



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 02:22 PM EDT

PDB ID : 8H3Z / pdb_00008h3z
Title : Crystal structure of the effector-binding domain of the LysR-type transcription factor NtcB from *Anabaena* PCC 7120
Authors : Han, S.J.; Jiang, Y.L.; Zhou, C.Z.
Deposited on : 2022-10-09
Resolution : 2.35 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

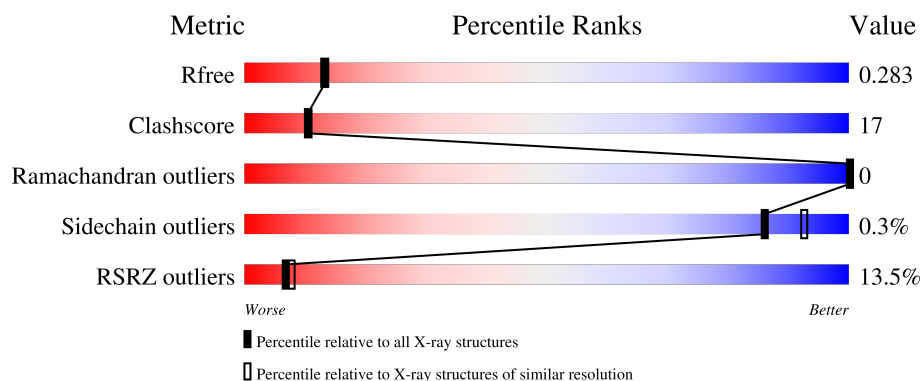
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	228	10% 71% 18% 10%
1	B	228	14% 59% 26% 14%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	A	311	-	-	X	-
2	IOD	B	305	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3310 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 NtcB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1627	1044	285	291	7			
1	B	196	Total	C	N	O	S	0	0	0
			1556	997	273	279	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q9L3R4
A	-4	HIS	-	expression tag	UNP Q9L3R4
A	-3	HIS	-	expression tag	UNP Q9L3R4
A	-2	HIS	-	expression tag	UNP Q9L3R4
A	-1	HIS	-	expression tag	UNP Q9L3R4
A	0	HIS	-	expression tag	UNP Q9L3R4
B	-5	HIS	-	expression tag	UNP Q9L3R4
B	-4	HIS	-	expression tag	UNP Q9L3R4
B	-3	HIS	-	expression tag	UNP Q9L3R4
B	-2	HIS	-	expression tag	UNP Q9L3R4
B	-1	HIS	-	expression tag	UNP Q9L3R4
B	0	HIS	-	expression tag	UNP Q9L3R4

- Molecule 2 is IODIDE ION (CCD ID: IOD) (formula: I) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	I	0	0
			12	12		
2	B	13	Total	I	0	0
			13	13		

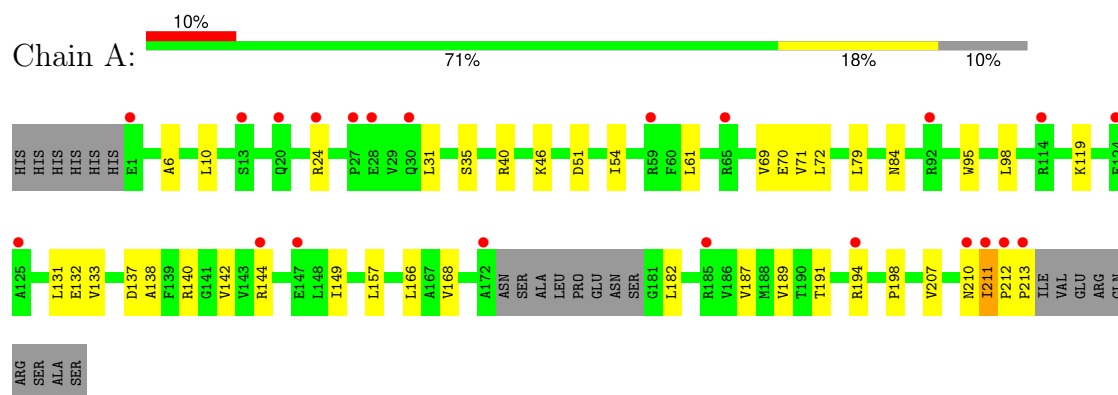
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	55	Total 55	O 55	0	0
3	B	47	Total 47	O 47	0	0

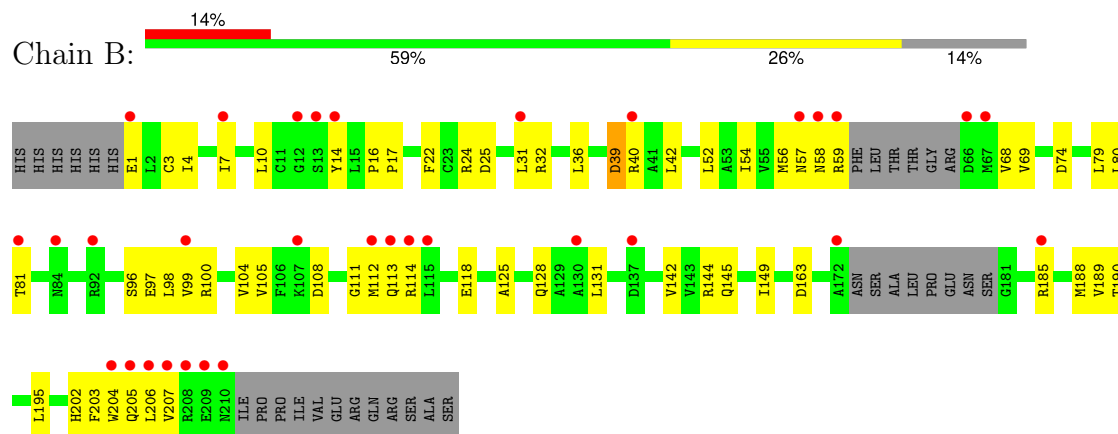
3 Residue-property plots [i](#)

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: NtcB



• Molecule 1: NtcB



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.70Å 69.41Å 114.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.35 50.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.0 (50.00-2.35) 91.0 (50.00-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	19.01 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.204 , 0.243 0.239 , 0.283	Depositor DCC
R_{free} test set	955 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3310	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: IOD

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	0.63	0/1658	1.05	1/2257 (0.0%)
1	B	0.64	0/1583	1.07	2/2151 (0.1%)
All	All	0.64	0/3241	1.06	3/4408 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	PRO	N-CA-C	5.82	117.80	110.70
1	B	118	GLU	CB-CG-CD	5.44	121.85	112.60
1	B	39	ASP	CB-CA-C	5.21	119.14	110.90

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	1627	0	1685	46	0
1	B	1556	0	1609	65	0
2	A	12	0	0	2	0
2	B	13	0	0	5	0
3	A	55	0	0	2	0
3	B	47	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3310	0	3294	110	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 17.

All (110) 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:74:ASP:OD1	1:B:185:ARG:HG2	1.37	1.21
1:B:52:LEU:HD11	1:B:188:MET:HE2	1.46	0.95
1:A:10:LEU:HD11	1:A:54:ILE:HG21	1.50	0.93
1:A:119:LYS:HE3	1:A:182:LEU:CD2	2.00	0.91
1:A:119:LYS:HE3	1:A:182:LEU:HD21	1.51	0.90
1:B:36:LEU:HD22	1:B:40:ARG:HD3	1.56	0.88
1:A:24:ARG:HG2	3:A:430:HOH:O	1.76	0.85
1:B:202:HIS:O	1:B:206:LEU:HG	1.79	0.82
1:A:79:LEU:HD13	1:A:98:LEU:HD11	1.63	0.81
1:B:39:ASP:OD1	1:B:59:ARG:HD2	1.82	0.79
1:B:4:ILE:HD13	1:B:203:PHE:CZ	2.18	0.78
1:A:10:LEU:HD11	1:A:54:ILE:CG2	2.13	0.78
1:A:95:TRP:CZ2	1:A:182:LEU:HD23	2.21	0.75
1:A:69:VAL:HG13	1:A:187:VAL:HG11	1.68	0.75
1:A:46:LYS:HG2	2:A:311:IOD:I	2.57	0.75
1:A:95:TRP:HZ2	1:A:182:LEU:HD23	1.52	0.74
1:B:108:ASP:HB3	3:B:420:HOH:O	1.87	0.74
1:B:202:HIS:CD2	1:B:205:GLN:HE21	2.08	0.71
1:A:133:VAL:CG1	1:A:138:ALA:HB3	2.21	0.71
1:B:79:LEU:HD11	1:B:149:ILE:HD12	1.74	0.70
1:B:39:ASP:OD1	1:B:59:ARG:CD	2.40	0.69
1:B:24:ARG:HD2	2:B:312:IOD:I	2.64	0.68
1:A:79:LEU:HD22	1:A:98:LEU:HD13	1.76	0.68
1:B:202:HIS:HD2	1:B:205:GLN:HE21	1.41	0.67
1:A:119:LYS:CE	1:A:182:LEU:HD21	2.25	0.66
1:B:104:VAL:HG22	1:B:142:VAL:HG11	1.77	0.65
1:B:104:VAL:CG2	1:B:142:VAL:HG11	2.26	0.65
1:A:212:PRO:HB2	1:A:213:PRO:HD3	1.80	0.64
1:B:202:HIS:HD2	1:B:205:GLN:NE2	1.95	0.64
1:B:99:VAL:CG2	1:B:125:ALA:HB1	2.28	0.63
1:A:119:LYS:HG2	1:A:182:LEU:HD21	1.81	0.62
1:B:22:PHE:CD1	1:B:31:LEU:HD21	2.35	0.61
1:A:119:LYS:HE3	1:A:182:LEU:HD22	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:ASN:ND2	3:A:401:HOH:O	2.34	0.61
1:B:203:PHE:HA	1:B:206:LEU:HD12	1.82	0.60
1:B:97:GLU:OE2	1:B:100:ARG:NH1	2.34	0.60
1:B:68:VAL:HG11	1:B:195:LEU:HD11	1.84	0.60
1:A:137:ASP:OD1	1:A:140:ARG:NH2	2.34	0.59
1:A:131:LEU:HD23	1:A:142:VAL:HG11	1.84	0.58
1:A:133:VAL:CG1	1:A:138:ALA:CB	2.82	0.58
1:A:140:ARG:HB3	1:A:144:ARG:CZ	2.35	0.57
1:B:57:ASN:OD1	1:B:57:ASN:O	2.21	0.57
1:B:99:VAL:HG21	1:B:125:ALA:CB	2.34	0.57
1:B:188:MET:HE1	1:B:204:TRP:HA	1.85	0.57
1:A:207:VAL:HG13	1:A:211:ILE:HG12	1.86	0.57
1:B:69:VAL:HG22	1:B:189:VAL:HG22	1.87	0.57
1:B:96:SER:O	1:B:99:VAL:HG12	2.05	0.57
1:A:69:VAL:CG1	1:A:187:VAL:HG11	2.36	0.56
1:A:79:LEU:CD1	1:A:98:LEU:HD11	2.34	0.55
1:B:188:MET:HG2	1:B:204:TRP:CZ3	2.42	0.55
1:B:36:LEU:HD22	1:B:40:ARG:CD	2.34	0.54
1:B:57:ASN:HB3	2:B:307:IOD:I	2.77	0.54
1:B:1:GLU:OE1	1:B:32:ARG:NH2	2.40	0.54
1:A:51:ASP:O	1:A:194:ARG:HD2	2.08	0.54
1:B:202:HIS:CE1	1:B:206:LEU:HD21	2.43	0.54
1:B:10:LEU:CD1	1:B:54:ILE:HG21	2.39	0.53
1:B:57:ASN:C	1:B:59:ARG:N	2.64	0.53
1:B:99:VAL:CG2	1:B:125:ALA:CB	2.87	0.53
1:A:140:ARG:HB3	1:A:144:ARG:NH2	2.24	0.52
1:A:31:LEU:HD23	1:B:131:LEU:HD13	1.91	0.52
1:A:69:VAL:HG13	1:A:187:VAL:CG1	2.38	0.52
1:A:211:ILE:O	1:A:212:PRO:C	2.52	0.51
1:A:133:VAL:HG13	1:A:138:ALA:CB	2.41	0.51
1:B:7:ILE:HG23	2:B:305:IOD:I	2.80	0.51
1:B:190:THR:HG22	1:B:204:TRP:CZ3	2.45	0.51
1:B:22:PHE:CE1	1:B:31:LEU:HD21	2.46	0.50
1:A:207:VAL:HG13	1:A:211:ILE:CG1	2.42	0.50
1:A:210:ASN:C	1:A:213:PRO:HD2	2.36	0.50
1:B:104:VAL:CG2	1:B:142:VAL:CG1	2.90	0.49
1:B:98:LEU:HD23	1:B:98:LEU:C	2.37	0.49
1:A:70:GLU:O	1:A:187:VAL:HG13	2.11	0.49
1:B:42:LEU:HD12	1:B:59:ARG:HG2	1.94	0.49
1:B:25:ASP:OD2	1:B:202:HIS:HE1	1.97	0.48
1:B:80:LEU:C	1:B:81:THR:HG23	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:ILE:CD1	1:B:203:PHE:CZ	2.92	0.48
1:B:97:GLU:CD	1:B:100:ARG:HH12	2.22	0.48
1:B:58:ASN:HB3	1:B:114:ARG:NH2	2.29	0.48
1:B:99:VAL:HG21	1:B:125:ALA:HB1	1.96	0.47
1:A:132:GLU:C	1:A:133:VAL:HG23	2.40	0.47
1:A:40:ARG:HG3	1:A:40:ARG:NH1	2.28	0.47
1:A:40:ARG:HG3	1:A:40:ARG:HH11	1.80	0.47
1:B:16:PRO:HB2	1:B:17:PRO:HD3	1.98	0.46
1:B:7:ILE:HD11	1:B:56:MET:HG3	1.96	0.46
1:B:57:ASN:O	1:B:58:ASN:C	2.57	0.46
1:B:145:GLN:NE2	3:B:402:HOH:O	2.36	0.46
1:A:191:THR:OG1	1:A:194:ARG:HG3	2.16	0.45
1:A:46:LYS:HA	2:A:311:IOD:I	2.87	0.45
1:B:74:ASP:OD1	1:B:185:ARG:CG	2.33	0.45
1:B:144:ARG:NH1	1:B:163:ASP:OD2	2.49	0.45
1:B:128:GLN:HB3	2:B:309:IOD:I	2.86	0.45
1:B:14:TYR:O	1:B:17:PRO:HD2	2.17	0.45
1:A:70:GLU:C	1:A:187:VAL:HG13	2.42	0.45
1:B:104:VAL:HG12	1:B:105:VAL:N	2.32	0.45
1:A:71:VAL:HA	1:A:187:VAL:HG22	1.97	0.45
1:A:61:LEU:HD22	1:A:189:VAL:HG21	1.98	0.44
1:A:144:ARG:HG3	1:A:166:LEU:HD21	1.98	0.44
1:A:157:LEU:HD13	1:A:168:VAL:HG13	1.99	0.44
1:B:108:ASP:HA	1:B:113:GLN:OE1	2.18	0.44
1:B:39:ASP:OD1	1:B:59:ARG:HD3	2.17	0.44
1:B:202:HIS:HA	1:B:205:GLN:HG2	1.99	0.44
1:B:1:GLU:CG	1:B:3:CYS:SG	3.07	0.43
1:A:98:LEU:HD12	1:A:149:ILE:HD12	2.00	0.43
1:B:206:LEU:O	1:B:207:VAL:C	2.62	0.43
1:B:10:LEU:HD11	1:B:54:ILE:HG21	2.01	0.42
1:A:72:LEU:HD13	1:A:211:ILE:HG21	2.02	0.41
1:B:10:LEU:CD1	1:B:54:ILE:CG2	2.98	0.41
1:B:7:ILE:CD1	1:B:56:MET:HG3	2.51	0.41
1:B:7:ILE:CG2	2:B:305:IOD:I	3.39	0.41
1:B:111:GLY:O	1:B:112:MET:C	2.64	0.41
1:A:6:ALA:O	1:A:35:SER:HA	2.21	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	201/228 (88%)	198 (98%)	3 (2%)	0	100	100
1	B	190/228 (83%)	182 (96%)	8 (4%)	0	100	100
All	All	391/456 (86%)	380 (97%)	11 (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	179/200 (90%)	178 (99%)	1 (1%)	78	87
1	B	171/200 (86%)	171 (100%)	0	100	100
All	All	350/400 (88%)	349 (100%)	1 (0%)	86	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	211	ILE

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

Mol	Chain	Res	Type
1	A	205	GLN
1	B	8	HIS

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Mol	Chain	Res	Type
1	B	30	GLN
1	B	57	ASN
1	B	128	GLN
1	B	202	HIS

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 25 ligands modelled in this entry, 25 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

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	205/228 (89%)	0.69	22 (10%)	11 13	20, 34, 54, 74	0
1	B	196/228 (85%)	0.97	32 (16%)	4 5	23, 36, 58, 81	0
All	All	401/456 (87%)	0.83	54 (13%)	7 8	20, 35, 57, 81	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	210	ASN	6.7
1	B	208	ARG	5.0
1	B	209	GLU	4.9
1	B	185	ARG	4.8
1	B	57	ASN	4.7
1	B	58	ASN	4.6
1	A	144	ARG	4.5
1	B	114	ARG	4.3
1	A	213	PRO	4.2
1	B	206	LEU	4.0
1	B	137	ASP	3.9
1	B	13	SER	3.9
1	B	7	ILE	3.7
1	A	125	ALA	3.6
1	B	115	LEU	3.6
1	A	59	ARG	3.5
1	B	205	GLN	3.4
1	B	14	TYR	3.4
1	A	211	ILE	3.3
1	A	124	GLU	3.3
1	A	212	PRO	3.3
1	B	59	ARG	3.3
1	B	81	THR	3.2
1	B	40	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	99	VAL	3.0
1	B	113	GLN	3.0
1	A	28	GLU	3.0
1	B	66	ASP	2.8
1	A	24	ARG	2.8
1	A	172	ALA	2.8
1	A	92	ARG	2.8
1	B	172	ALA	2.7
1	A	27	PRO	2.7
1	A	185	ARG	2.6
1	B	204	TRP	2.6
1	B	92	ARG	2.6
1	A	13	SER	2.6
1	A	194	ARG	2.6
1	B	1	GLU	2.5
1	A	114	ARG	2.5
1	A	65	ARG	2.5
1	B	207	VAL	2.5
1	B	67	MET	2.4
1	A	210	ASN	2.4
1	B	12	GLY	2.3
1	B	130	ALA	2.2
1	A	30	GLN	2.2
1	B	31	LEU	2.1
1	B	112	MET	2.1
1	A	1	GLU	2.1
1	A	20	GLN	2.1
1	B	107	LYS	2.1
1	A	147	GLU	2.1
1	B	84	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

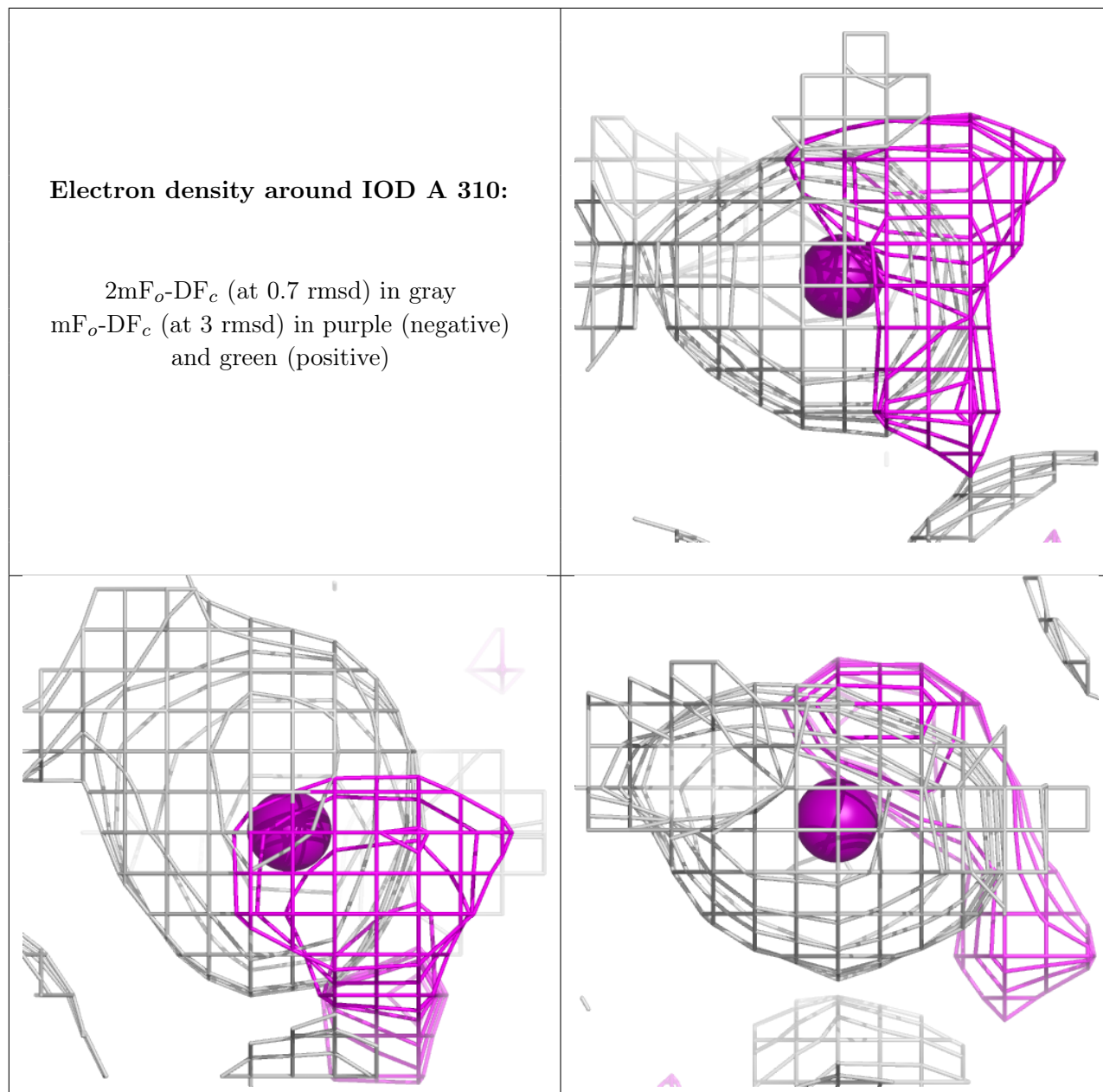
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	IOD	A	310	1/1	0.92	0.27	99,99,99,99	0
2	IOD	B	308	1/1	0.93	0.11	94,94,94,94	0
2	IOD	A	311	1/1	0.95	0.16	94,94,94,94	0
2	IOD	B	304	1/1	0.96	0.20	77,77,77,77	0
2	IOD	A	308	1/1	0.96	0.09	81,81,81,81	0
2	IOD	B	313	1/1	0.96	0.12	67,67,67,67	0
2	IOD	A	312	1/1	0.97	0.15	73,73,73,73	0
2	IOD	B	309	1/1	0.97	0.09	85,85,85,85	0
2	IOD	B	311	1/1	0.97	0.08	62,62,62,62	0
2	IOD	A	309	1/1	0.97	0.16	74,74,74,74	0
2	IOD	A	303	1/1	0.98	0.15	72,72,72,72	0
2	IOD	B	301	1/1	0.98	0.04	49,49,49,49	0
2	IOD	A	307	1/1	0.98	0.10	58,58,58,58	0
2	IOD	B	312	1/1	0.98	0.08	73,73,73,73	0
2	IOD	B	306	1/1	0.98	0.05	54,54,54,54	0
2	IOD	B	307	1/1	0.99	0.05	42,42,42,42	0
2	IOD	A	302	1/1	0.99	0.06	48,48,48,48	0
2	IOD	B	302	1/1	0.99	0.07	54,54,54,54	0
2	IOD	B	310	1/1	0.99	0.05	52,52,52,52	0
2	IOD	B	303	1/1	0.99	0.04	48,48,48,48	0
2	IOD	A	305	1/1	0.99	0.09	54,54,54,54	0
2	IOD	A	306	1/1	0.99	0.06	61,61,61,61	0
2	IOD	B	305	1/1	1.00	0.01	33,33,33,33	0
2	IOD	A	301	1/1	1.00	0.01	28,28,28,28	0
2	IOD	A	304	1/1	1.00	0.04	48,48,48,48	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.

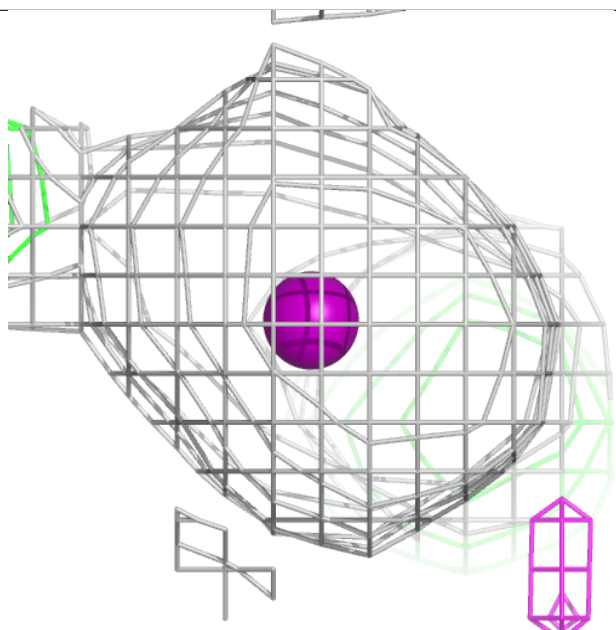
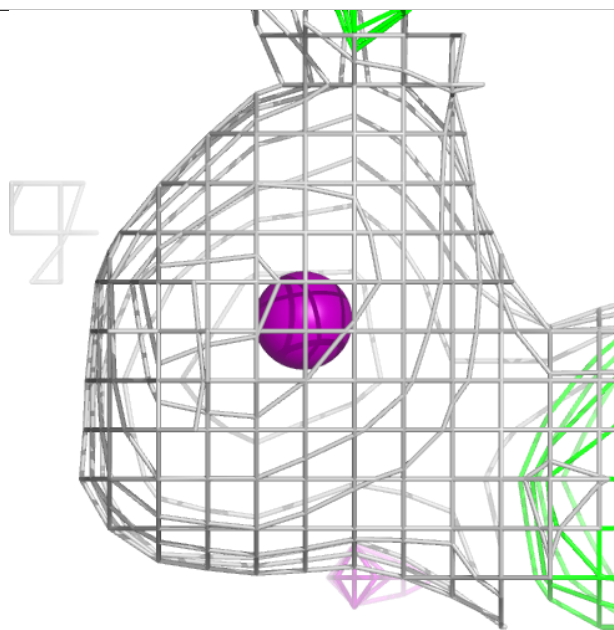
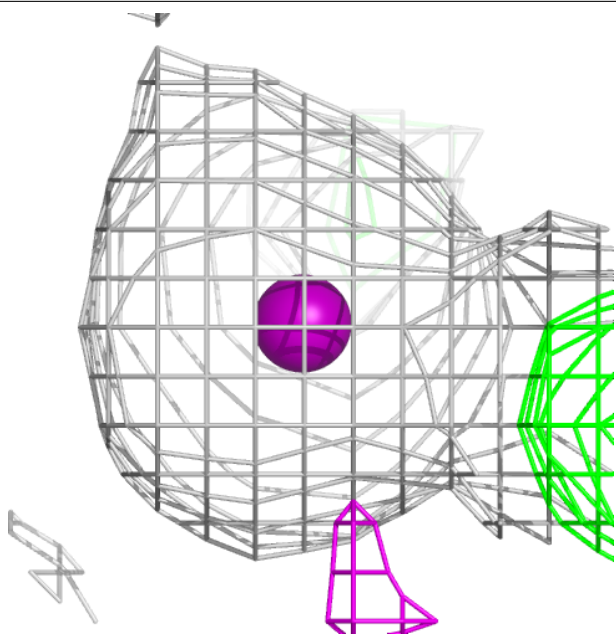
Electron density around IOD A 310:

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



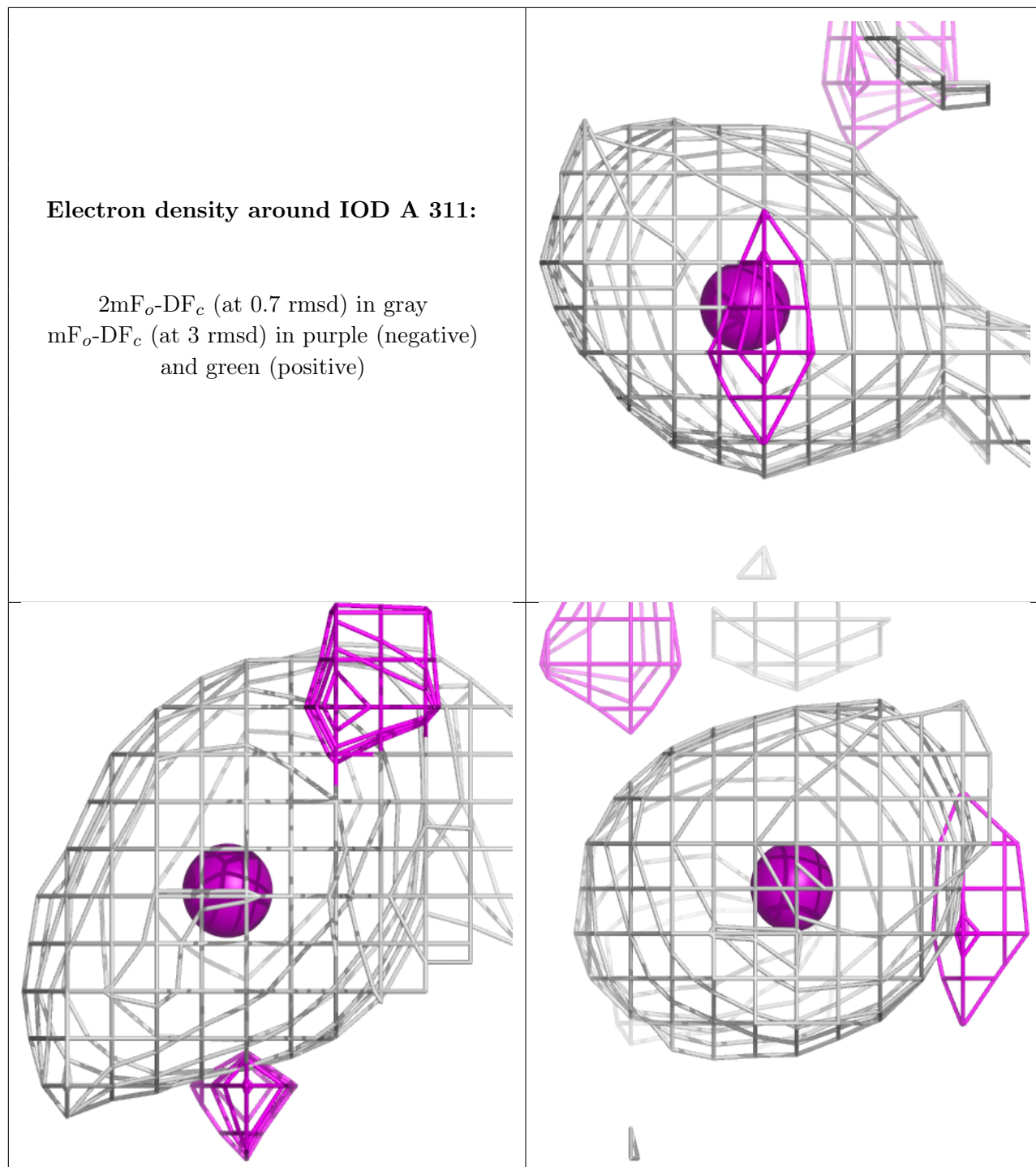
Electron density around IOD B 308:

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and green (positive)



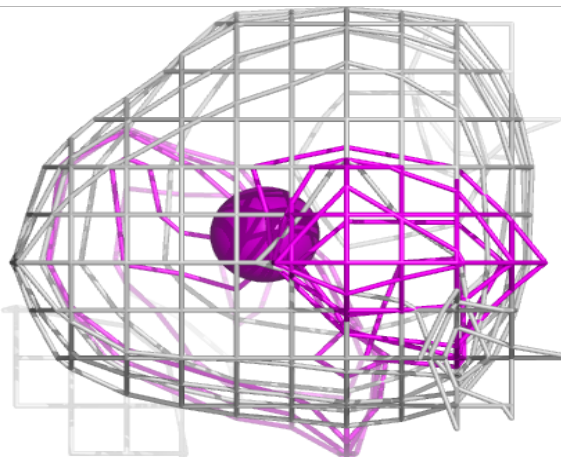
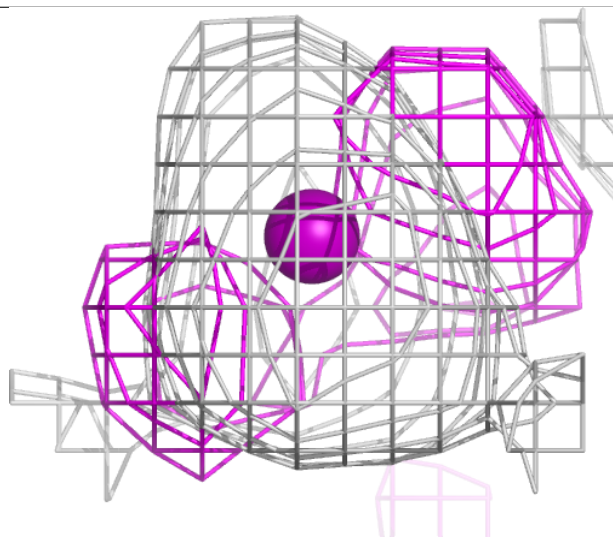
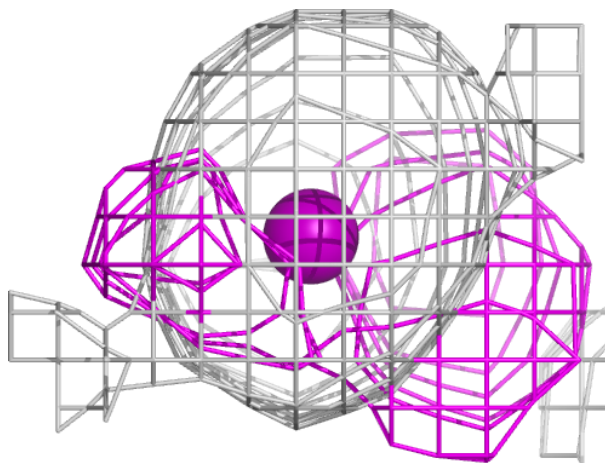
Electron density around IOD A 311:

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



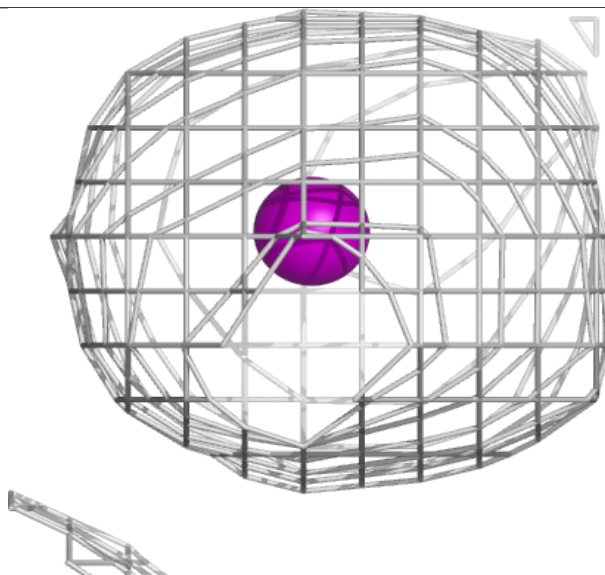
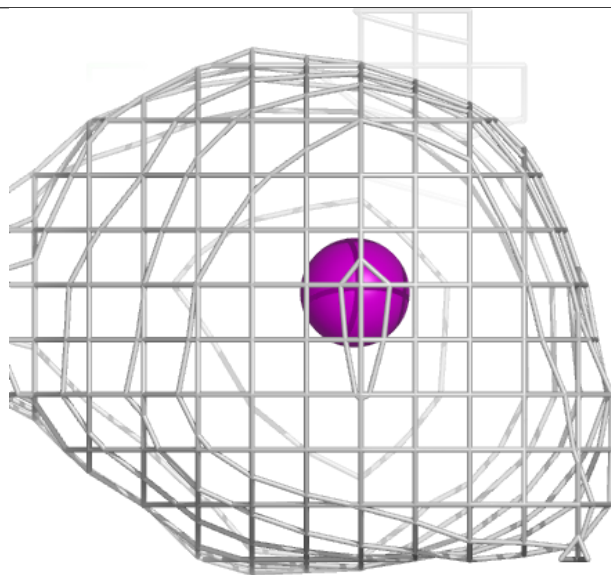
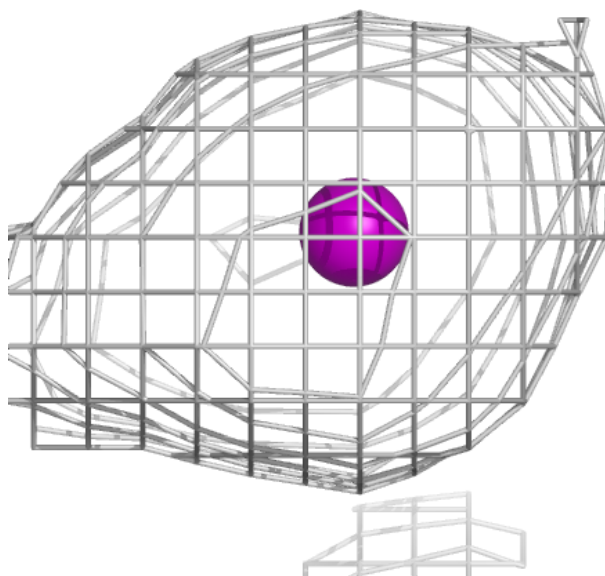
Electron density around IOD B 304:

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



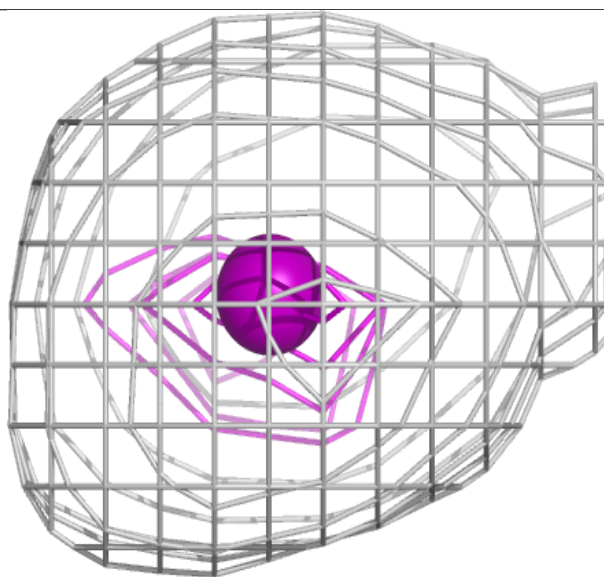
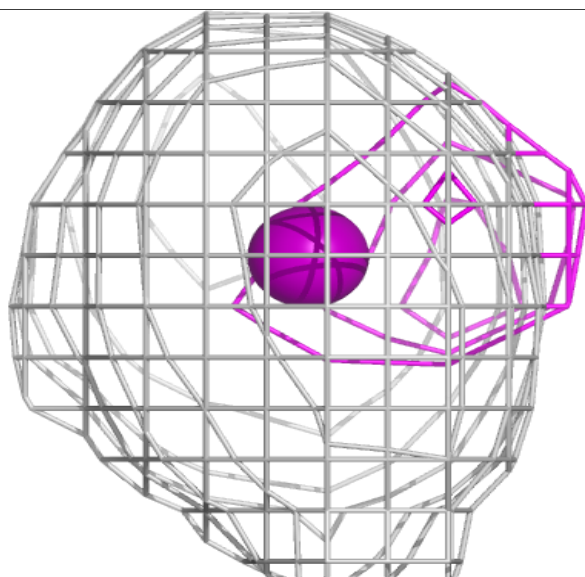
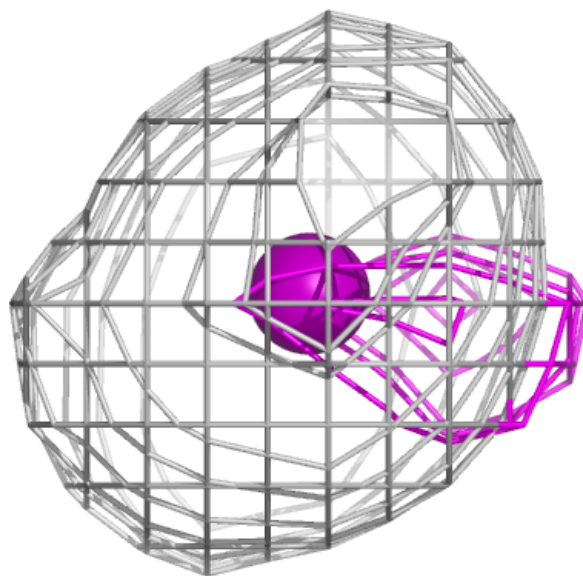
Electron density around IOD A 308:

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



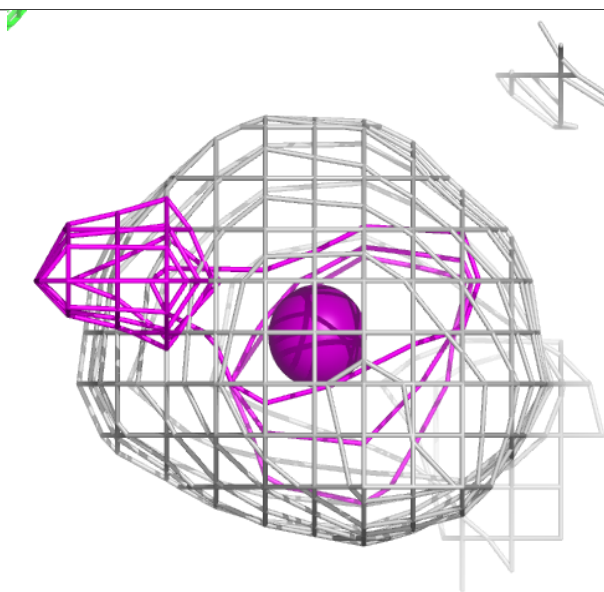
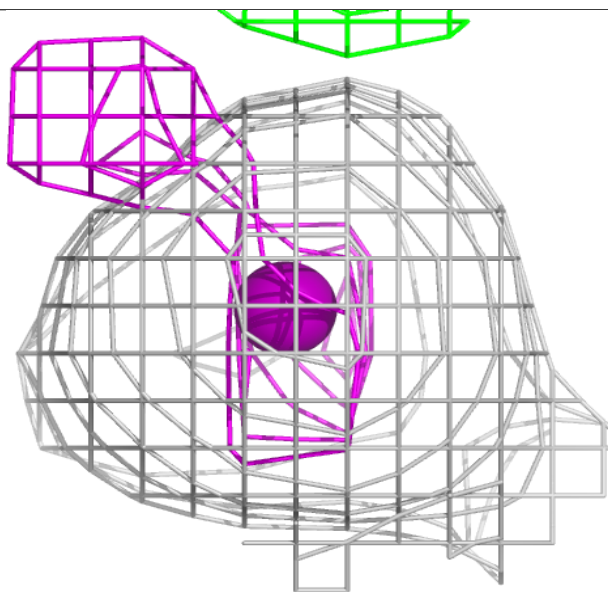
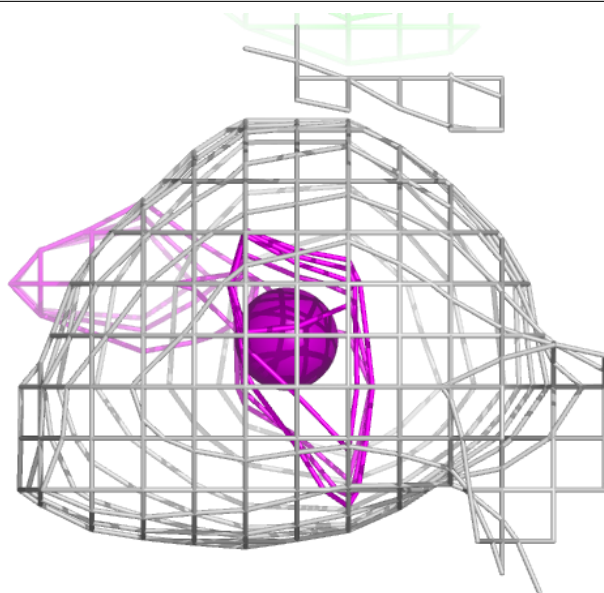
Electron density around IOD B 313:

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



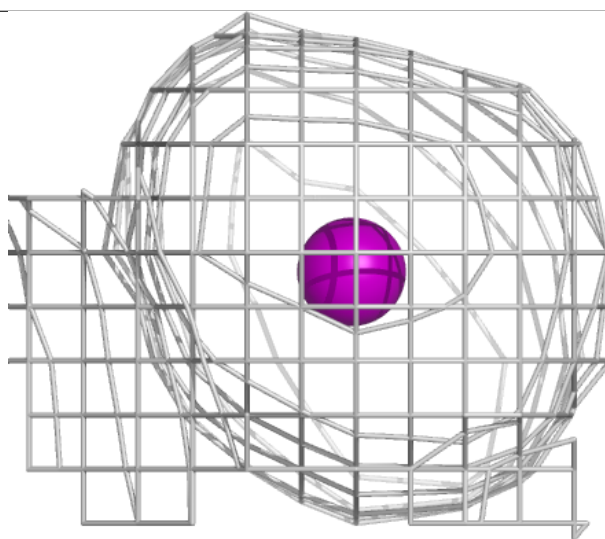
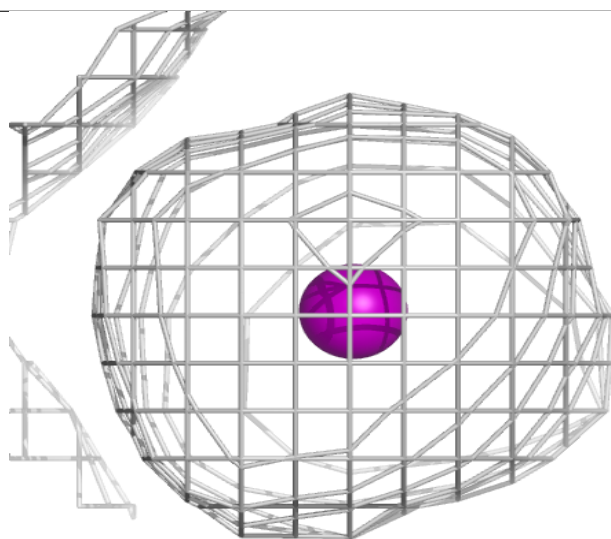
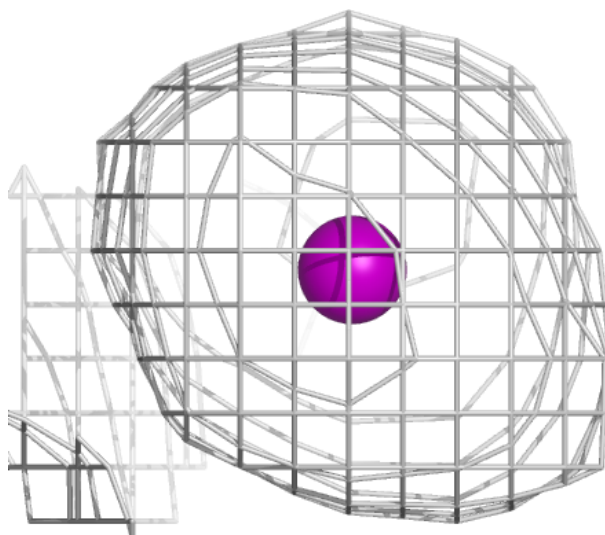
Electron density around IOD A 312:

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



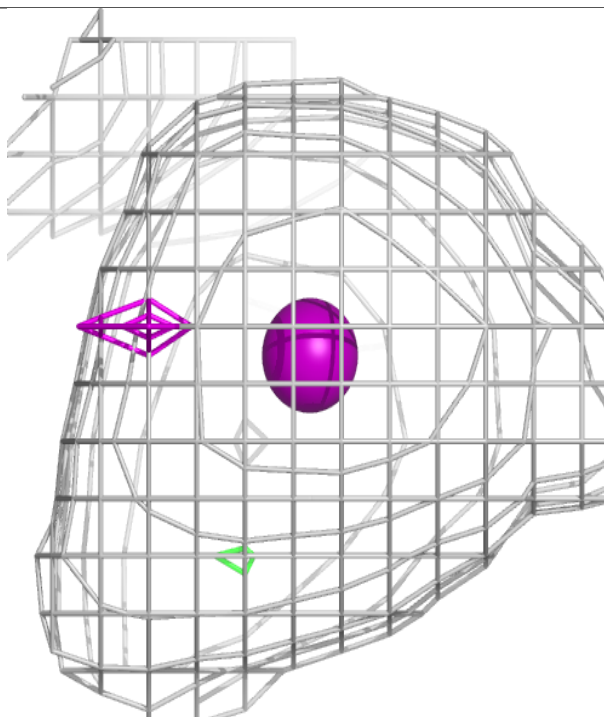
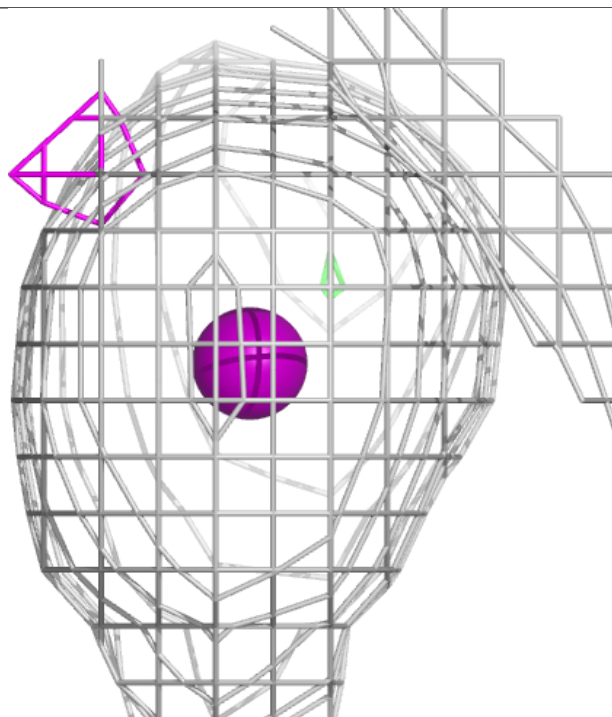
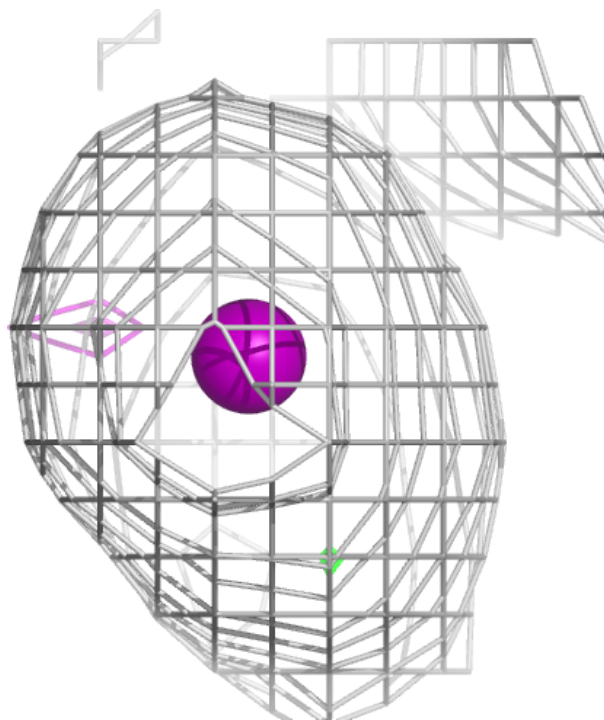
Electron density around IOD B 309:

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



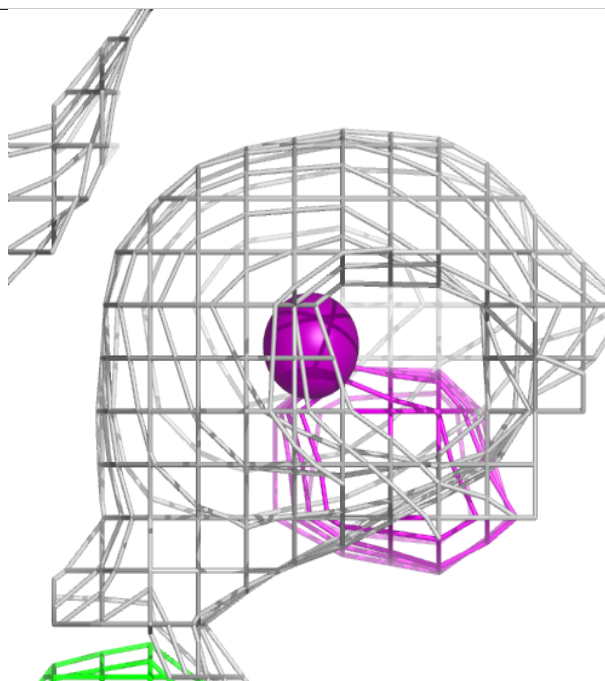
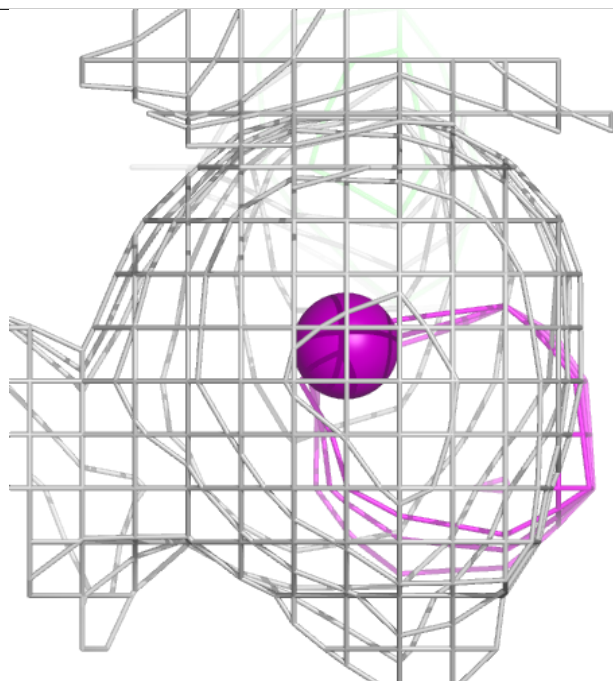
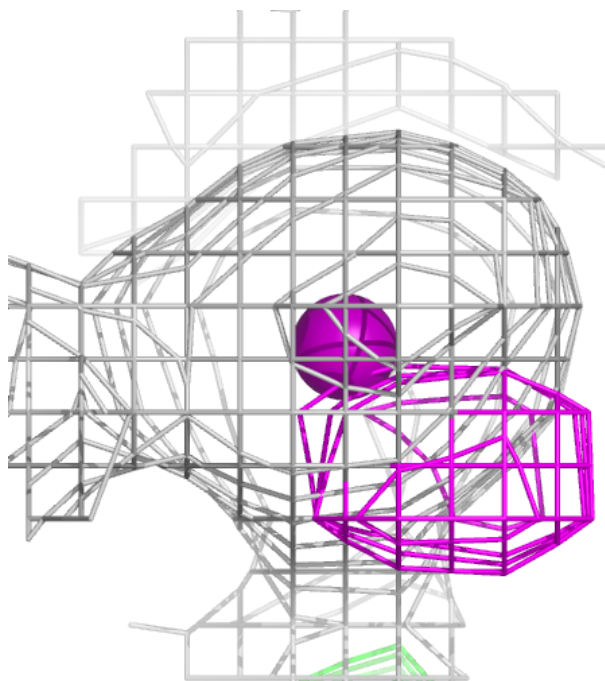
Electron density around IOD B 311:

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and green (positive)



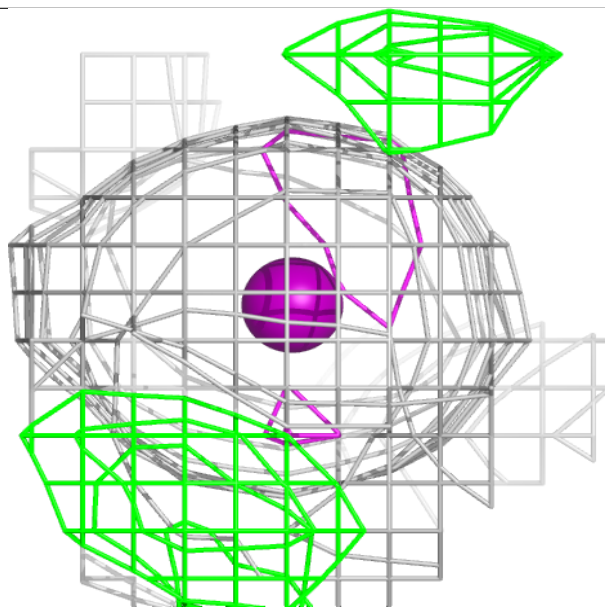
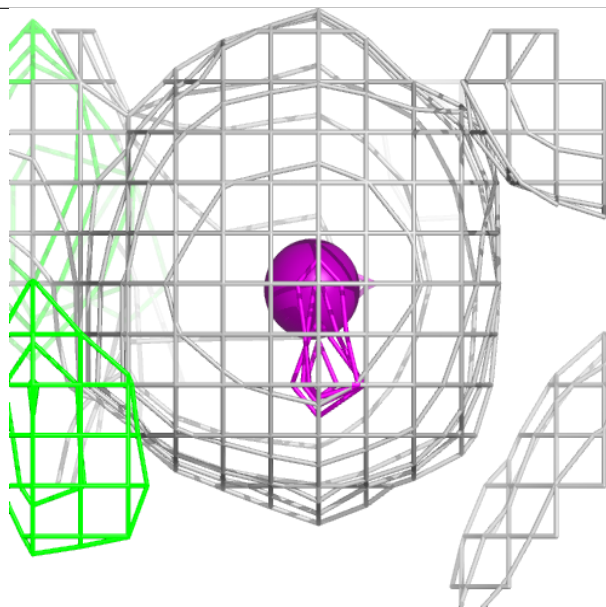
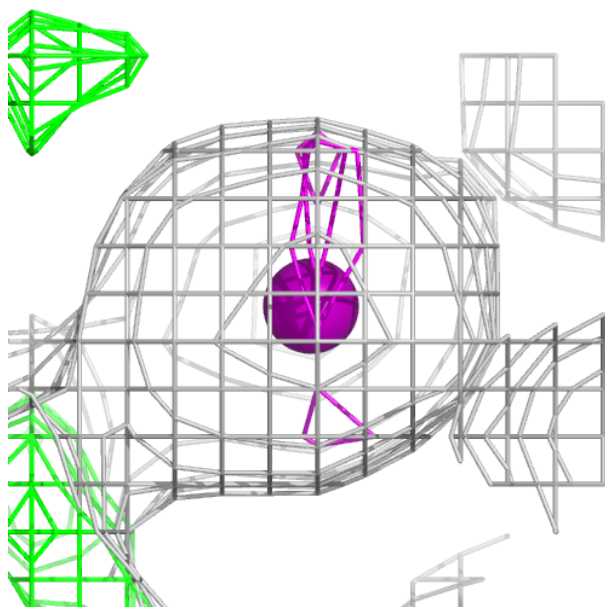
Electron density around IOD A 309:

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



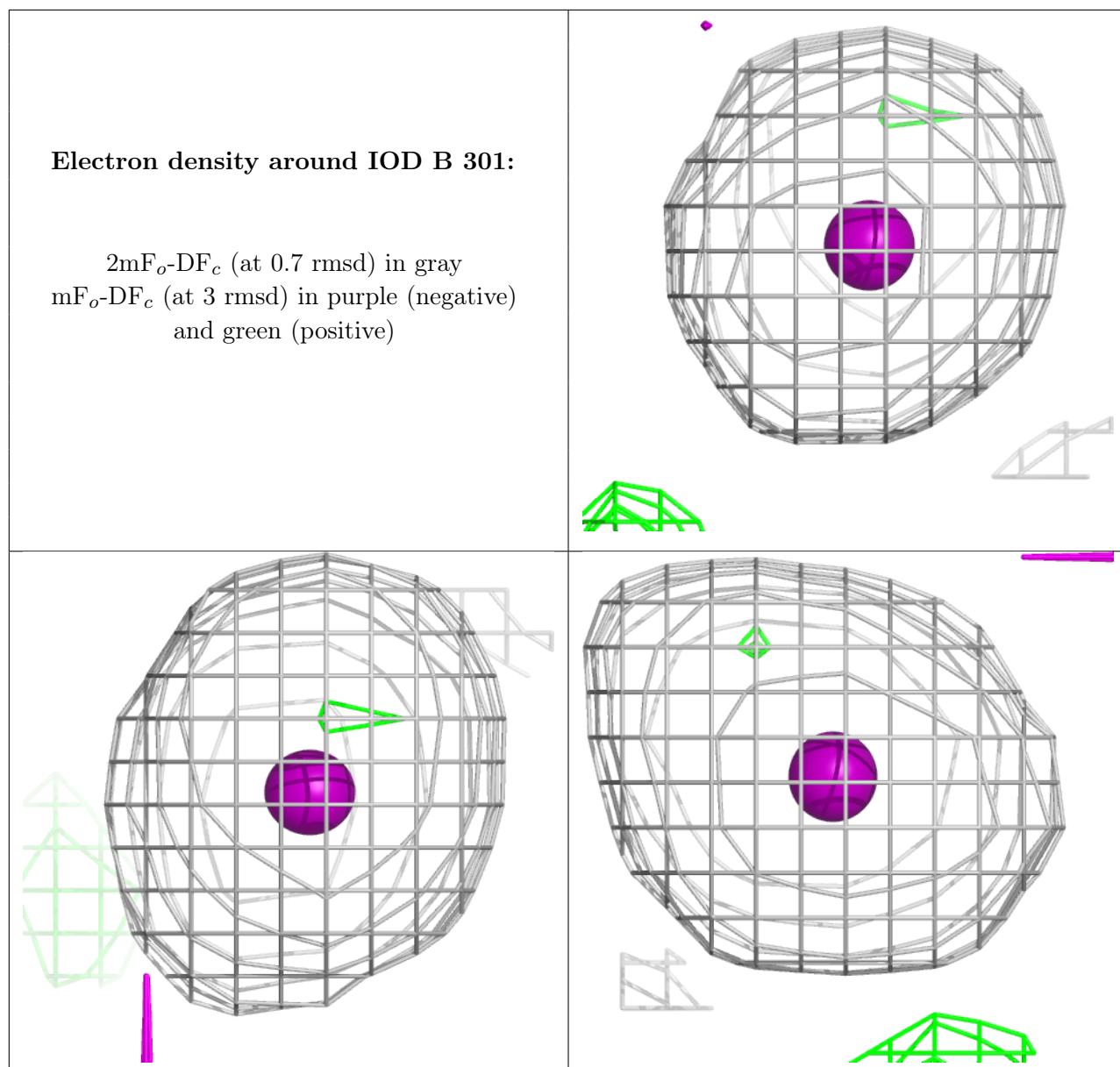
Electron density around IOD A 303:

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



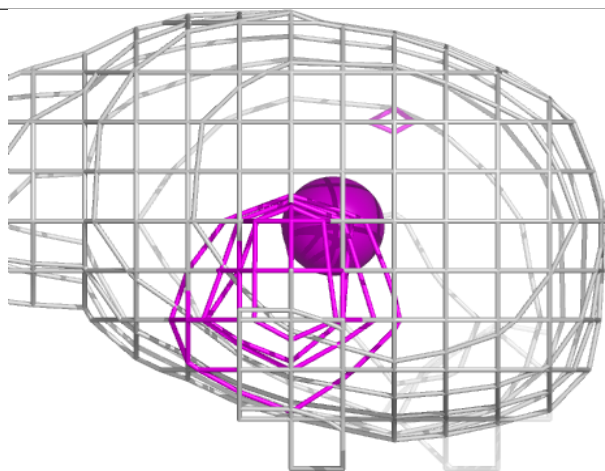
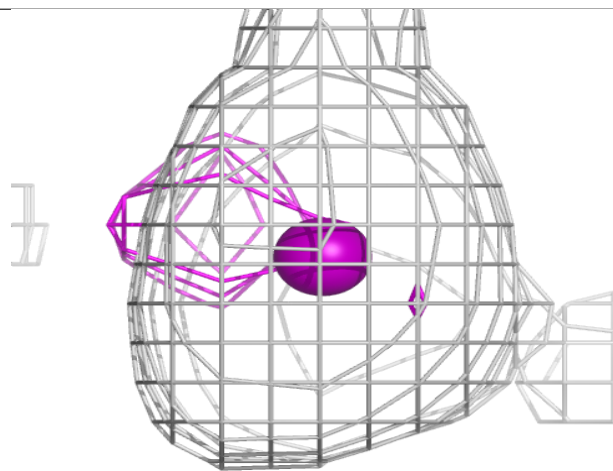
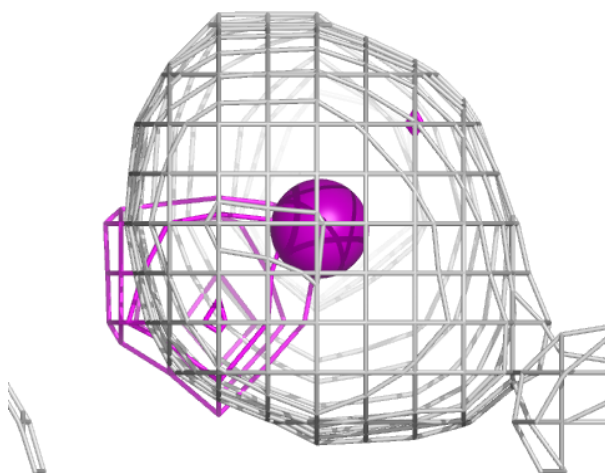
Electron density around IOD B 301:

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



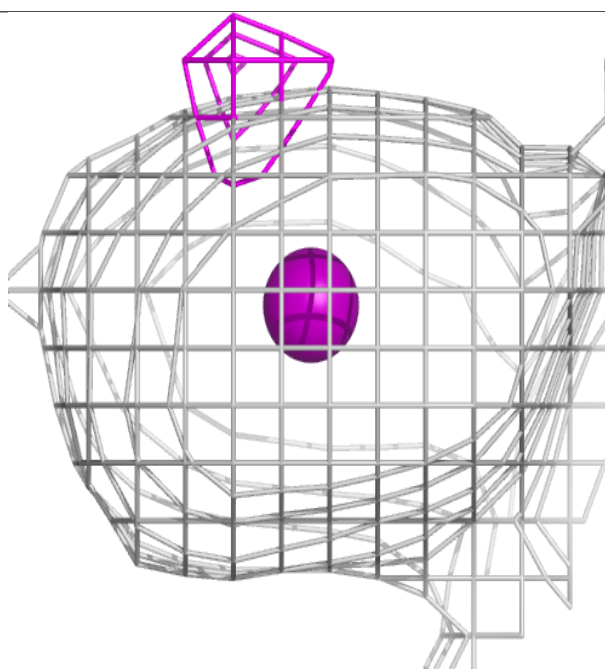
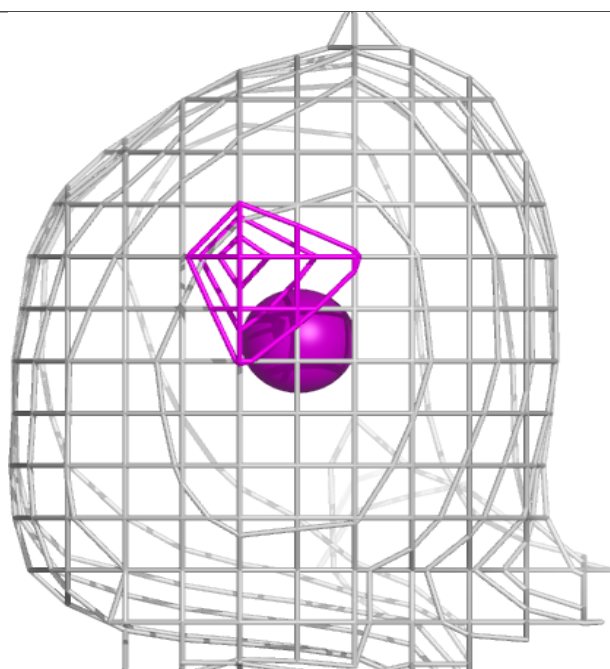
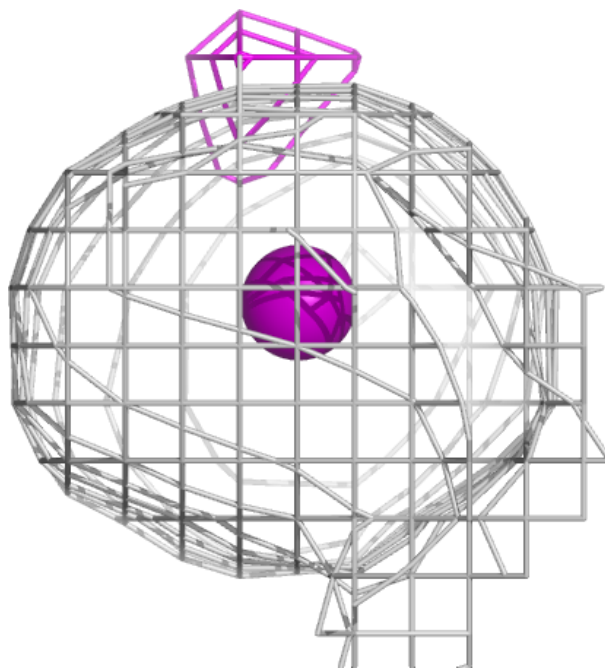
Electron density around IOD A 307:

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



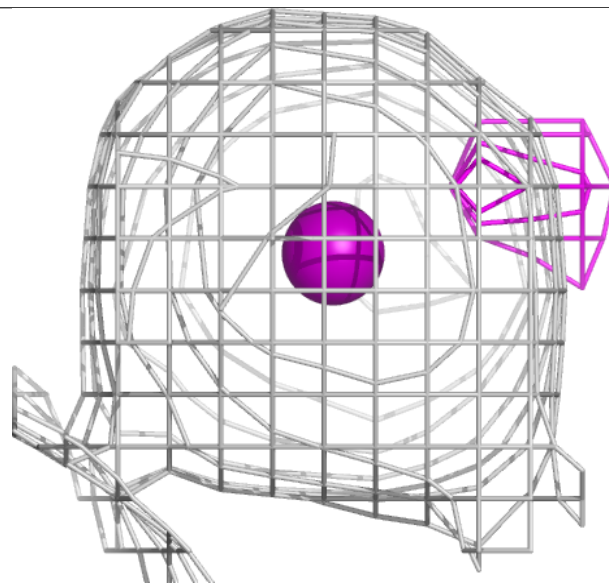
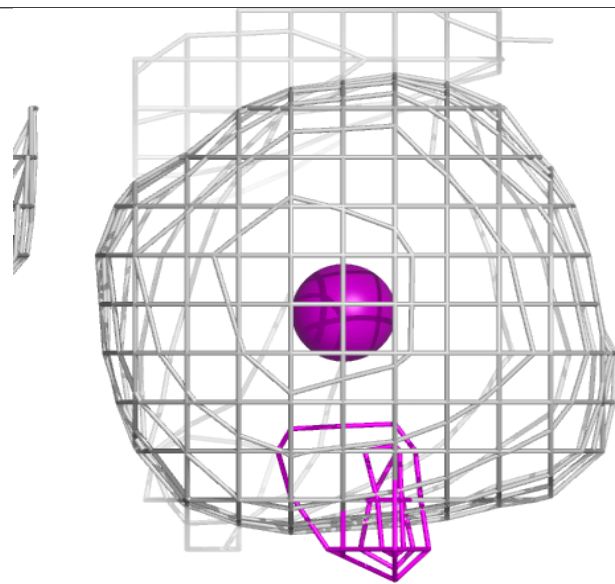
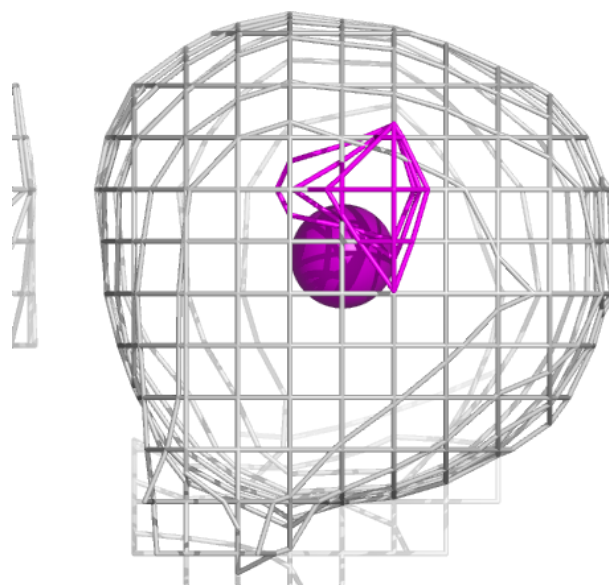
Electron density around IOD B 312:

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and green (positive)



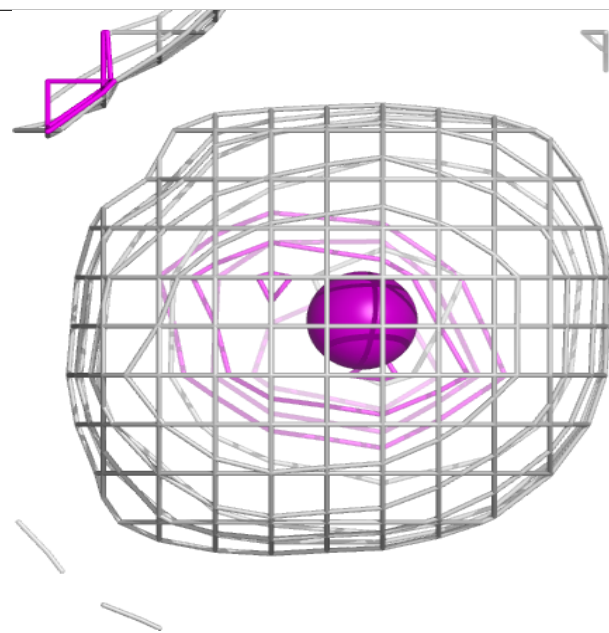
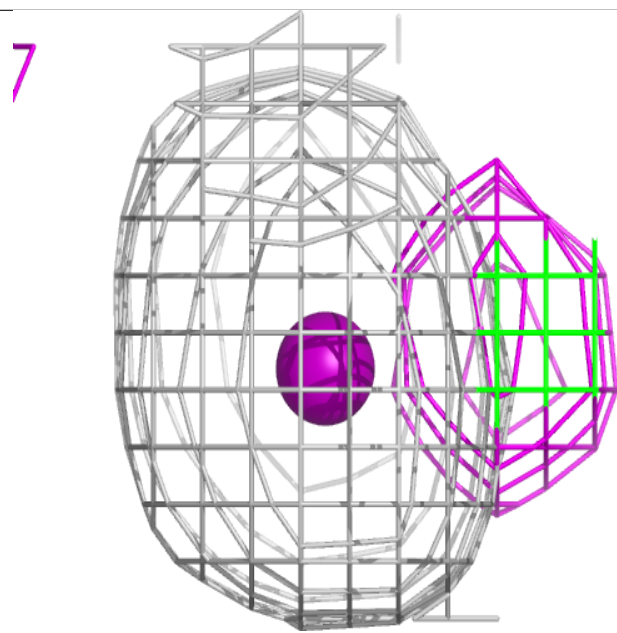
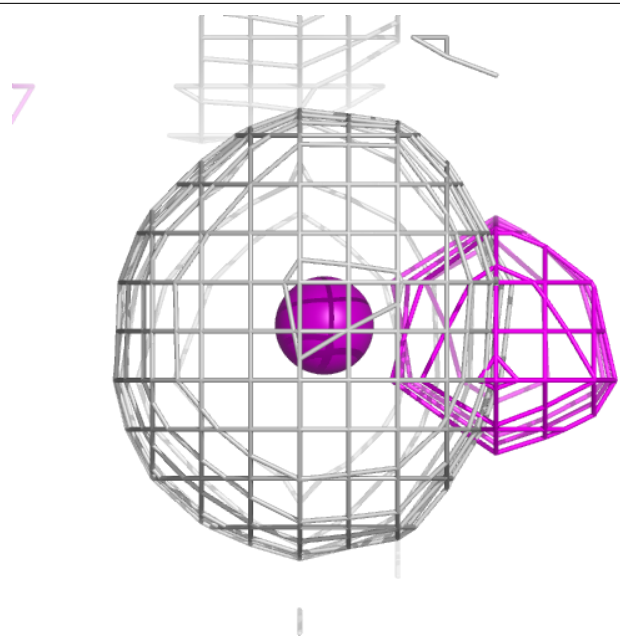
Electron density around IOD B 306:

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



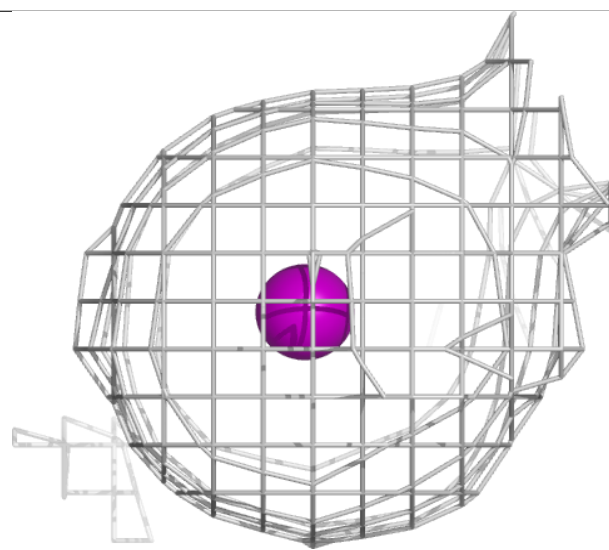
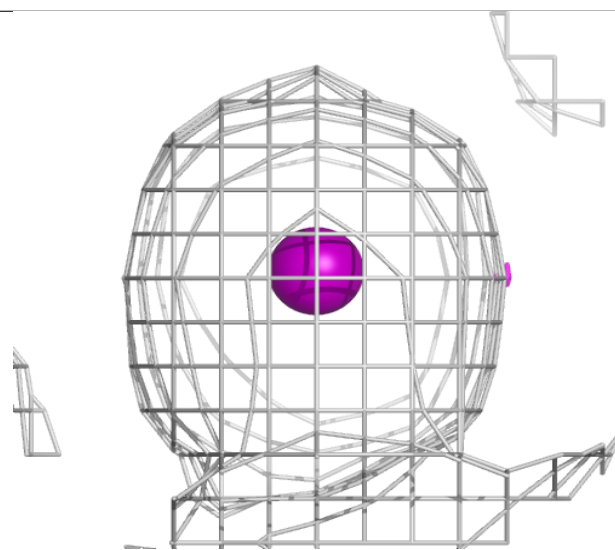
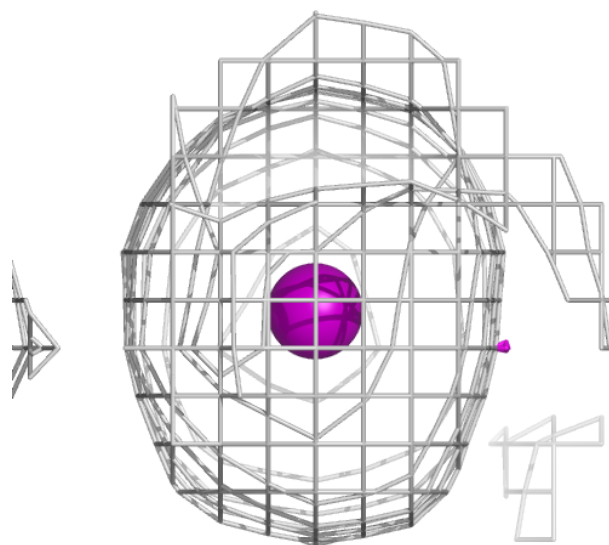
Electron density around IOD B 307:

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



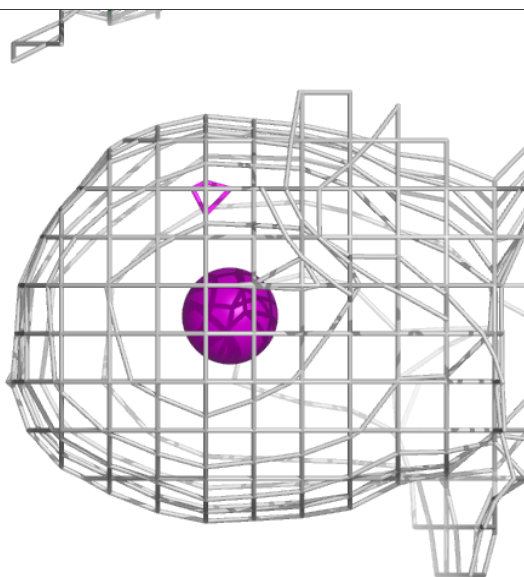
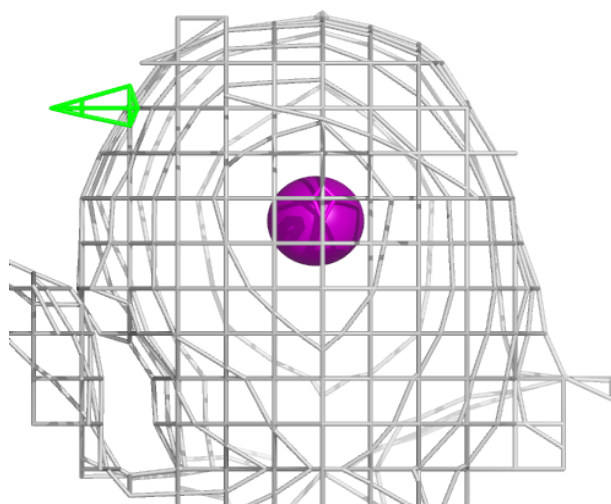
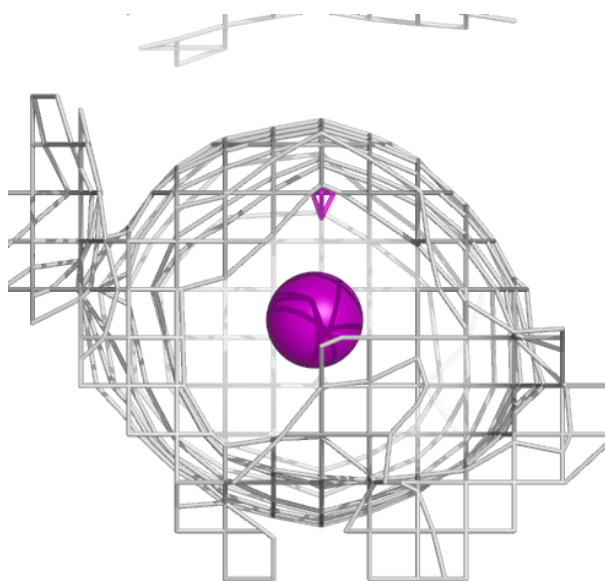
Electron density around IOD A 302:

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and green (positive)



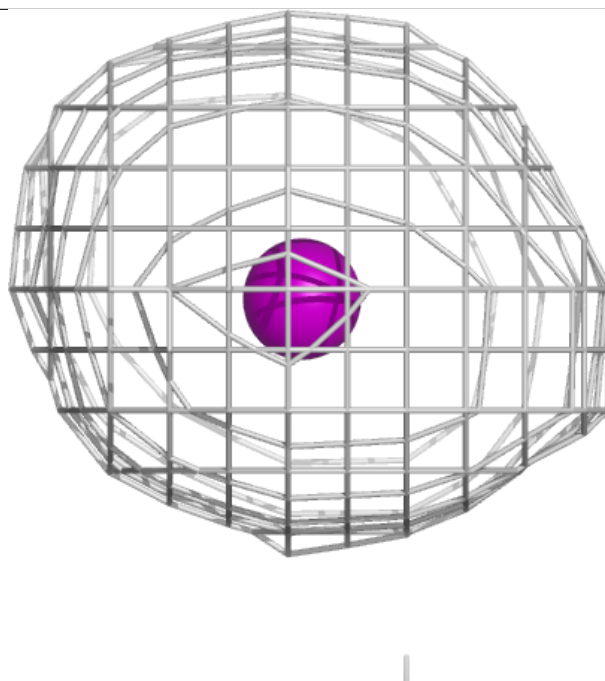
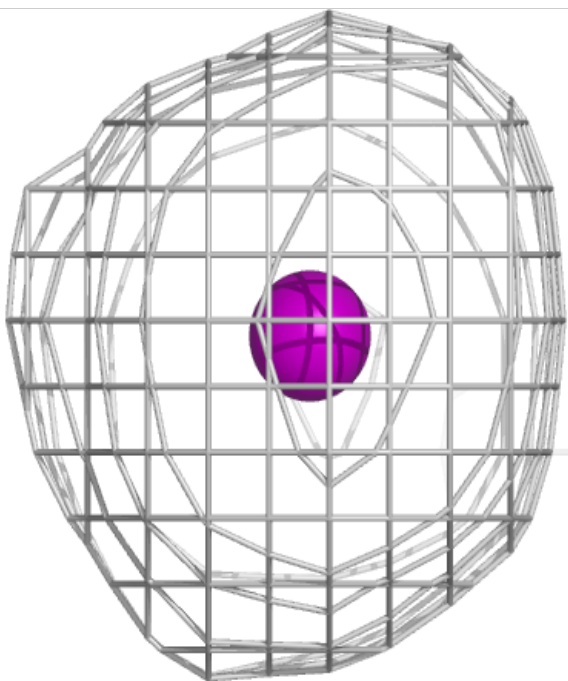
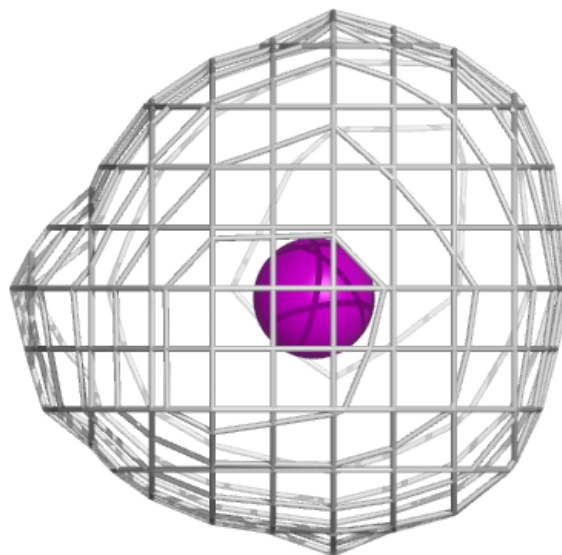
Electron density around IOD B 302:

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and green (positive)



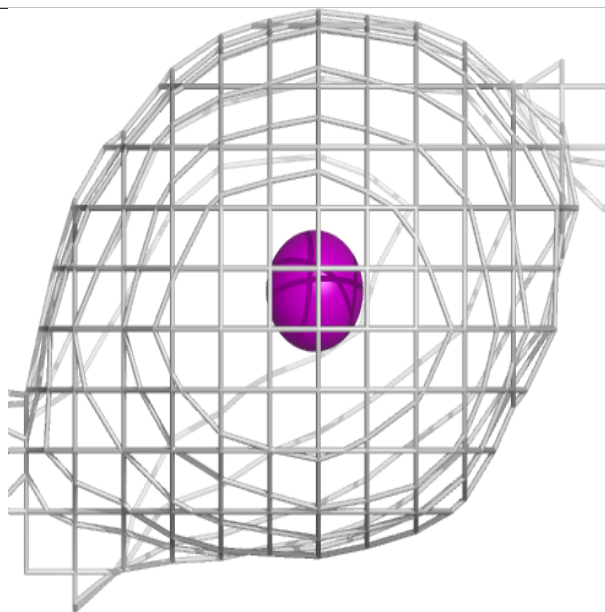
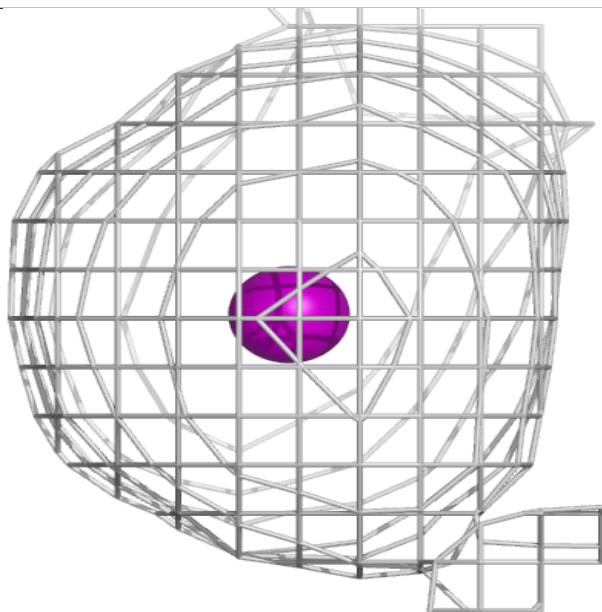
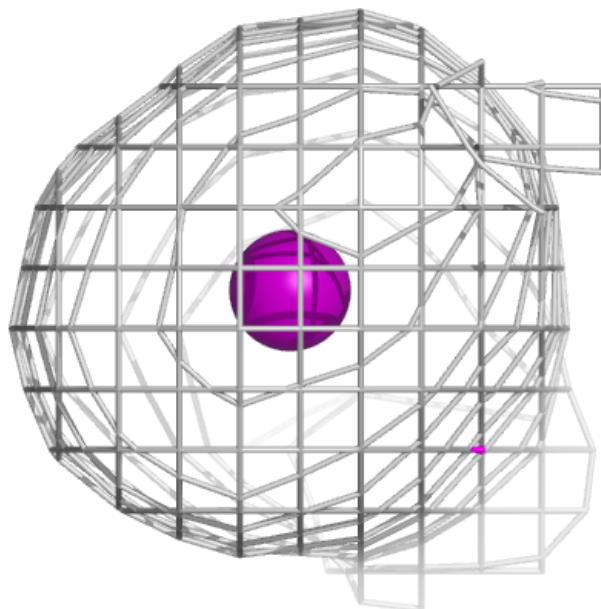
Electron density around IOD B 310:

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and green (positive)



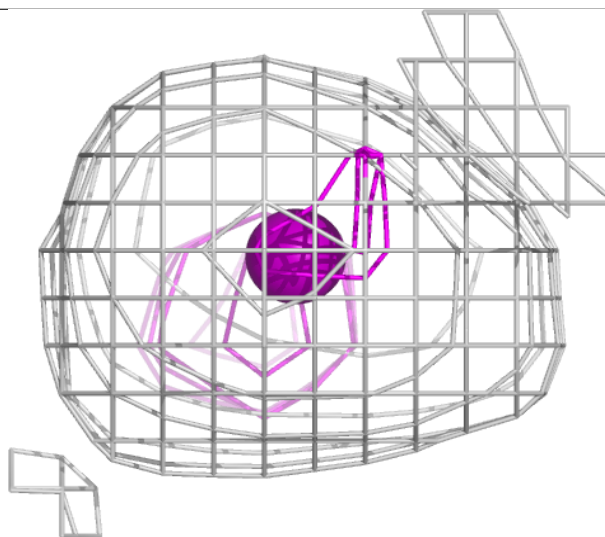
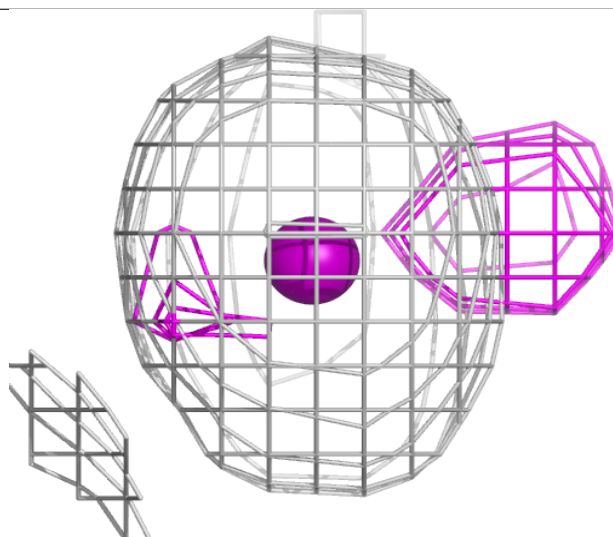
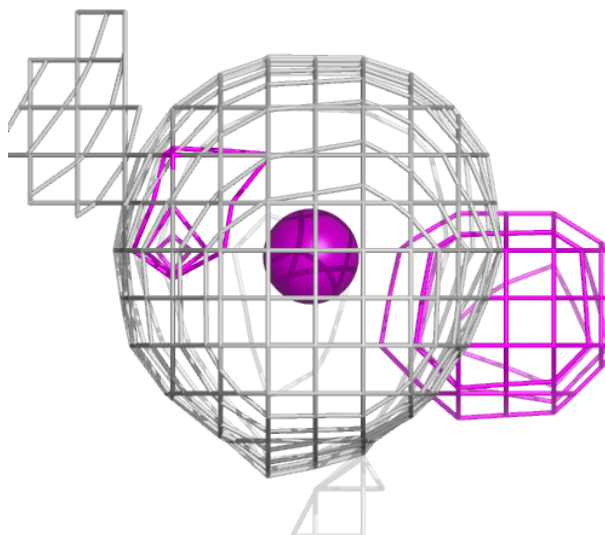
Electron density around IOD B 303:

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



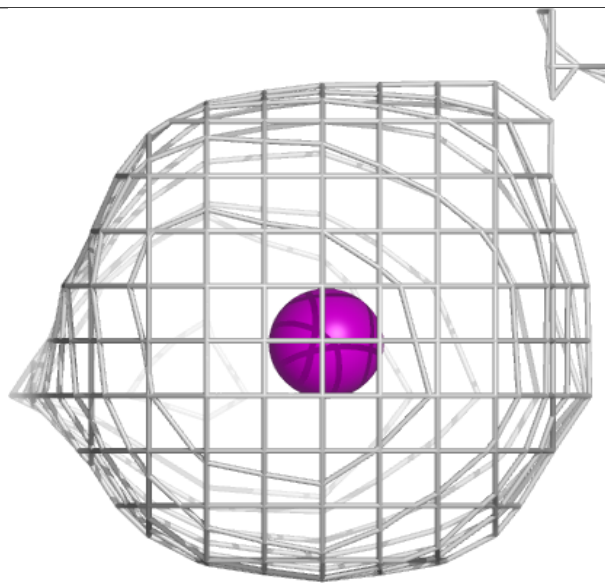
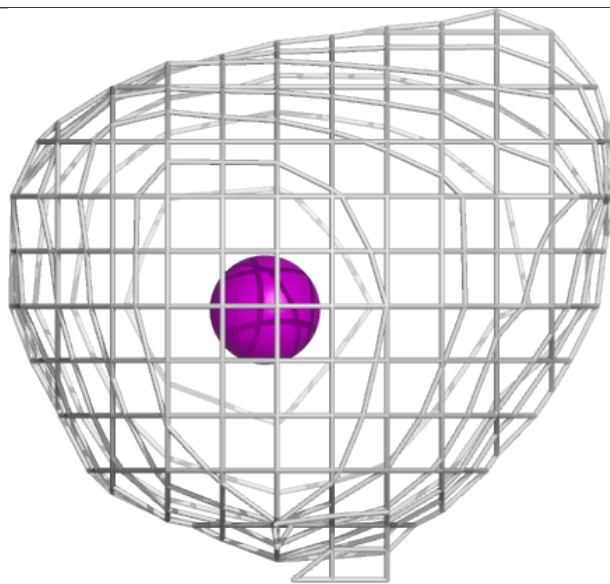
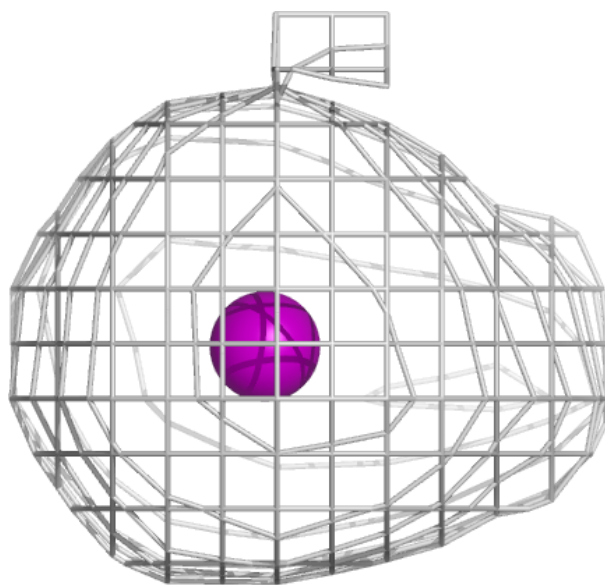
Electron density around IOD A 305:

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and green (positive)



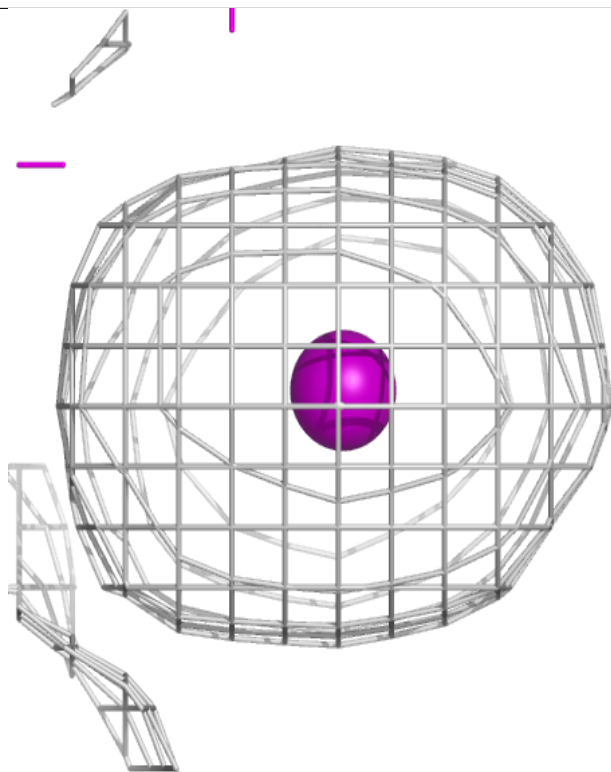
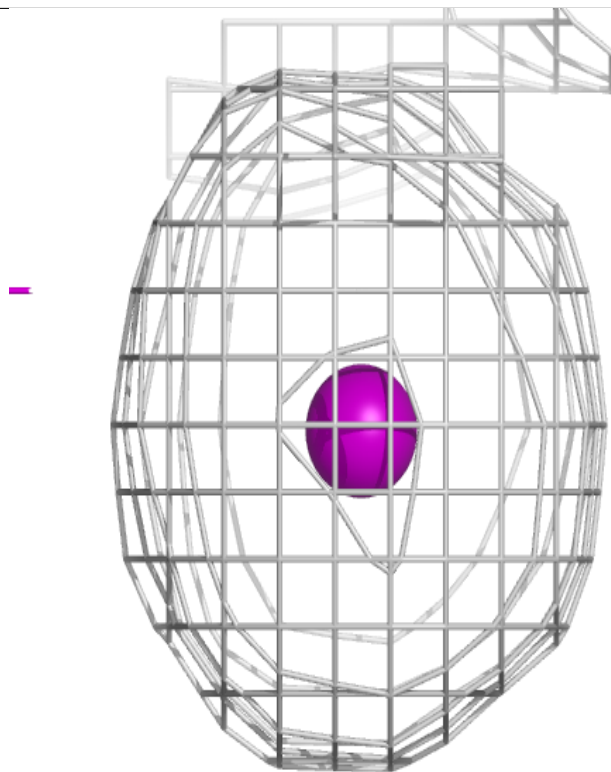
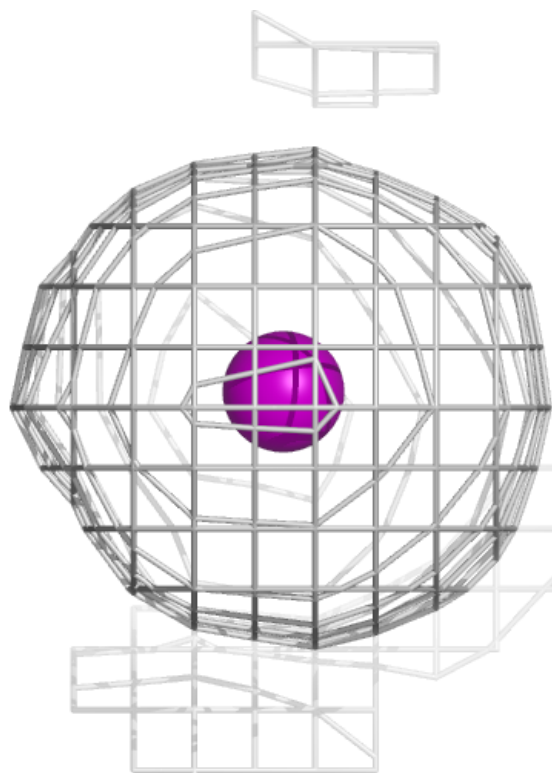
Electron density around IOD A 306:

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



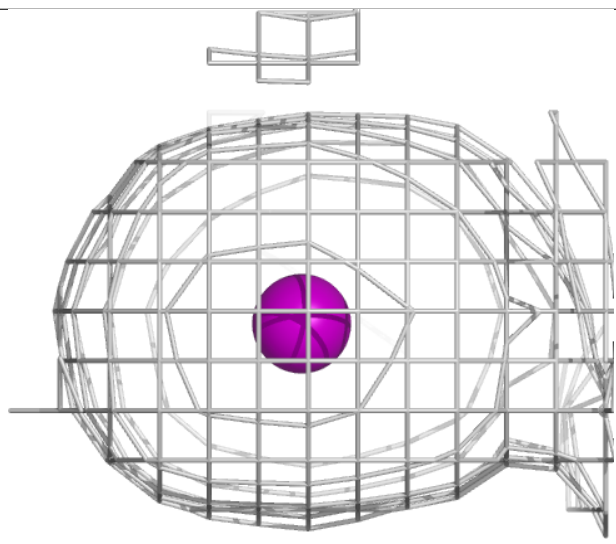
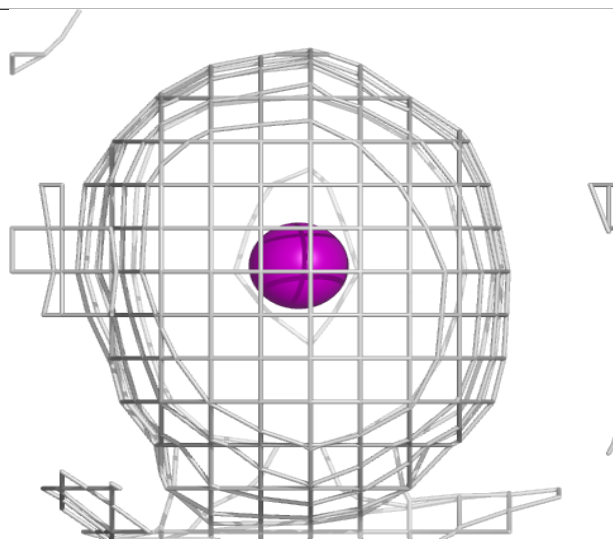
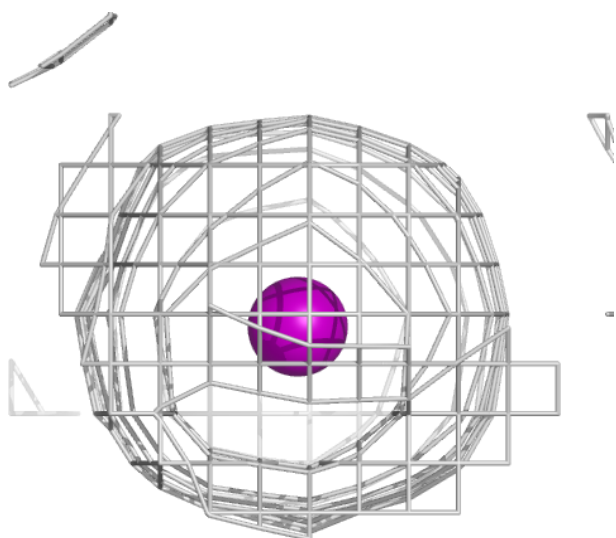
Electron density around IOD B 305:

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



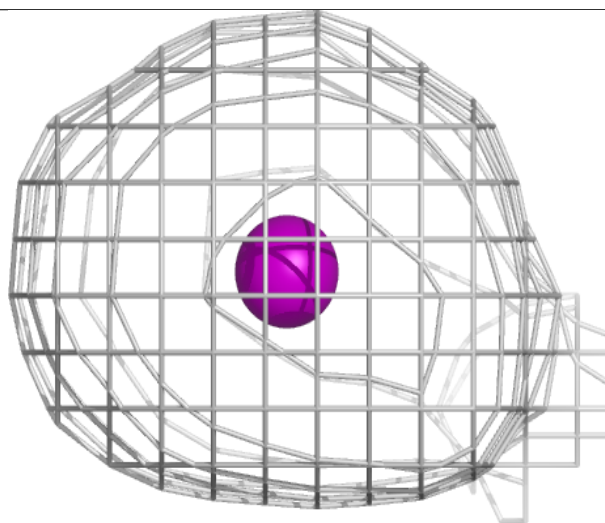
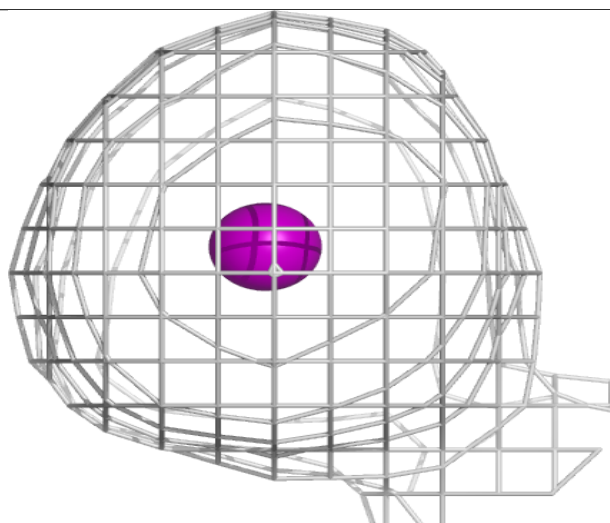
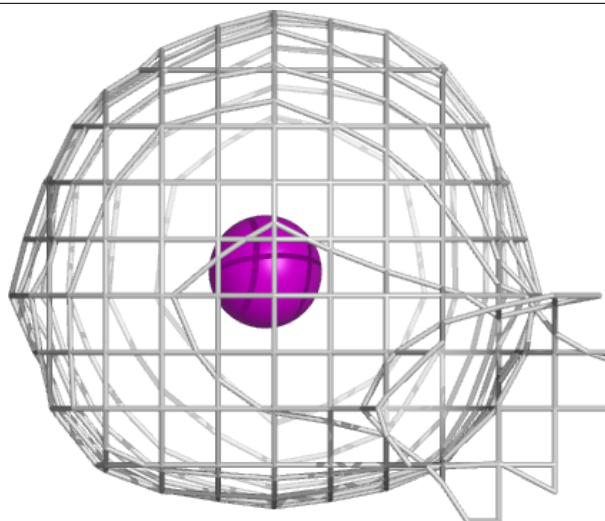
Electron density around IOD A 301:

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



Electron density around IOD A 304:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.