



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 20, 2024 – 12:29 pm BST

PDB ID : 8OT7
Title : Crystal structure of an 8-repeat consensus TPR superhelix with Barium
Authors : Liutkus, M.; Rojas, A.L.; Cortajarena, A.L.
Deposited on : 2023-04-20
Resolution : 3.30 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 : 2.36.2
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) : 2.36.2

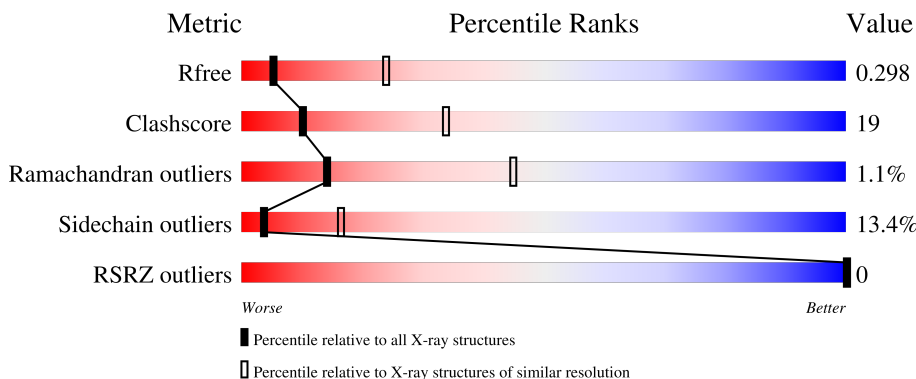
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	292	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2304 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 Consensus tetratricopeptide repeat protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	272	2296	1472	352	472	0	0	0

- Molecule 2 is BARIUM ION (three-letter code: BA) (formula: Ba) (labeled as "Ligand of Interest" by depositor).

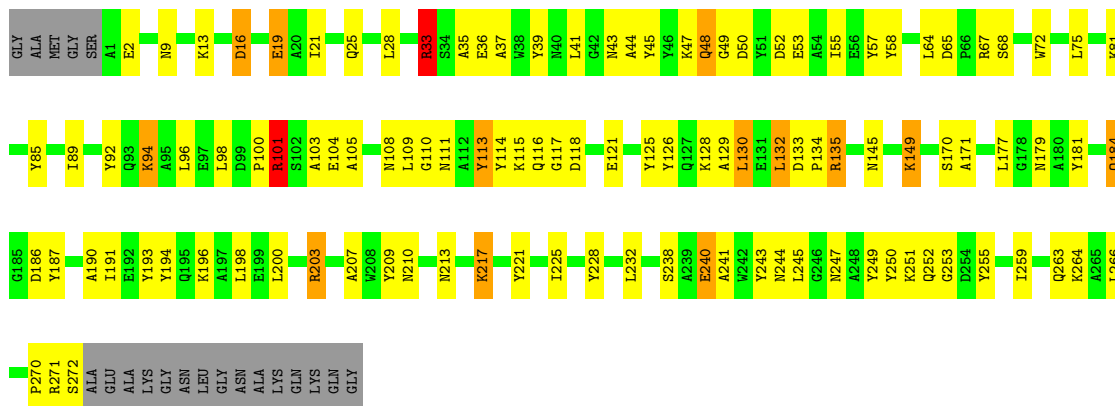
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	8	Total	Ba	0	0
			8	8		

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: Consensus tetratricopeptide repeat protein

Chain A:  55% 33% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	70.24Å 70.24Å 73.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.83 – 3.30 60.83 – 3.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (60.83-3.30) 99.9 (60.83-3.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.33Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.187 , 0.299 0.186 , 0.298	Depositor DCC
R_{free} test set	350 reflections (5.73%)	wwPDB-VP
Wilson B-factor (Å ²)	134.5	Xtrriage
Anisotropy	0.037	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 70.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.042 for -h,-k,l 0.388 for h,-h-k,-l 0.053 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2304	wwPDB-VP
Average B, all atoms (Å ²)	153.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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: BA

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	0.65	0/2367	0.89	3/3221 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	33	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	A	101	ARG	CG-CD-NE	-5.63	99.98	111.80
1	A	203	ARG	CG-CD-NE	5.31	122.95	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	GLY	Peptide
1	A	253	GLY	Peptide

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	2296	0	2034	82	0
2	A	8	0	0	0	0
All	All	2304	0	2034	82	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 19.

All (82) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ASN:ND2	1:A:58:TYR:OH	1.97	0.97
1:A:128:LYS:O	1:A:132:LEU:HD21	1.72	0.87
1:A:135:ARG:O	1:A:135:ARG:NH1	2.09	0.86
1:A:133:ASP:OD2	1:A:134:PRO:CD	2.27	0.83
1:A:128:LYS:O	1:A:132:LEU:CD2	2.26	0.82
1:A:132:LEU:HD22	1:A:132:LEU:H	1.44	0.81
1:A:108:ASN:HA	1:A:111:ASN:HD22	1.44	0.81
1:A:133:ASP:OD2	1:A:134:PRO:HD3	1.84	0.77
1:A:255:TYR:O	1:A:259:ILE:HG13	1.87	0.75
1:A:50:ASP:HB3	1:A:53:GLU:HG3	1.74	0.70
1:A:85:TYR:O	1:A:89:ILE:HG13	1.92	0.69
1:A:50:ASP:HB3	1:A:53:GLU:CG	2.25	0.67
1:A:133:ASP:OD2	1:A:134:PRO:HD2	1.94	0.66
1:A:52:ASP:HA	1:A:55:ILE:HD12	1.78	0.66
1:A:103:ALA:HB2	1:A:132:LEU:HD23	1.78	0.66
1:A:210:ASN:HA	1:A:213:ASN:HD22	1.62	0.65
1:A:179:ASN:ND2	1:A:194:TYR:OH	2.30	0.64
1:A:198:LEU:HD21	1:A:207:ALA:HB3	1.80	0.63
1:A:9:ASN:O	1:A:13:LYS:HG2	1.99	0.63
1:A:225:ILE:HG23	1:A:245:LEU:HD11	1.82	0.61
1:A:85:TYR:O	1:A:89:ILE:CG1	2.49	0.60
1:A:240:GLU:HA	1:A:243:TYR:HB3	1.83	0.60
1:A:228:TYR:O	1:A:232:LEU:HG	2.03	0.58
1:A:240:GLU:HA	1:A:243:TYR:CB	2.34	0.58
1:A:244:ASN:HA	1:A:247:ASN:HD22	1.68	0.57
1:A:171:ALA:HB2	1:A:200:LEU:HB2	1.87	0.57
1:A:101:ARG:HB3	1:A:101:ARG:CZ	2.34	0.56
1:A:47:LYS:O	1:A:49:GLY:N	2.39	0.54
1:A:132:LEU:HD22	1:A:132:LEU:N	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ALA:HB2	1:A:64:LEU:HB2	1.89	0.54
1:A:21:ILE:HD11	1:A:44:ALA:O	2.08	0.54
1:A:21:ILE:HD13	1:A:45:TYR:CE1	2.43	0.54
1:A:72:TRP:CD2	1:A:94:LYS:HG3	2.43	0.53
1:A:33:ARG:NE	1:A:33:ARG:HA	2.25	0.52
1:A:210:ASN:HA	1:A:213:ASN:ND2	2.25	0.52
1:A:98:LEU:O	1:A:100:PRO:HD3	2.10	0.52
1:A:238:SER:HB3	1:A:241:ALA:HB3	1.91	0.52
1:A:225:ILE:HG23	1:A:245:LEU:CD1	2.39	0.51
1:A:65:ASP:OD2	1:A:68:SER:HB2	2.11	0.51
1:A:110:GLY:O	1:A:114:TYR:HB2	2.11	0.51
1:A:41:LEU:HD23	1:A:57:TYR:CG	2.45	0.50
1:A:92:TYR:HB3	1:A:109:LEU:HD13	1.94	0.50
1:A:181:TYR:HB3	1:A:186:ASP:O	2.12	0.49
1:A:33:ARG:NE	1:A:33:ARG:CA	2.76	0.49
1:A:45:TYR:C	1:A:47:LYS:H	2.16	0.49
1:A:118:ASP:OD1	1:A:121:GLU:CG	2.61	0.48
1:A:113:TYR:CD2	1:A:125:TYR:CE2	3.02	0.48
1:A:238:SER:CB	1:A:241:ALA:HB3	2.43	0.48
1:A:132:LEU:CD2	1:A:132:LEU:H	2.23	0.47
1:A:103:ALA:HB2	1:A:132:LEU:CG	2.45	0.47
1:A:103:ALA:HB2	1:A:132:LEU:CD2	2.43	0.46
1:A:36:GLU:O	1:A:39:TYR:HB3	2.15	0.46
1:A:209:TYR:OH	1:A:244:ASN:ND2	2.49	0.46
1:A:232:LEU:HD12	1:A:245:LEU:HD22	1.96	0.46
1:A:116:GLN:HB2	1:A:118:ASP:HB3	1.96	0.46
1:A:16:ASP:HB3	1:A:19:GLU:HB3	1.98	0.45
1:A:85:TYR:O	1:A:89:ILE:CD1	2.64	0.45
1:A:130:LEU:C	1:A:130:LEU:HD23	2.37	0.45
1:A:47:LYS:C	1:A:49:GLY:N	2.70	0.45
1:A:118:ASP:OD1	1:A:121:GLU:HG2	2.17	0.45
1:A:85:TYR:O	1:A:89:ILE:HD12	2.16	0.45
1:A:45:TYR:C	1:A:47:LYS:N	2.70	0.44
1:A:96:LEU:HD21	1:A:105:ALA:HB3	2.00	0.44
1:A:101:ARG:CZ	1:A:101:ARG:CB	2.96	0.44
1:A:145:ASN:O	1:A:149:LYS:HG2	2.18	0.44
1:A:116:GLN:HB2	1:A:118:ASP:CB	2.48	0.43
1:A:270:PRO:HG2	1:A:271:ARG:NH1	2.34	0.43
1:A:130:LEU:HD23	1:A:130:LEU:O	2.20	0.42
1:A:47:LYS:C	1:A:49:GLY:H	2.23	0.41
1:A:177:LEU:HD23	1:A:193:TYR:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:TYR:O	1:A:190:ALA:HB3	2.21	0.41
1:A:238:SER:OG	1:A:241:ALA:HB3	2.20	0.41
1:A:89:ILE:CG2	1:A:113:TYR:CE2	3.04	0.41
1:A:221:TYR:CE2	1:A:251:LYS:CB	3.04	0.41
1:A:108:ASN:HA	1:A:111:ASN:ND2	2.24	0.41
1:A:126:TYR:O	1:A:129:ALA:HB3	2.20	0.41
1:A:89:ILE:HG21	1:A:113:TYR:CE2	2.57	0.40
1:A:109:LEU:HD23	1:A:125:TYR:CD1	2.56	0.40
1:A:28:LEU:HD21	1:A:37:ALA:HB3	2.03	0.40
1:A:238:SER:OG	1:A:241:ALA:CB	2.69	0.40
1:A:263:GLN:HA	1:A:266:LEU:HB2	2.04	0.40
1:A:217:LYS:HA	1:A:217:LYS:HE2	2.03	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	270/292 (92%)	238 (88%)	29 (11%)	3 (1%)	14 45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	184	GLN
1	A	191	ILE

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	216/227 (95%)	187 (87%)	29 (13%)	4 16

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	16	ASP
1	A	19	GLU
1	A	25	GLN
1	A	33	ARG
1	A	48	GLN
1	A	67	ARG
1	A	75	LEU
1	A	81	LYS
1	A	94	LYS
1	A	101	ARG
1	A	104	GLU
1	A	113	TYR
1	A	115	LYS
1	A	130	LEU
1	A	132	LEU
1	A	135	ARG
1	A	149	LYS
1	A	170	SER
1	A	184	GLN
1	A	196	LYS
1	A	203	ARG
1	A	217	LYS
1	A	240	GLU
1	A	249	TYR
1	A	250	TYR
1	A	252	GLN
1	A	264	LYS
1	A	272	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	77	ASN
1	A	108	ASN
1	A	111	ASN
1	A	142	ASN
1	A	179	ASN
1	A	244	ASN
1	A	247	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	272/292 (93%)	-0.11	0 100 100	108, 151, 188, 233	0

There are no RSRZ outliers to report.

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.

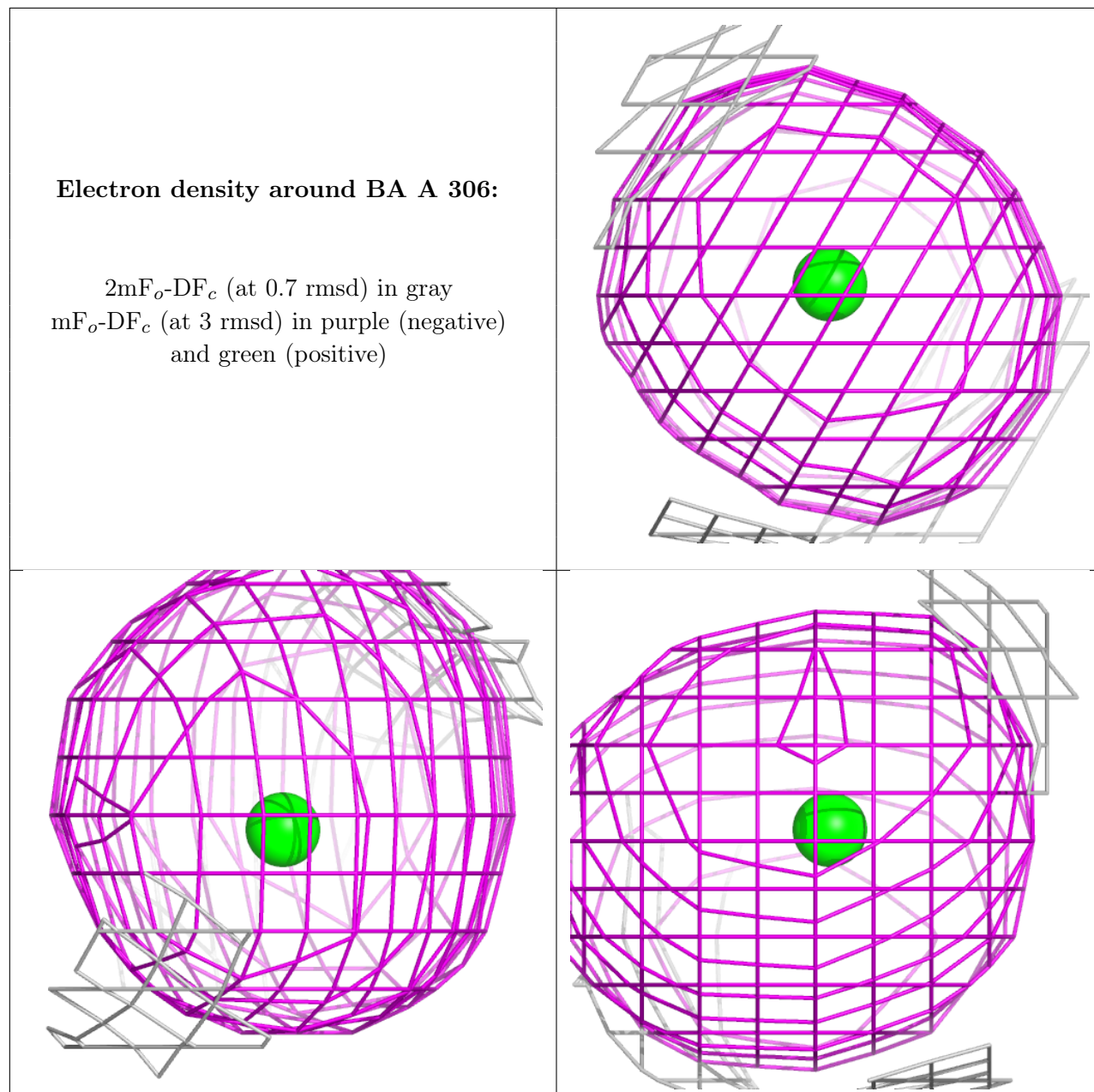
6.4 Ligands [i](#)

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, 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	BA	A	306	1/1	0.76	0.06	181,181,181,181	0
2	BA	A	302	1/1	0.77	0.21	142,142,142,142	1
2	BA	A	307	1/1	0.83	0.11	195,195,195,195	0
2	BA	A	303	1/1	0.95	0.04	176,176,176,176	0
2	BA	A	305	1/1	0.97	0.09	116,116,116,116	0
2	BA	A	304	1/1	0.98	0.02	131,131,131,131	1
2	BA	A	301	1/1	0.99	0.04	171,171,171,171	0
2	BA	A	308	1/1	0.99	0.10	164,164,164,164	0

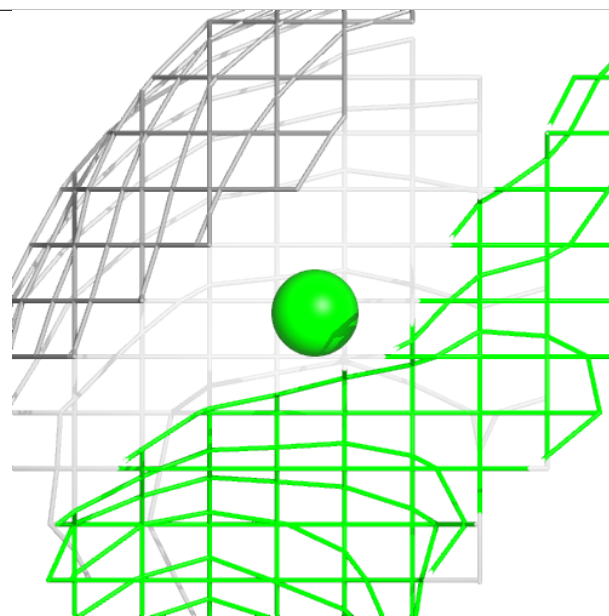
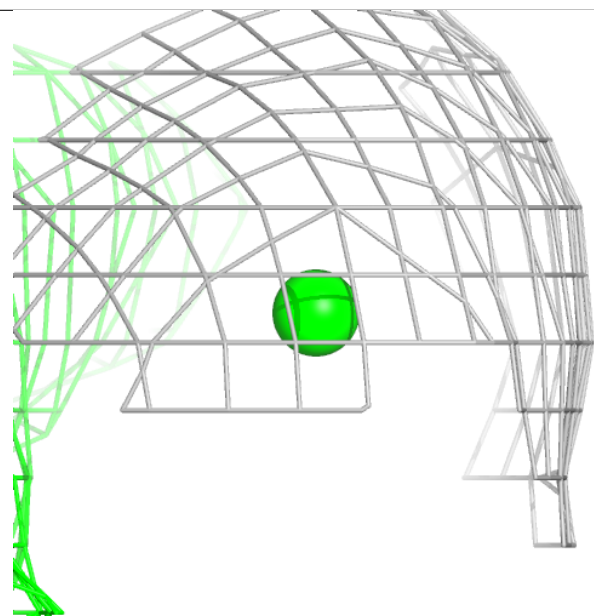
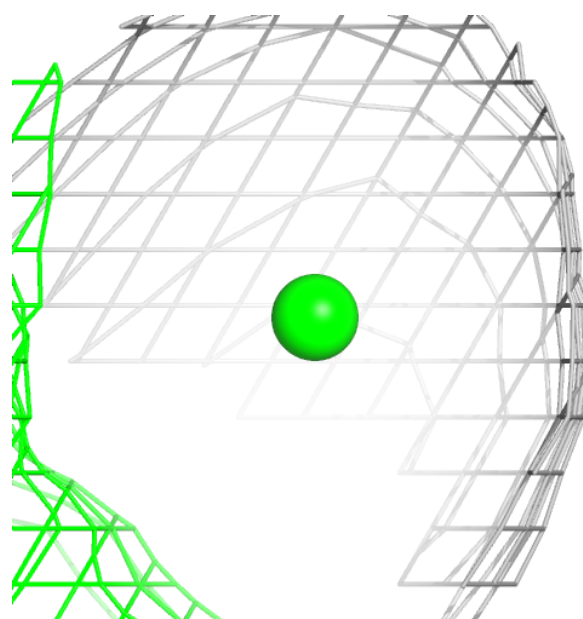
The following is a graphical depiction of the model fit to experimental electron density of all

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.



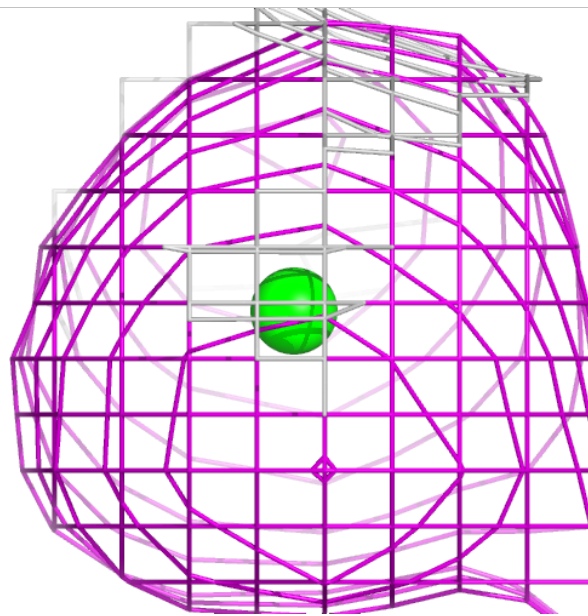
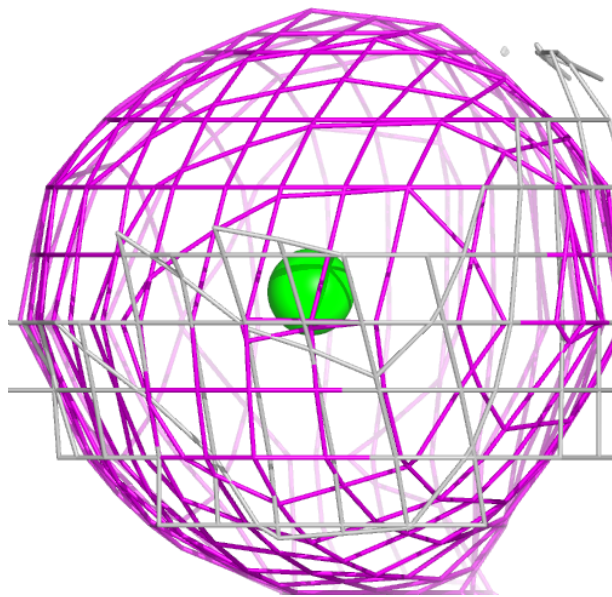
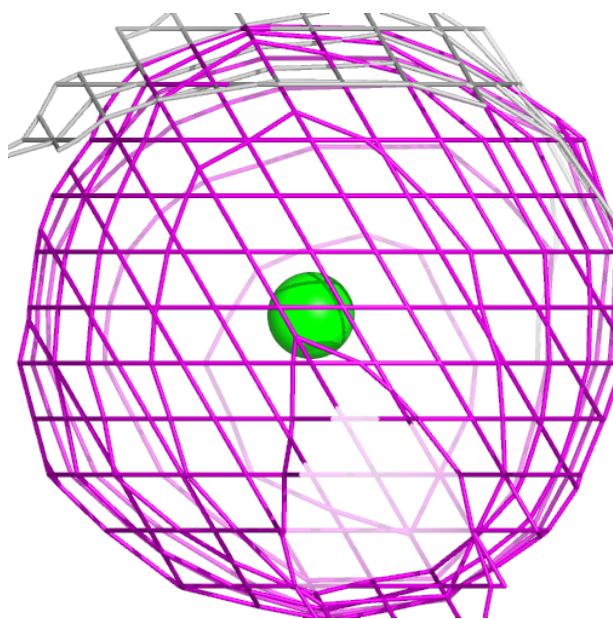
Electron density around BA A 302:

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



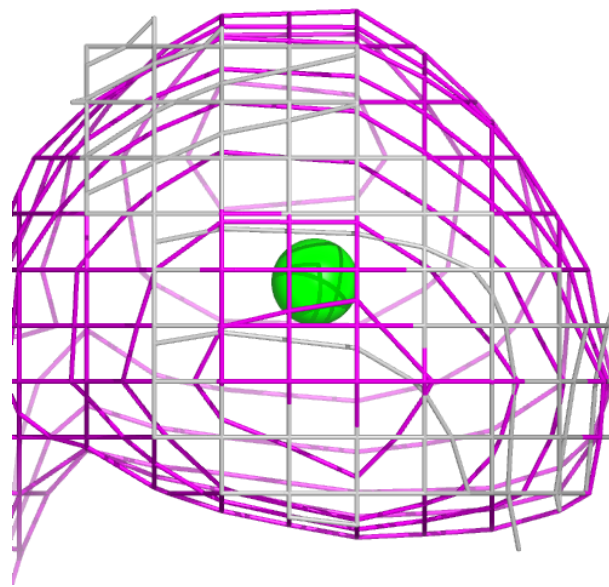
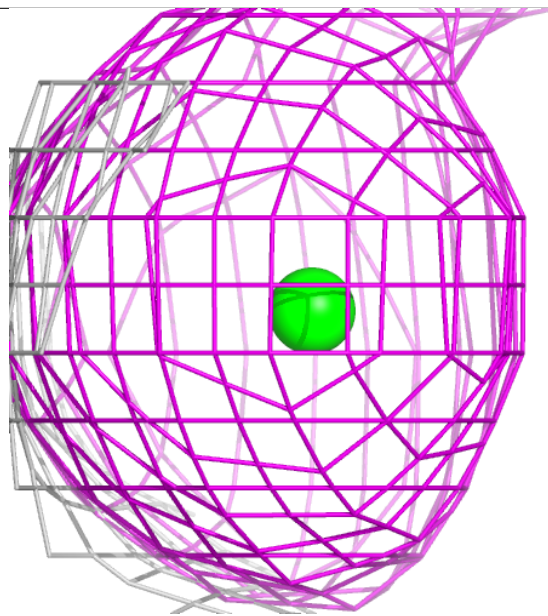
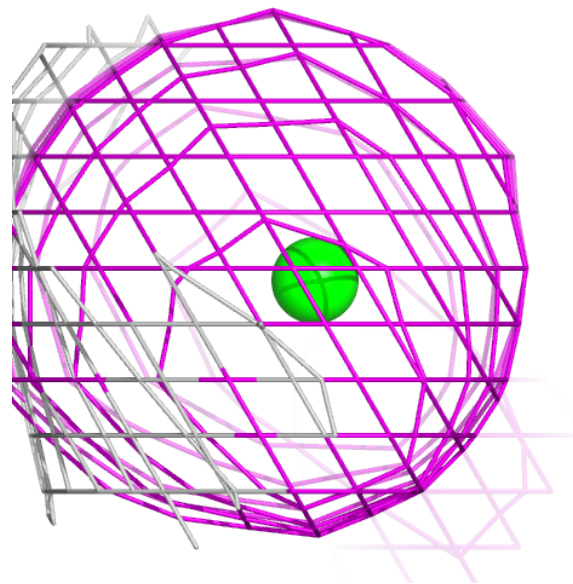
Electron density around BA A 307:

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



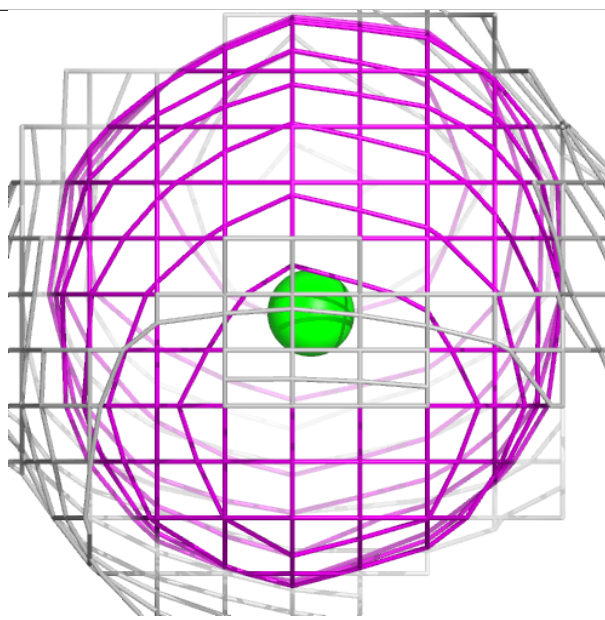
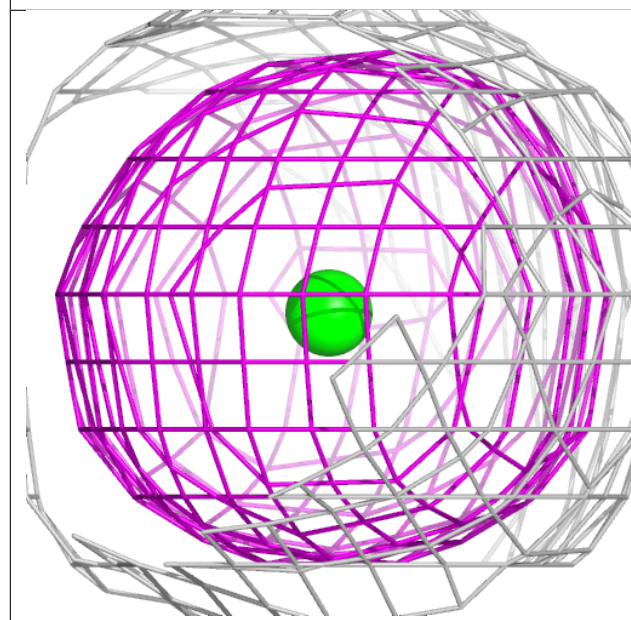
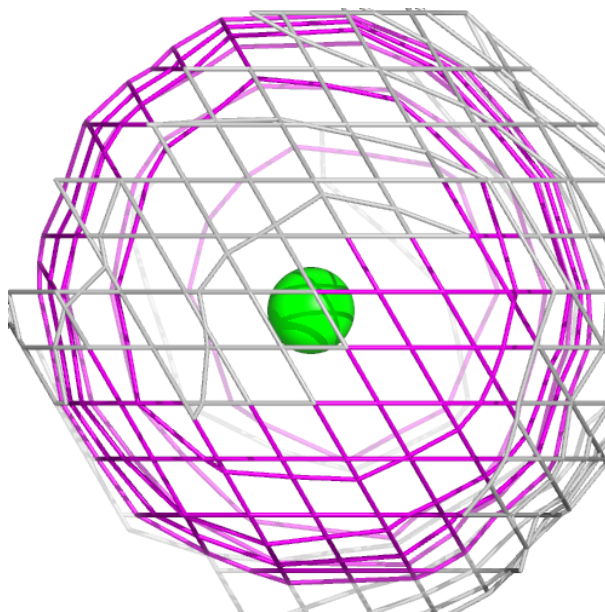
Electron density around BA A 303:

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



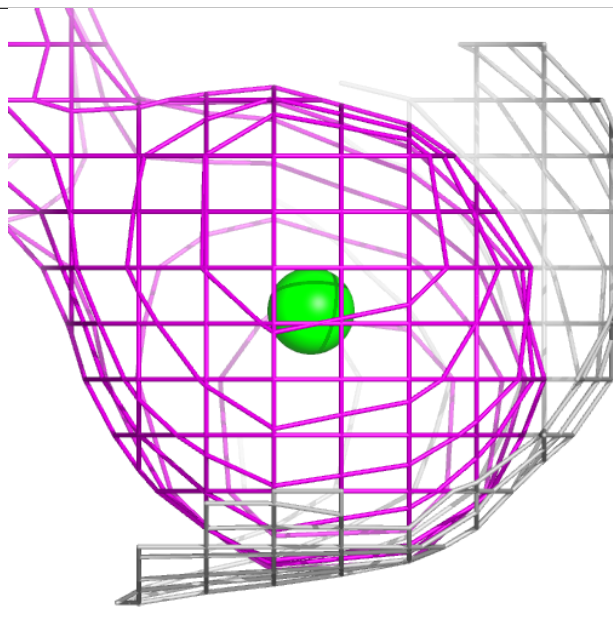
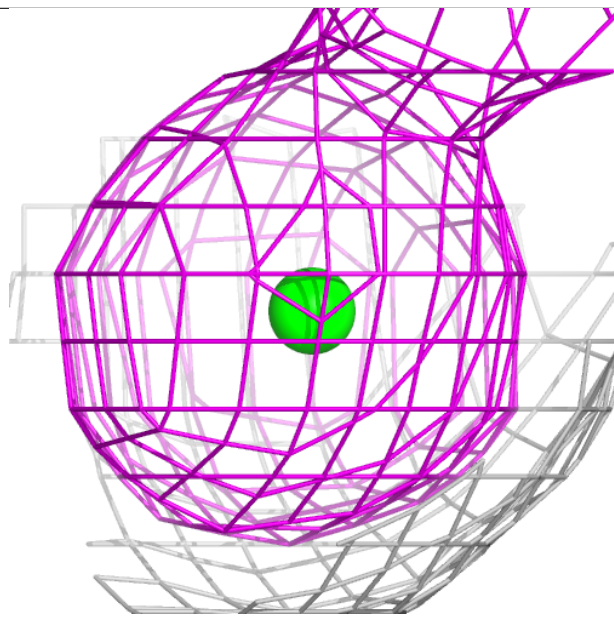
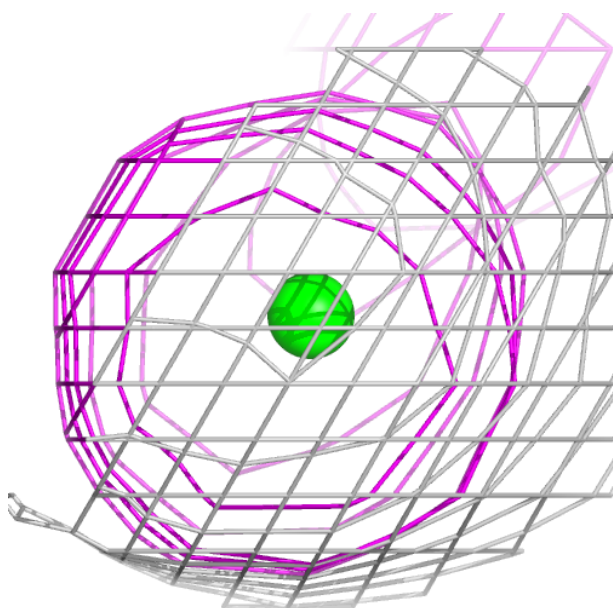
Electron density around BA A 305:

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



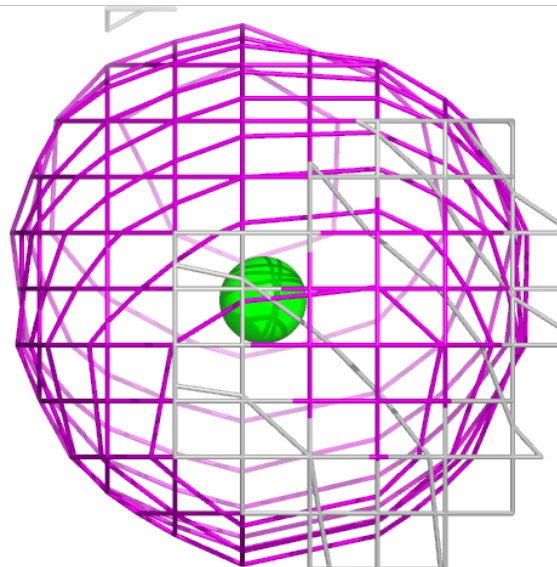
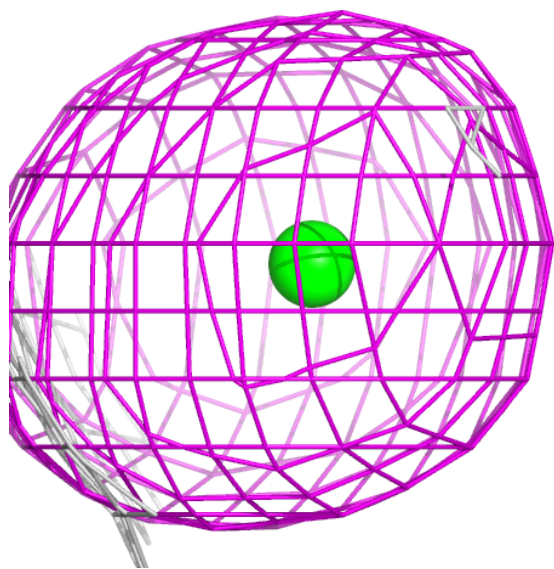
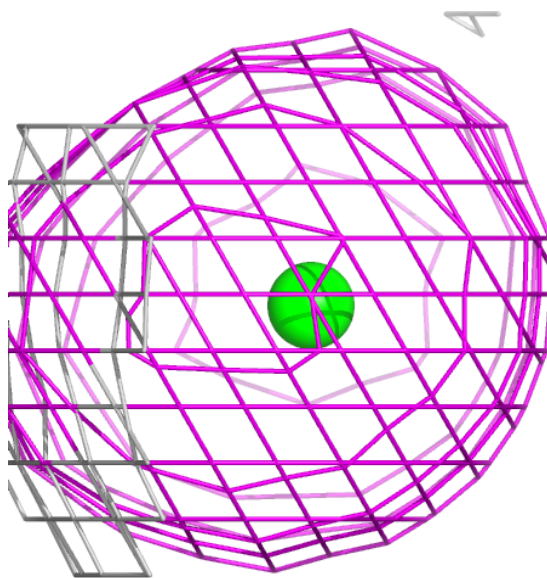
Electron density around BA A 304:

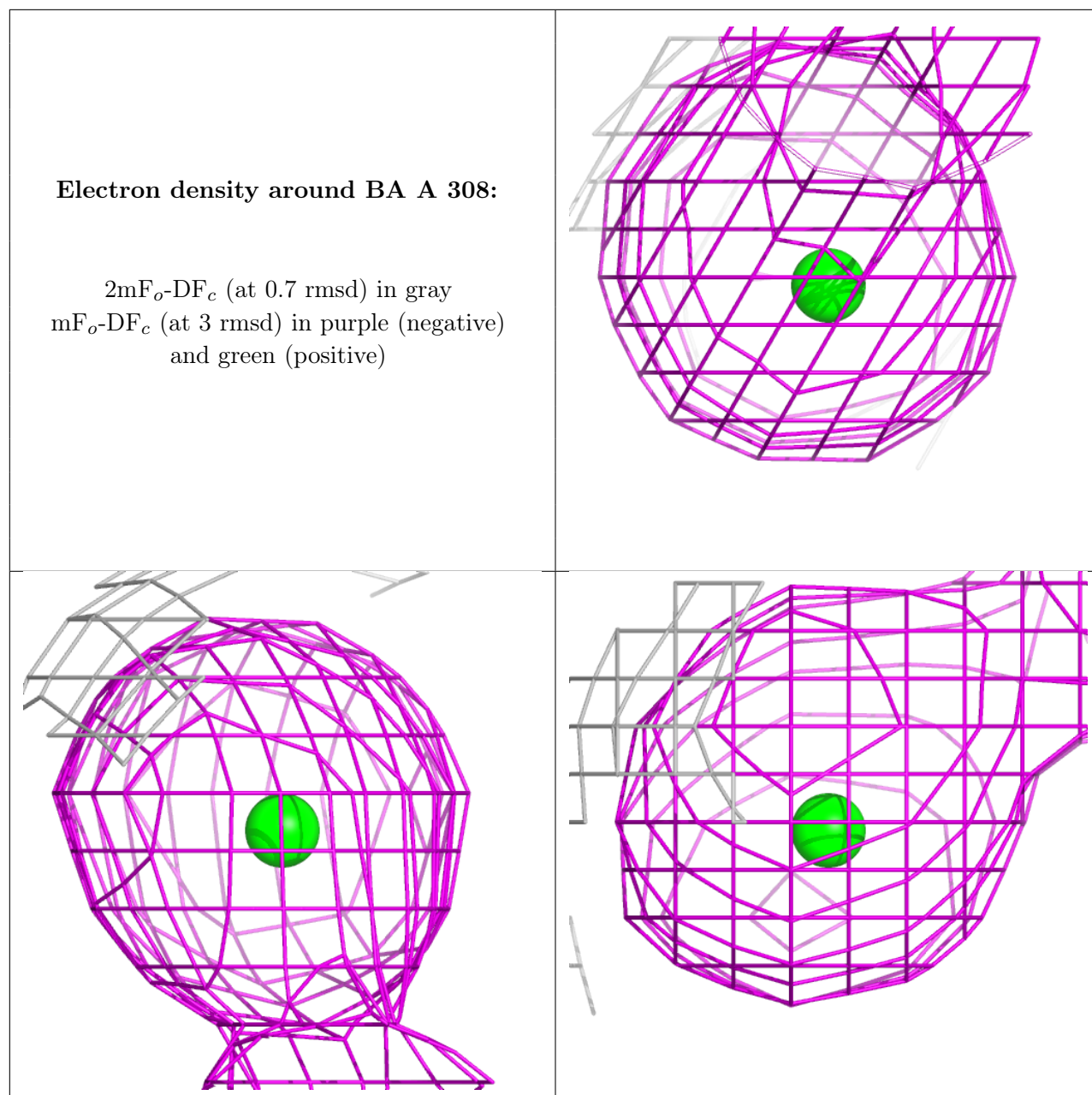
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around BA 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.