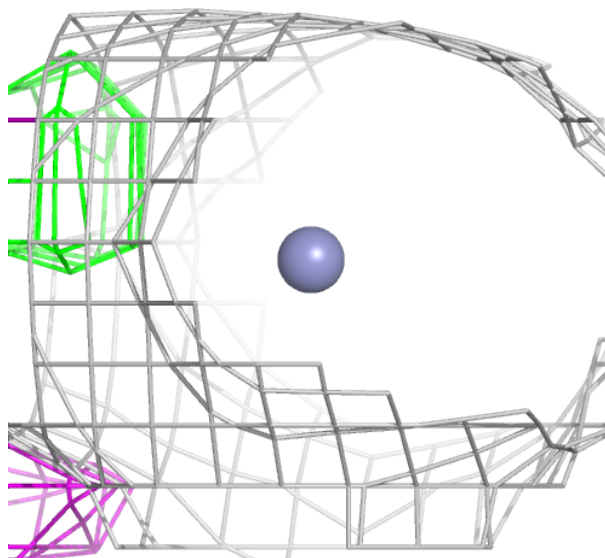
Electron density around ZN S 302:

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



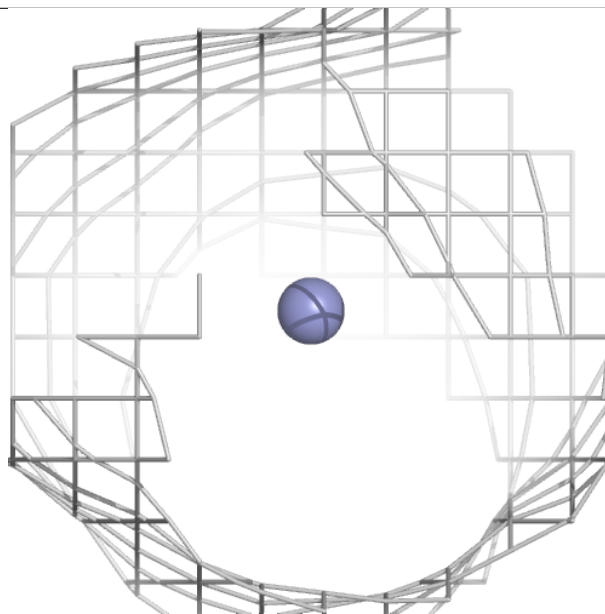
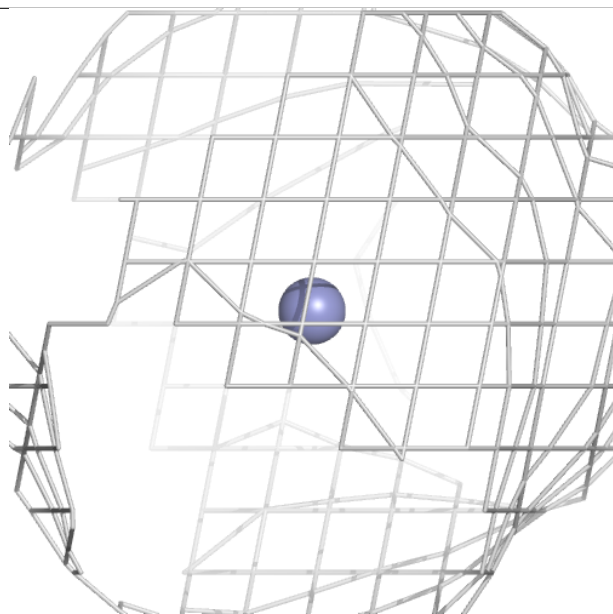
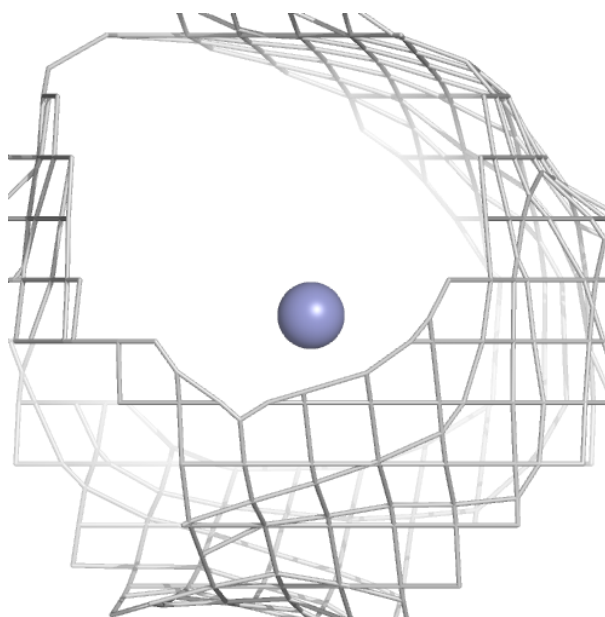
Electron density around ZN V 302:

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and green (positive)



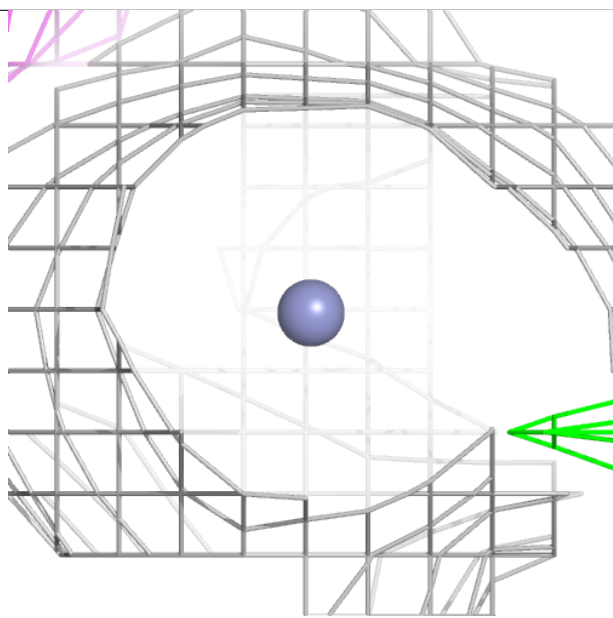
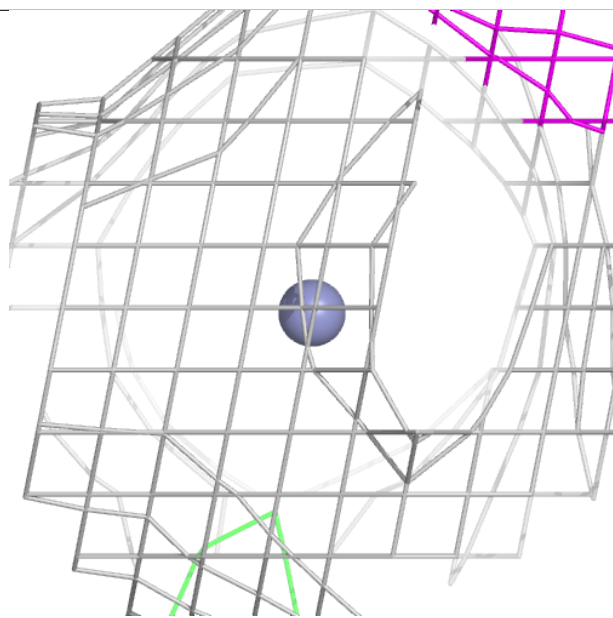
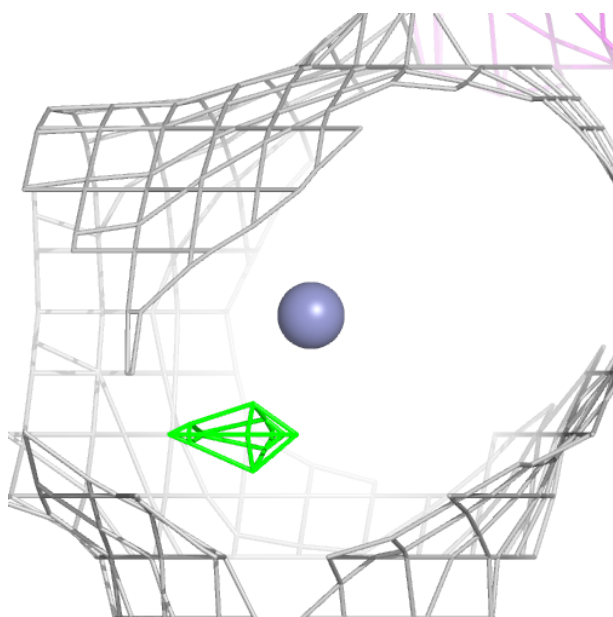
Electron density around ZN Y 301:

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



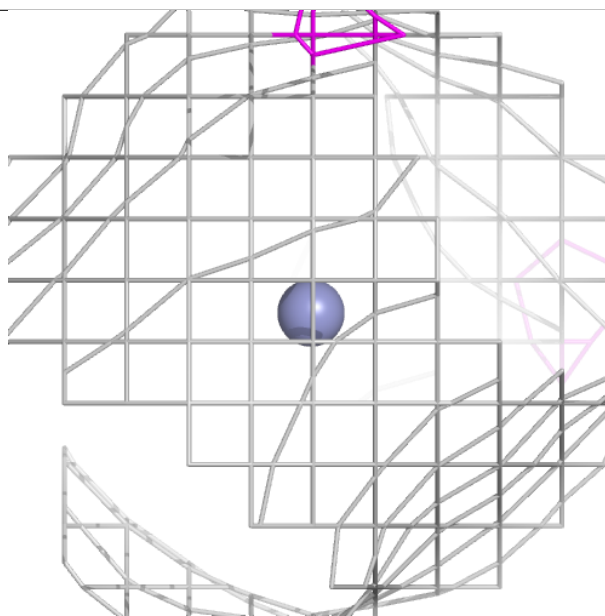
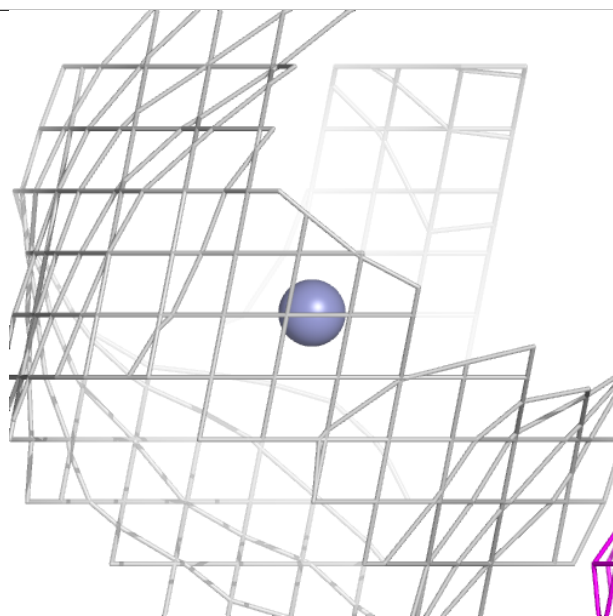
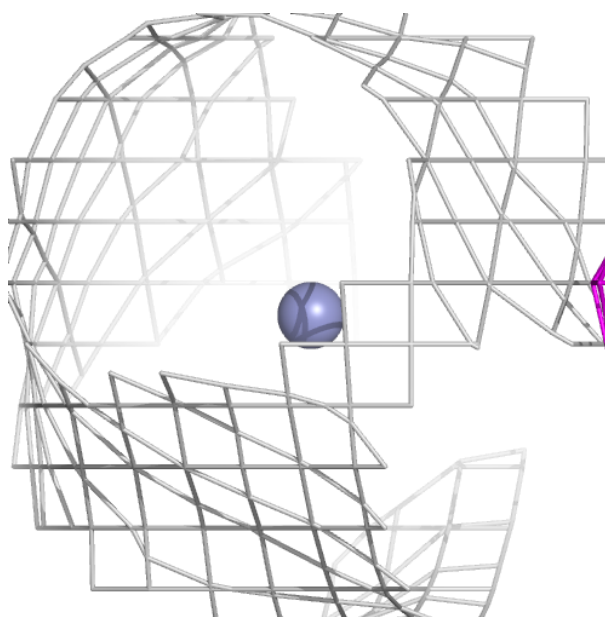
Electron density around ZN Y 302:

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



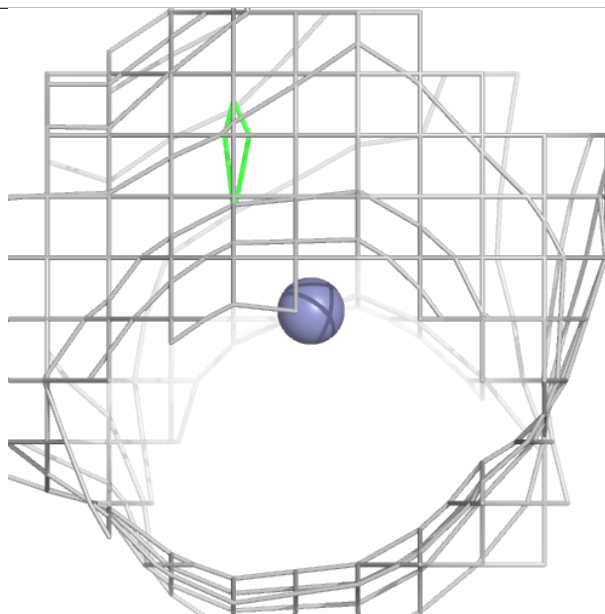
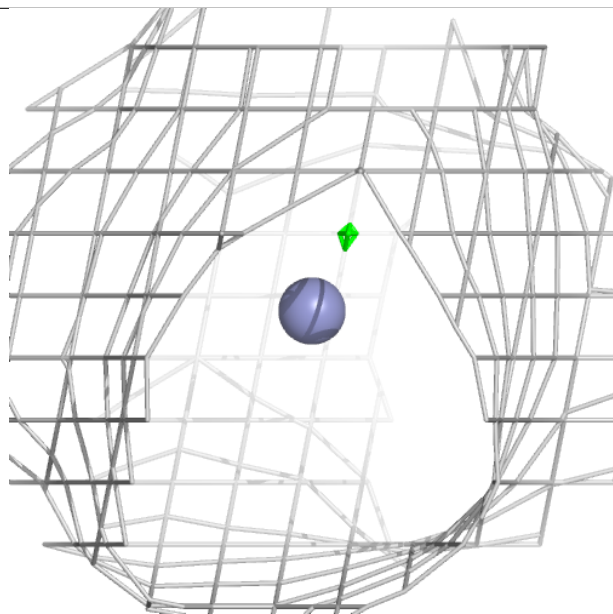
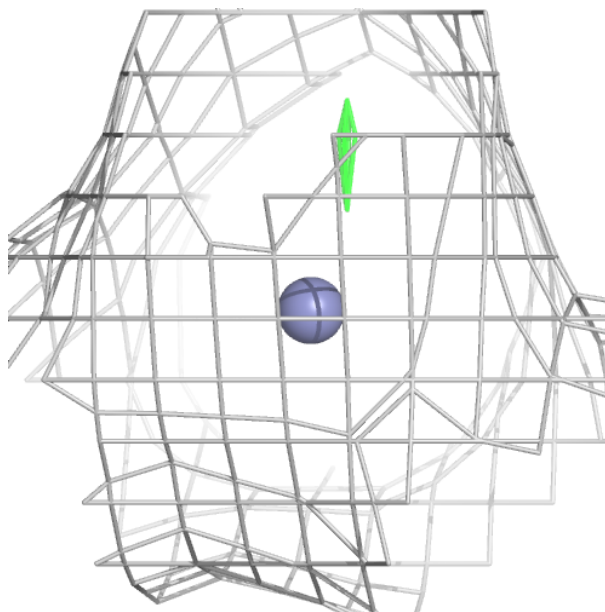
Electron density around ZN M 301:

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



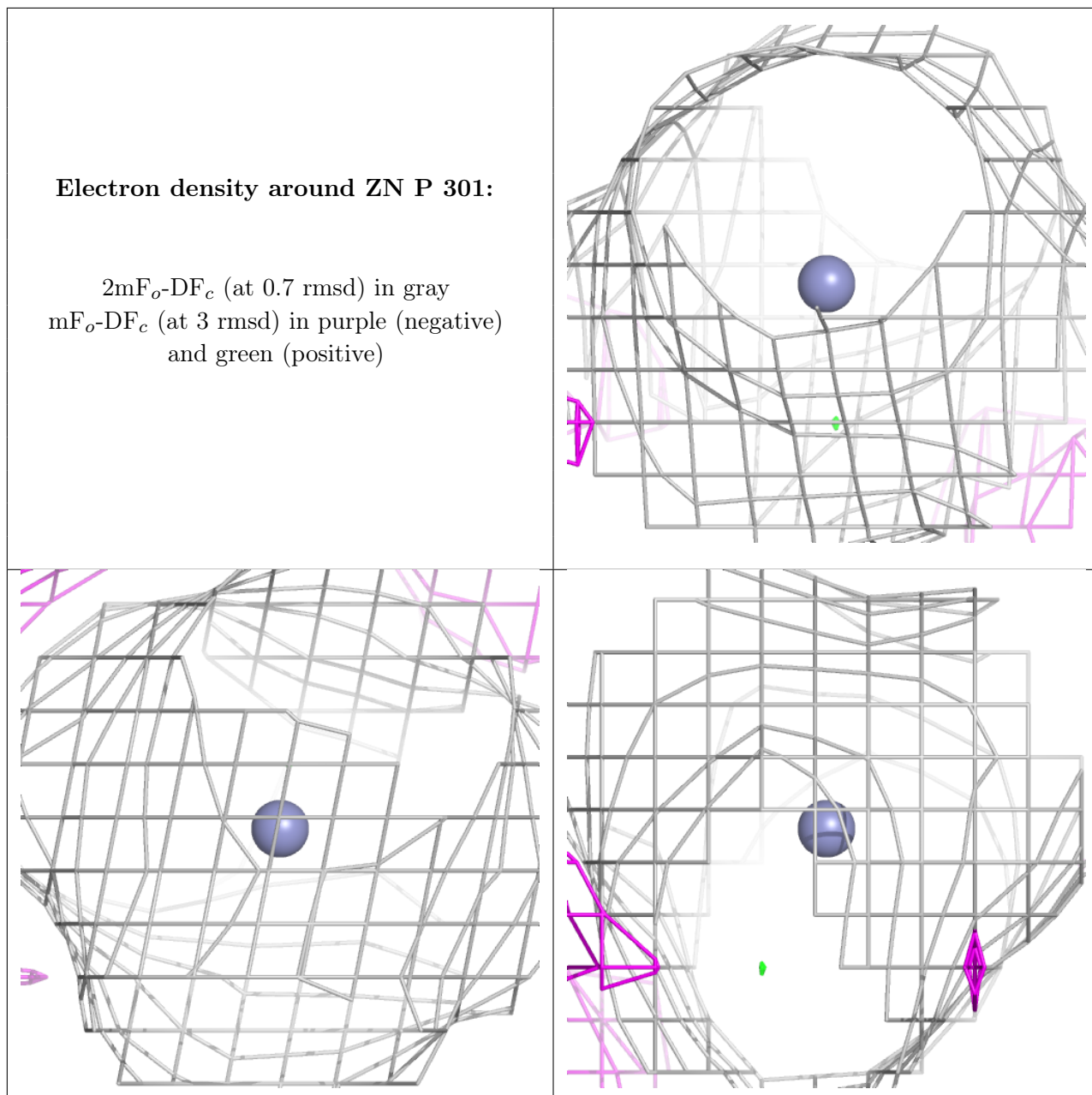
Electron density around ZN A 301:

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and green (positive)



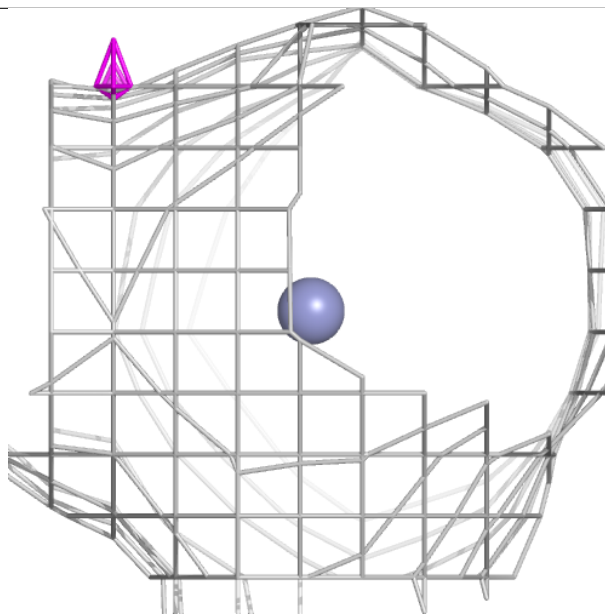
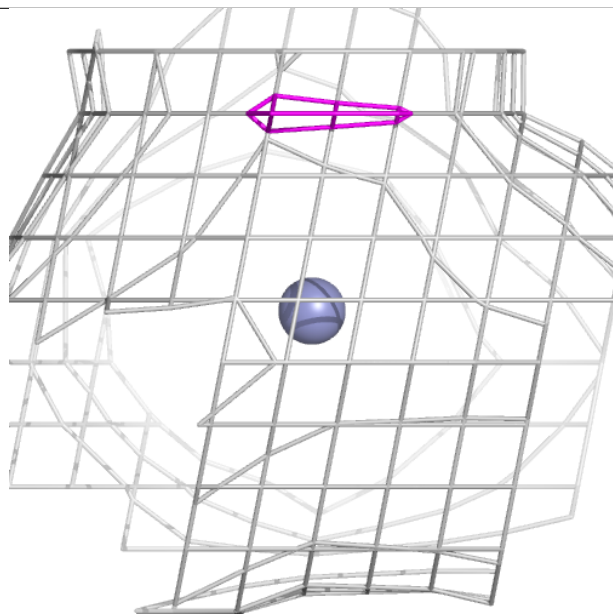
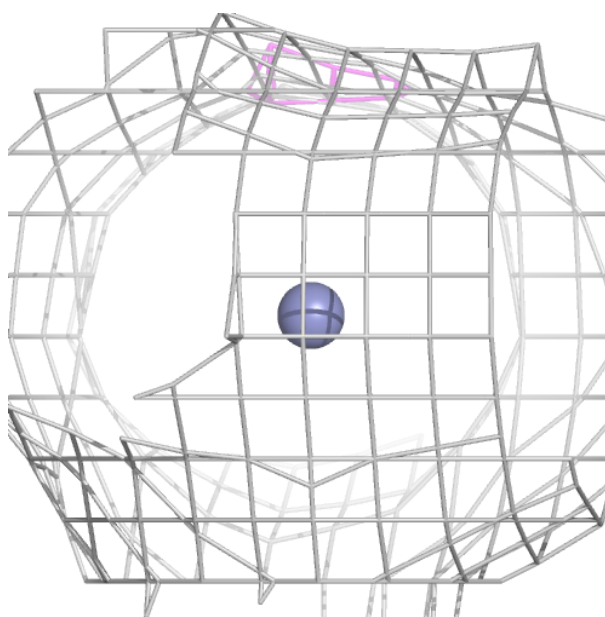
Electron density around ZN P 301:

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



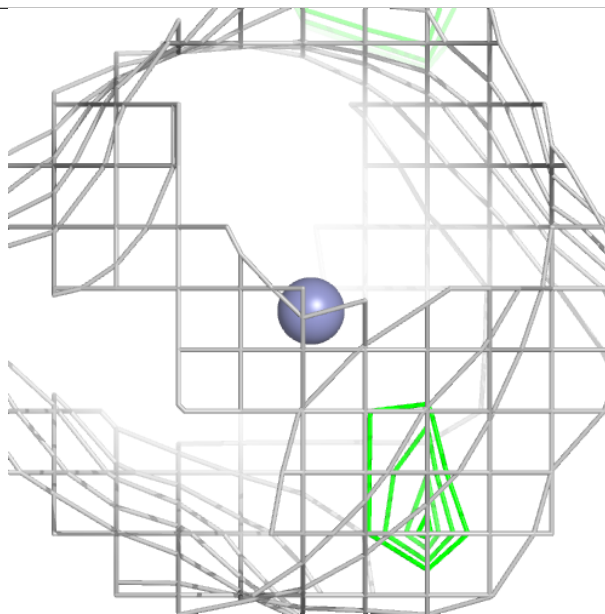
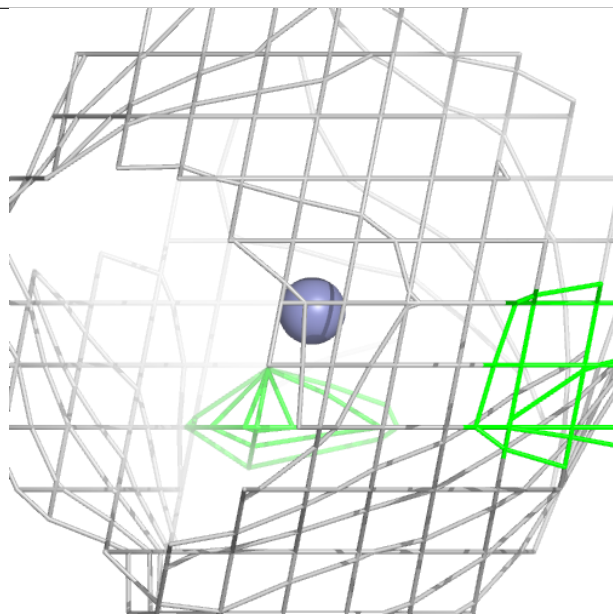
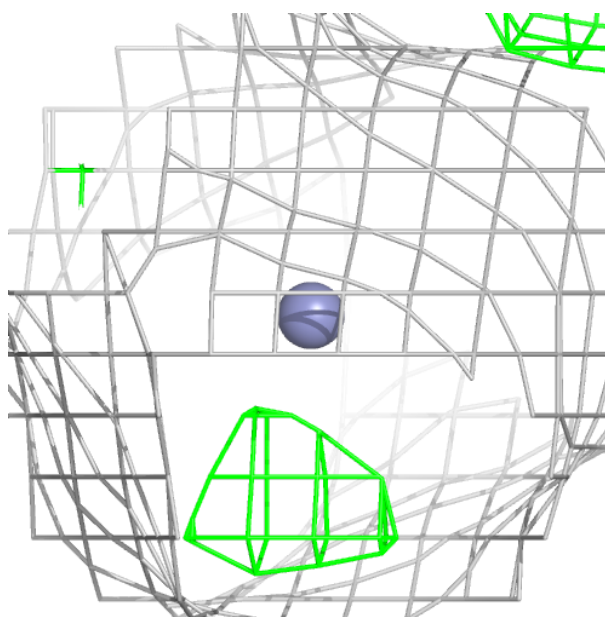
Electron density around ZN P 302:

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and green (positive)



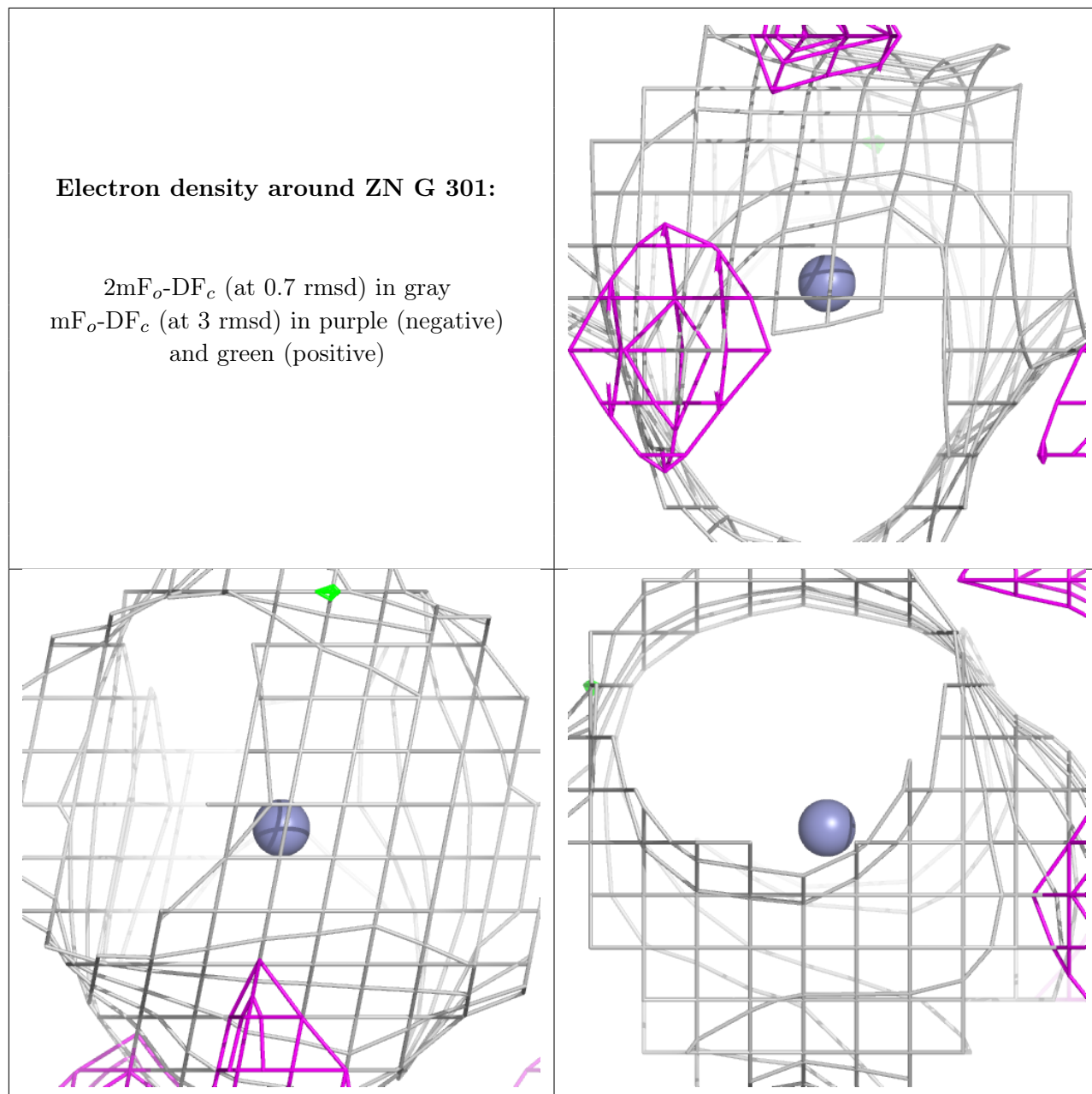
Electron density around ZN S 301:

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and green (positive)



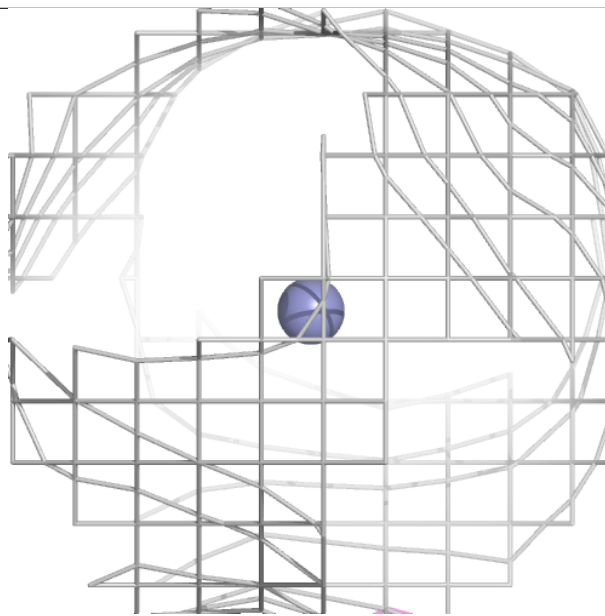
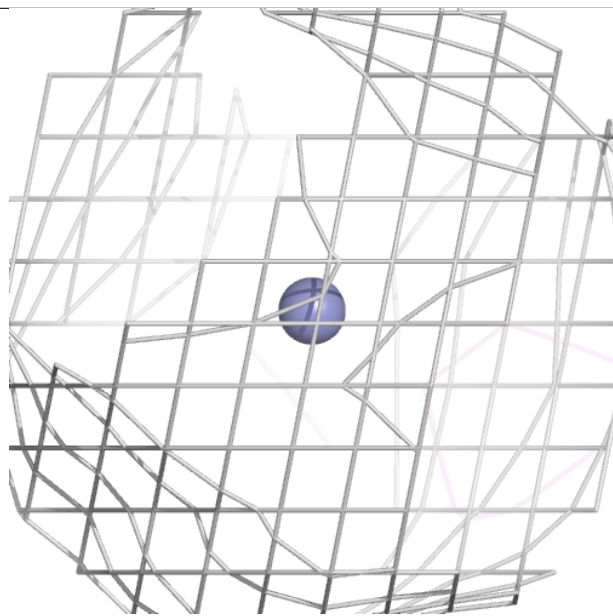
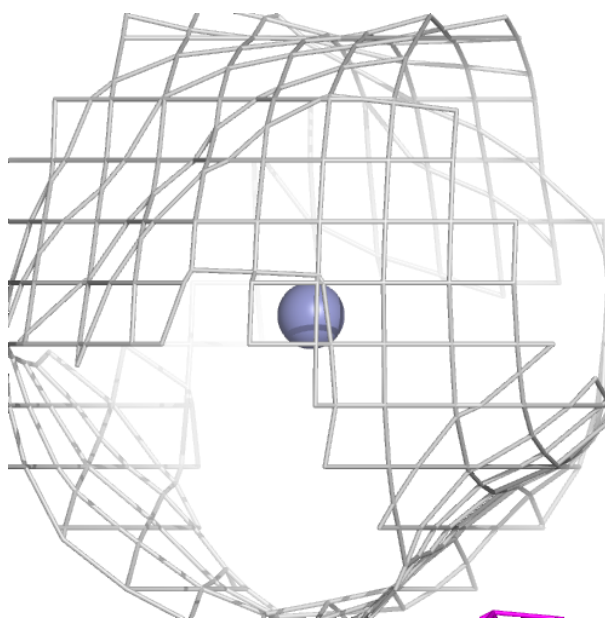
Electron density around ZN G 301:

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and green (positive)



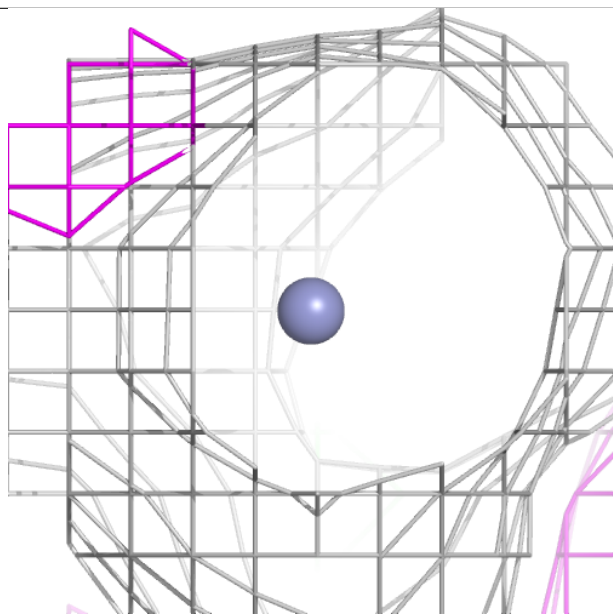
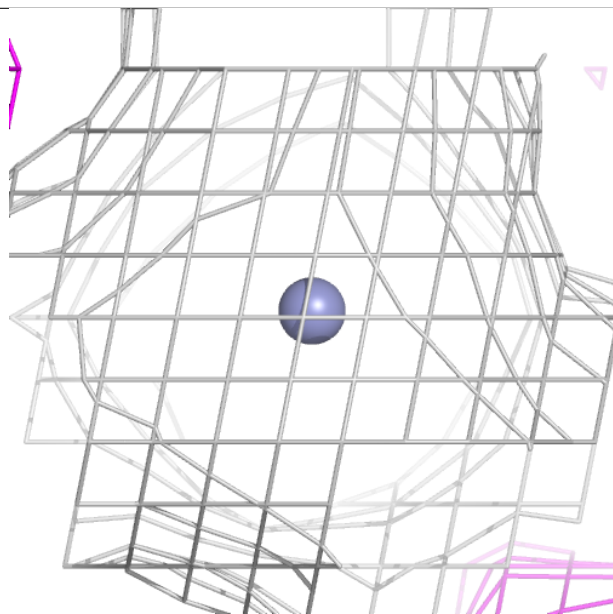
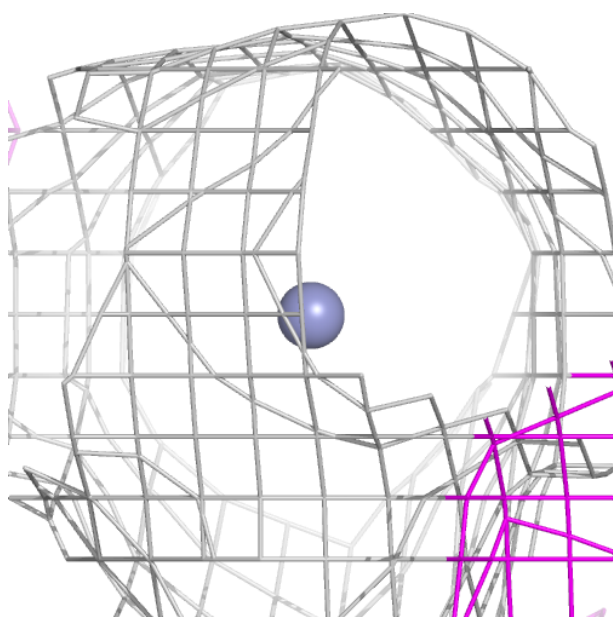
Electron density around ZN V 301:

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and green (positive)



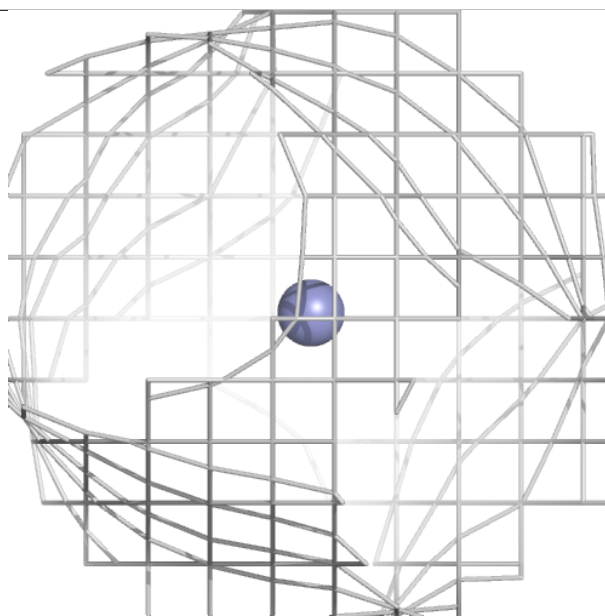
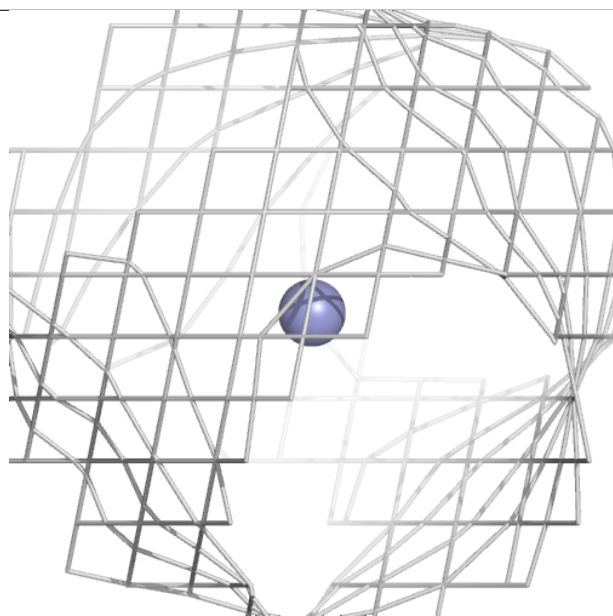
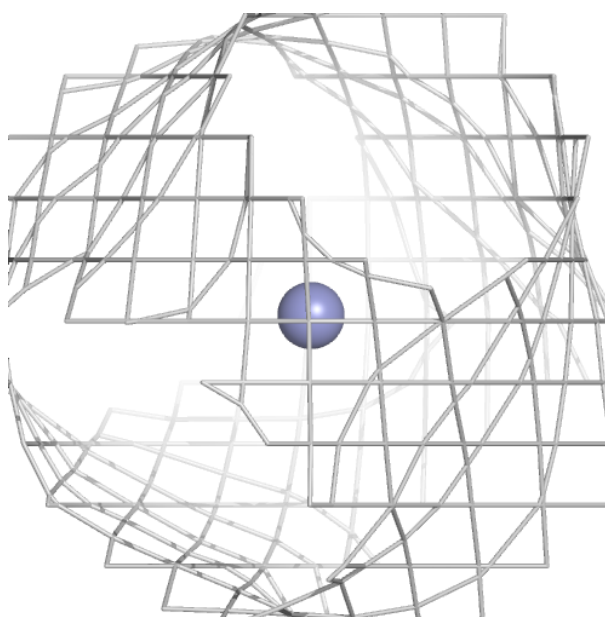
Electron density around ZN G 302:

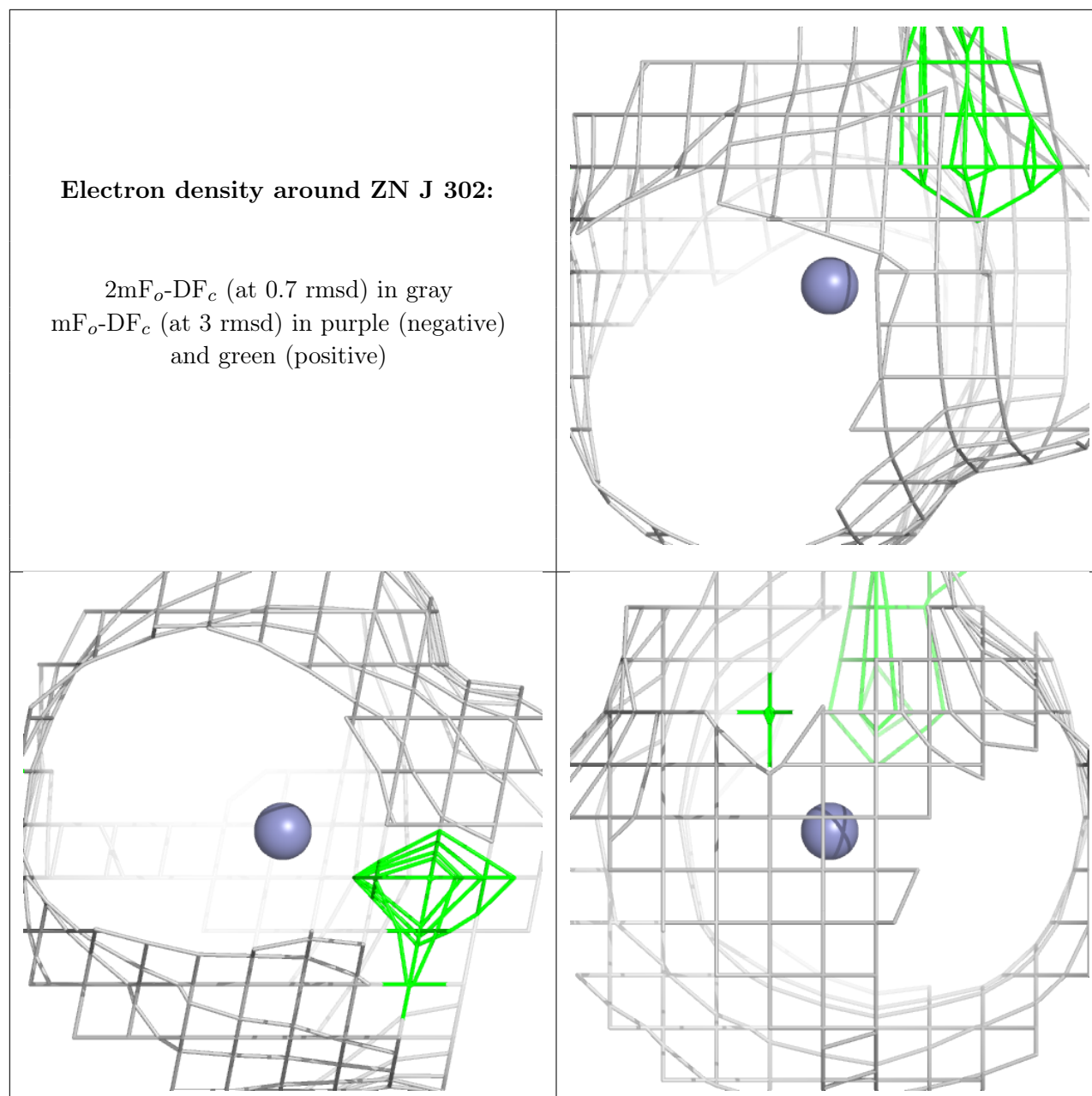
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN D 301:

$2mF_o-DF_c$ (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.