wwPDB X-ray Structure Validation Summary Report (i)

Jan 15, 2024 – 05:36 pm GMT

PDB ID	:	8C41
Title	:	High resolution structure of the Streptococcus pneumoniae topoisomerase IV-DNA complex with the novel fluoroquinolone Delafloxacin
Authors	:	Najmudin, S.; Pan, X.S.; Wang, B.; Chayen, N.E.; Fisher, L.M.; Sanderson, M.R.
Deposited on	:	2022-12-30
Resolution	:	2.39 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

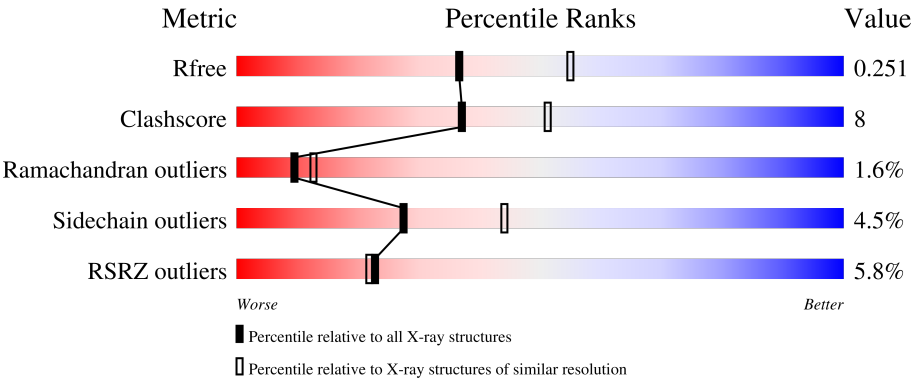
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	742	6% 74% 20%
1	B	742	5% 79% 17%
2	E	7	43% 57%
3	F	11	36% 45% 18%

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Mol	Chain	Length	Quality of chain
4	G	7	71% 29%
5	H	11	45% 36% 18%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 24852 atoms, of which 12136 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 Fused ParE30ParC55 CLEAVAGE COMPLEX of the TOPOISOMERASE IV.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	720	Total	C	H	N	O	S	321	2	0
			11587	3629	5843	1000	1091	24			
1	B	720	Total	C	H	N	O	S	319	0	0
			11549	3619	5819	996	1091	24			

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*AP*TP*GP*AP*AP*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	7	Total	C	H	N	O	P	1	0	0
			221	69	80	27	39	6			

- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*GP*TP*CP*AP*TP*TP*CP*AP*TP *G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	F	11	Total	C	H	N	O	P	1	0	0
			351	108	126	39	67	11			

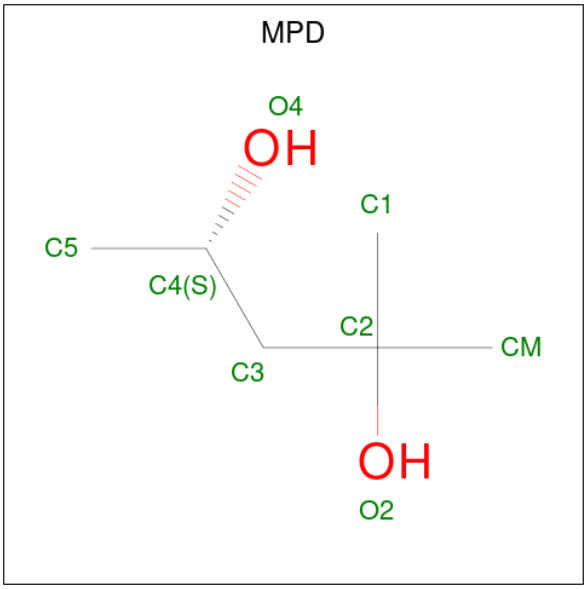
- Molecule 4 is a DNA chain called DNA (5'-D(*CP*GP*TP*GP*CP*AP*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	G	7	Total	C	H	N	O	P	1	0	0
			220	68	80	25	41	6			

- Molecule 5 is a DNA chain called DNA (5'-D(P*GP*AP*CP*TP*AP*TP*GP*CP*AP*CP *G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	H	11	Total	C	H	N	O	P	1	0	0
			350	107	124	43	65	11			

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C H O 22 6 14 2	1	0
6	A	1	Total C H O 22 6 14 2	1	0
6	B	1	Total C H O 22 6 14 2	1	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

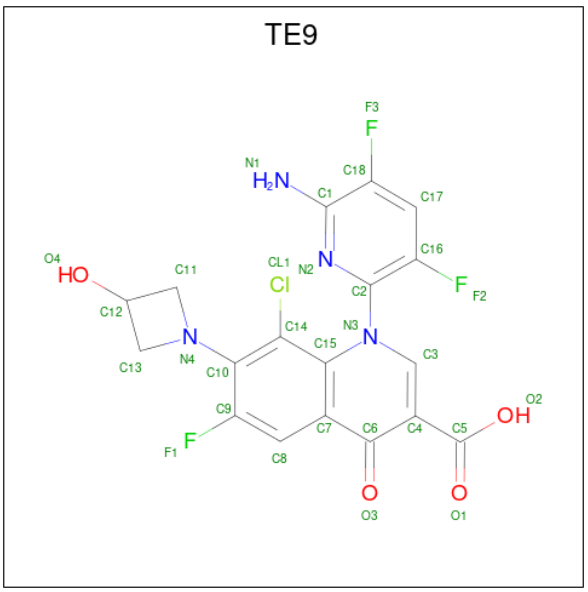
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	3	Total Mg 3 3	0	0
7	B	3	Total Mg 3 3	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0
8	B	1	Total Cl 1 1	0	0

- Molecule 9 is delafloxacin (three-letter code: TE9) (formula: $C_{18}H_{12}ClF_3N_4O_4$) (labeled as

"Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
9	F	1	Total	C	Cl	F	H	N	O	1	0
			41	18	1	3	11	4	4		
9	H	1	Total	C	Cl	F	H	N	O	1	0
			41	18	1	3	11	4	4		

- Molecule 10 is water.

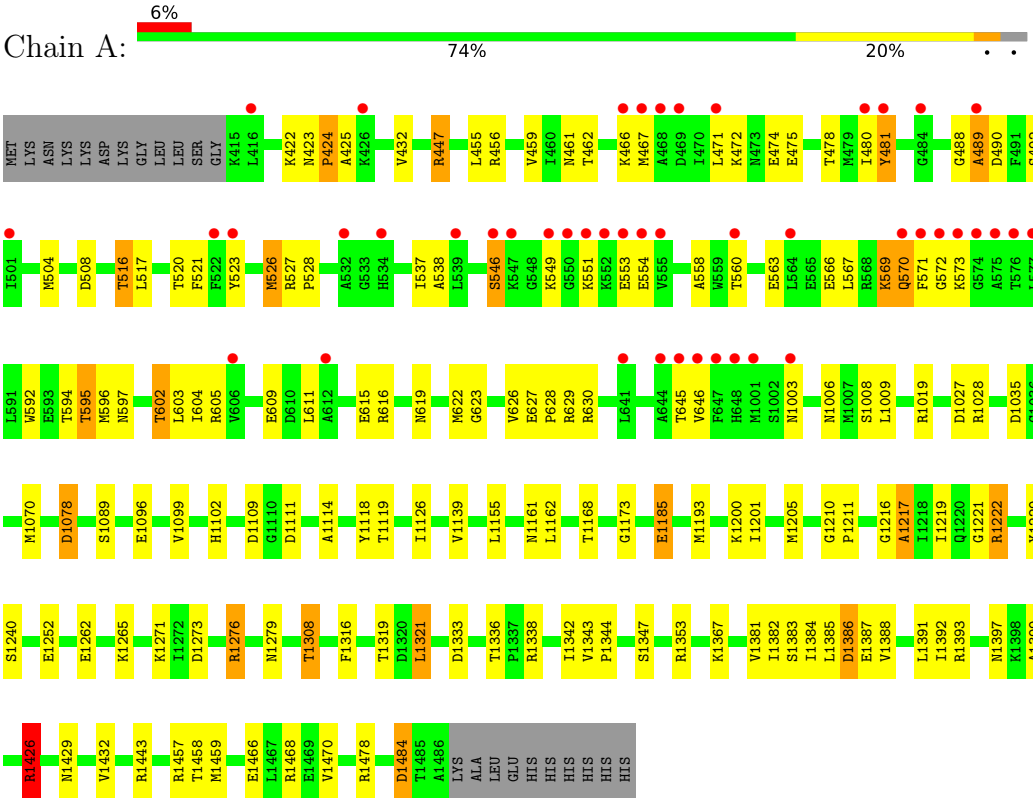
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	195	Total	O	0	0
			195	195		
10	B	195	Total	O	0	0
			195	195		
10	E	10	Total	O	0	0
			10	10		
10	F	7	Total	O	0	0
			7	7		
10	G	7	Total	O	0	0
			7	7		
10	H	4	Total	O	0	0
			4	4		

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.

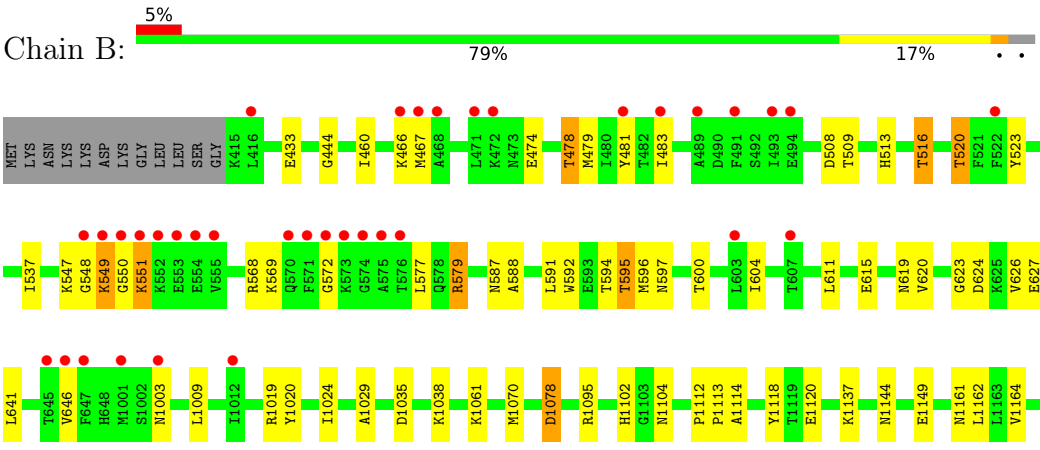
• Molecule 1: Fused ParE30ParC55 CLEAVAGE COMPLEX of the TOPOISOMERASE IV

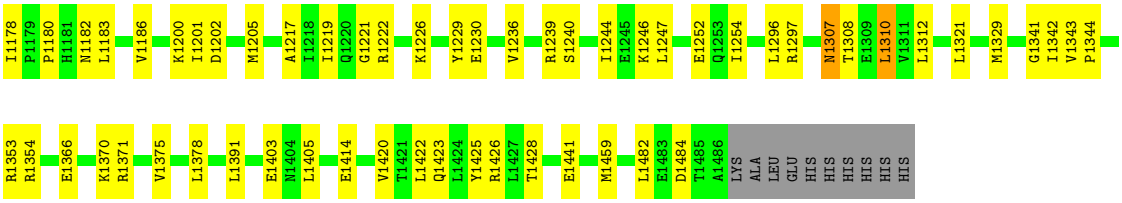
Chain A:



• Molecule 1: Fused ParE30ParC55 CLEAVAGE COMPLEX of the TOPOISOMERASE IV

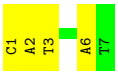
Chain B:





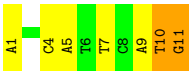
• Molecule 2: DNA (5'-D(*CP*AP*TP*GP*AP*AP*T)-3')

Chain E:



• Molecule 3: DNA (5'-D(P*AP*GP*TP*CP*AP*TP*TP*CP*AP*TP*G)-3')

Chain F:

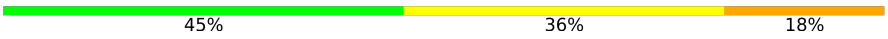


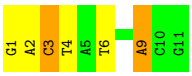
• Molecule 4: DNA (5'-D(*CP*GP*TP*GP*CP*AP*T)-3')

Chain G:

• Molecule 5: DNA (5'-D(P*GP*AP*CP*TP*AP*TP*GP*CP*AP*CP*G)-3')

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	157.47Å 157.47Å 212.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	115.01 – 2.39 114.75 – 2.39	Depositor EDS
% Data completeness (in resolution range)	58.9 (115.01-2.39) 58.9 (114.75-2.39)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.8.0352, PDB-REDO	Depositor
R, R_{free}	0.192 , 0.243 0.201 , 0.251	Depositor DCC
R_{free} test set	3458 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	34.9	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	24852	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TE9, MPD, MG, CL

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	0.45	1/5844 (0.0%)	0.78	4/7879 (0.1%)
1	B	0.45	2/5824 (0.0%)	0.76	1/7854 (0.0%)
2	E	0.81	0/158	1.34	2/242 (0.8%)
3	F	0.92	0/251	1.51	7/385 (1.8%)
4	G	0.87	0/156	1.58	1/239 (0.4%)
5	H	0.85	0/253	1.42	4/388 (1.0%)
All	All	0.49	3/12486 (0.0%)	0.84	19/16987 (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	7
1	B	0	2
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1403	GLU	CD-OE1	6.60	1.32	1.25
1	B	1414	GLU	CD-OE1	5.42	1.31	1.25
1	A	1185	GLU	CD-OE1	5.34	1.31	1.25

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1468	ARG	NE-CZ-NH2	-6.63	116.98	120.30
3	F	5	DA	P-O3'-C3'	-6.49	111.91	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	H	2	DA	P-O3'-C3'	-6.43	111.98	119.70
5	H	3	DC	C4'-C3'-C2'	-6.42	97.32	103.10
2	E	3	DT	O5'-P-OP2	-6.29	100.04	105.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1276	ARG	Sidechain
1	A	1353	ARG	Sidechain
1	A	1426	ARG	Sidechain
1	A	447	ARG	Sidechain
1	A	456	ARG	Sidechain

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	5744	5843	5833	94	0
1	B	5730	5819	5807	85	0
2	E	141	80	81	2	0
3	F	225	126	126	4	0
4	G	140	80	81	1	0
5	H	226	124	124	5	0
6	A	16	28	28	5	0
6	B	8	14	14	2	0
7	A	3	0	0	0	0
7	B	3	0	0	0	0
8	A	1	0	0	1	0
8	B	1	0	0	1	0
9	F	30	11	0	3	0
9	H	30	11	0	3	0
10	A	195	0	0	5	0
10	B	195	0	0	6	0
10	E	10	0	0	0	0
10	F	7	0	0	0	0
10	G	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H	4	0	0	1	0
All	All	12716	12136	12094	188	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 8.

The worst 5 of 188 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:1222:ARG:NH1	1:A:1484:ASP:OD1	2.04	0.90
1:B:508:ASP:OD2	10:B:1601:HOH:O	1.92	0.87
1:B:579:ARG:HH11	1:B:579:ARG:HB3	1.40	0.87
9:F:101:TE9:CL1	9:F:101:TE9:C2	2.63	0.84
1:A:594:THR:OG1	1:A:595:THR:HG22	1.77	0.83

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	720/742 (97%)	664 (92%)	42 (6%)	14 (2%)	8 10
1	B	718/742 (97%)	678 (94%)	31 (4%)	9 (1%)	12 17
All	All	1438/1484 (97%)	1342 (93%)	73 (5%)	23 (2%)	9 13

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	424	PRO
1	A	466	LYS
1	A	467	MET

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Mol	Chain	Res	Type
1	A	489	ALA
1	A	549	LYS

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	618/635 (97%)	580 (94%)	38 (6%)	18	30
1	B	616/635 (97%)	597 (97%)	19 (3%)	40	60
All	All	1234/1270 (97%)	1177 (95%)	57 (5%)	27	43

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1308	THR
1	B	1420	VAL
1	A	1386	ASP
1	B	1310	LEU
1	B	1168	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1102	HIS
1	B	619	ASN
1	A	1005	GLN
1	A	619	ASN
1	A	1102	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	MPD	A	1501	-	7,7,7	0.22	0	9,10,10	0.50	0
9	TE9	H	101	7	31,33,33	1.17	2 (6%)	37,51,51	1.31	5 (13%)
6	MPD	A	1502	-	7,7,7	0.14	0	9,10,10	0.78	0
9	TE9	F	101	7	31,33,33	1.20	4 (12%)	37,51,51	1.21	2 (5%)
6	MPD	B	1501	-	7,7,7	0.28	0	9,10,10	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MPD	A	1501	-	-	4/5/5/5	-
9	TE9	H	101	7	-	4/11/20/20	0/4/4/4
6	MPD	A	1502	-	-	2/5/5/5	-
9	TE9	F	101	7	-	7/11/20/20	0/4/4/4
6	MPD	B	1501	-	-	2/5/5/5	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	F	101	TE9	C2-C16	-3.00	1.38	1.42
9	H	101	TE9	C2-C16	-2.69	1.39	1.42
9	H	101	TE9	C1-C18	2.69	1.42	1.40
9	F	101	TE9	C3-N3	2.53	1.42	1.37
9	F	101	TE9	C1-C18	2.35	1.42	1.40

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	H	101	TE9	C17-C18-C1	-3.13	119.66	121.70
9	F	101	TE9	C17-C18-C1	-2.95	119.77	121.70
9	H	101	TE9	C4-C3-N3	-2.60	120.54	123.75
9	H	101	TE9	C3-C4-C6	2.28	121.58	119.88
9	H	101	TE9	O1-C5-C4	-2.24	117.54	122.46

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1502	MPD	C2-C3-C4-O4
9	F	101	TE9	C16-C2-N3-C15
9	F	101	TE9	N2-C2-N3-C3
9	H	101	TE9	C16-C2-N3-C15
9	H	101	TE9	N2-C2-N3-C3

There are no ring outliers.

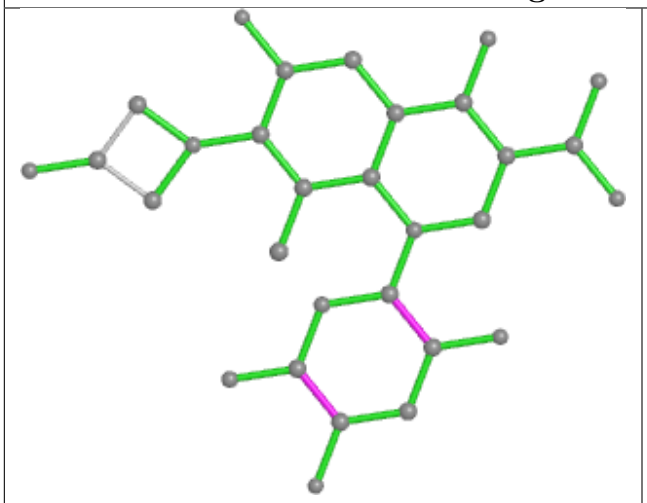
4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1501	MPD	5	0
9	H	101	TE9	3	0
9	F	101	TE9	3	0
6	B	1501	MPD	2	0

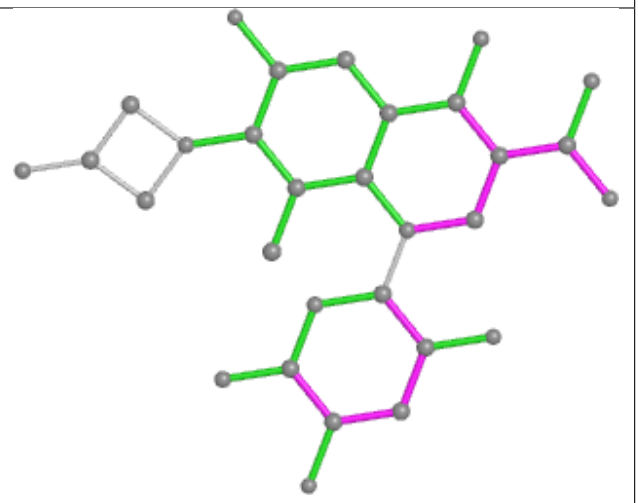
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

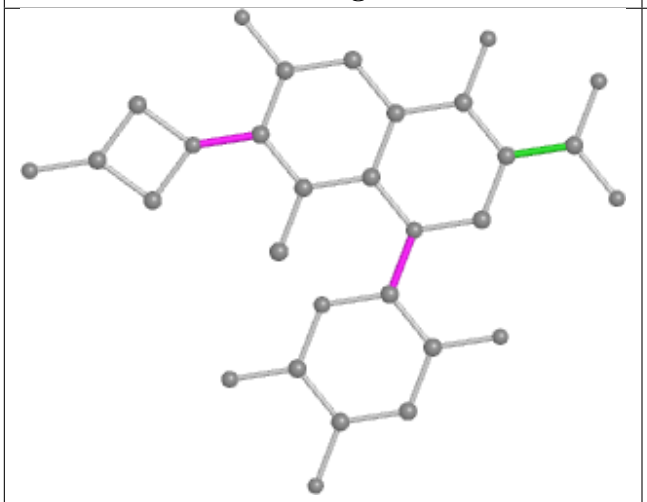
Ligand TE9 H 101



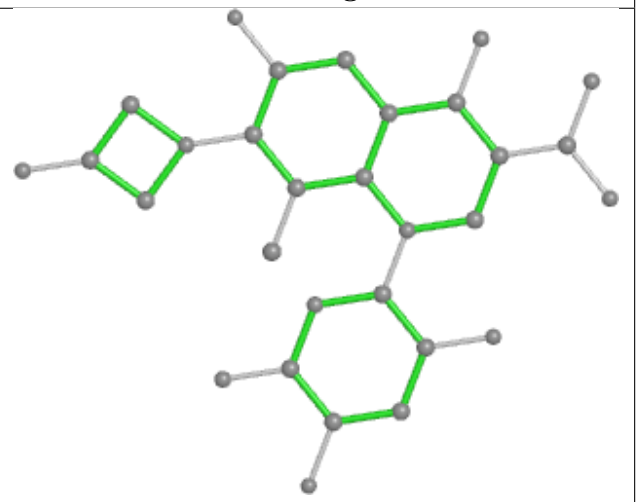
Bond lengths



Bond angles

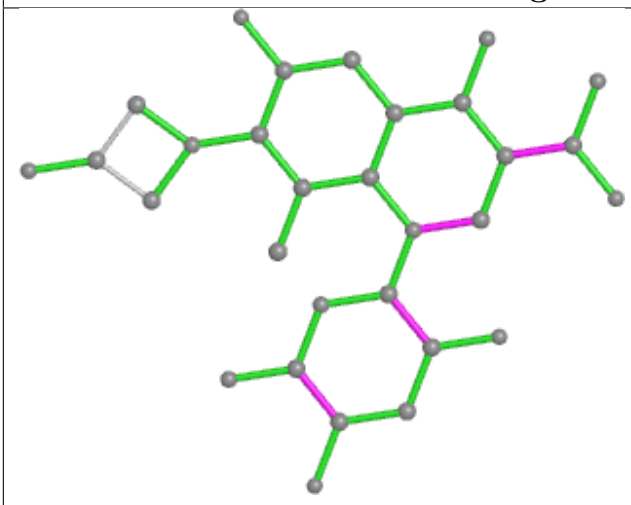


Torsions

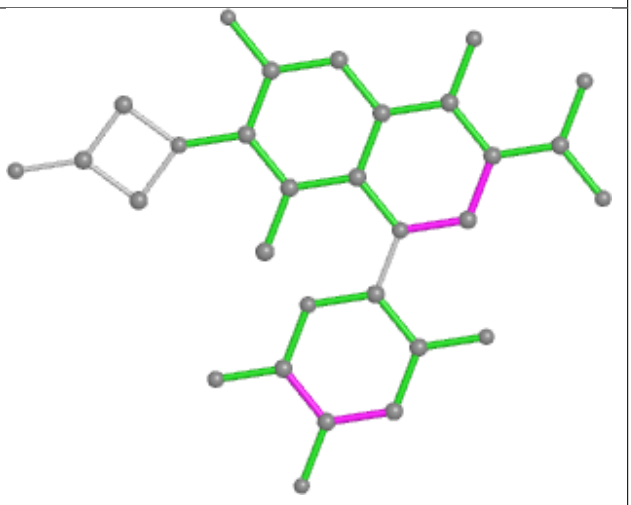


Rings

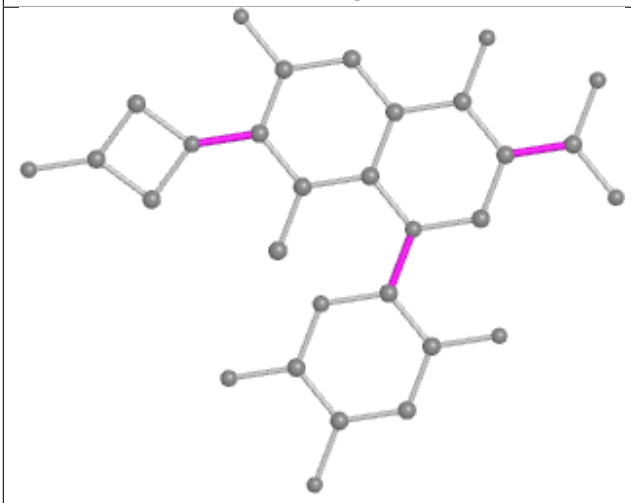
Ligand TE9 F 101



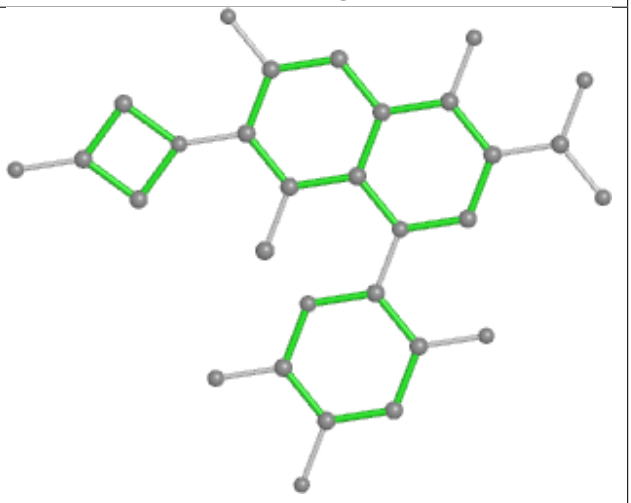
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	720/742 (97%)	0.39	48 (6%) 17 16	27, 46, 108, 155	0
1	B	720/742 (97%)	0.32	37 (5%) 28 26	27, 44, 105, 154	0
2	E	7/7 (100%)	0.10	0 100 100	42, 44, 65, 91	0
3	F	11/11 (100%)	0.08	0 100 100	46, 61, 93, 97	0
4	G	7/7 (100%)	0.06	0 100 100	37, 39, 67, 89	0
5	H	11/11 (100%)	0.18	0 100 100	48, 61, 91, 97	0
All	All	1476/1520 (97%)	0.35	85 (5%) 23 22	27, 46, 107, 155	0

The worst 5 of 85 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	572	GLY	13.1
1	A	571	PHE	12.4
1	B	571	PHE	9.7
1	A	553	GLU	9.3
1	A	549	LYS	9.1

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 monosaccharides in this entry.

6.4 Ligands (i)

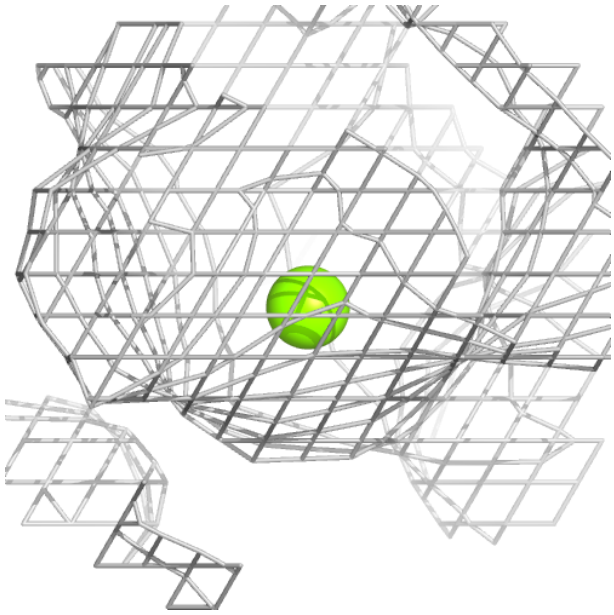
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

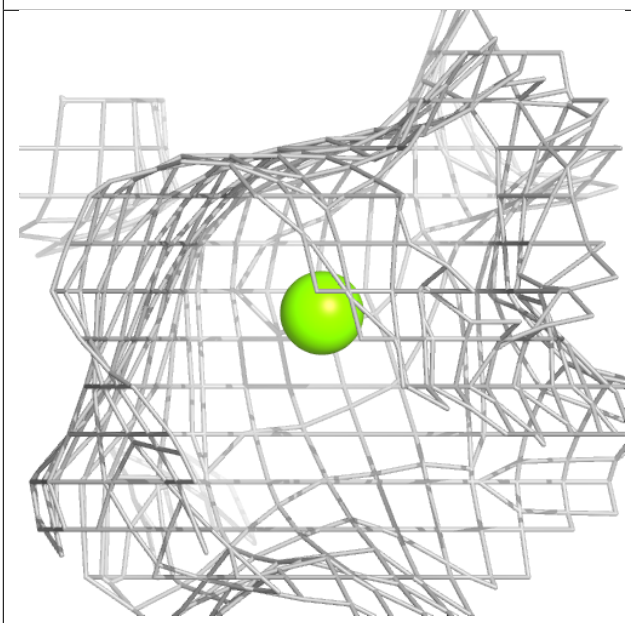
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MPD	A	1502	8/8	0.90	0.24	62,74,77,78	1
6	MPD	A	1501	8/8	0.95	0.19	46,48,48,49	1
6	MPD	B	1501	8/8	0.95	0.19	31,31,32,34	1
8	CL	A	1506	1/1	0.95	0.07	51,51,51,51	0
7	MG	A	1505	1/1	0.96	0.05	39,39,39,39	0
9	TE9	F	101	30/30	0.96	0.17	49,60,62,65	1
9	TE9	H	101	30/30	0.96	0.16	50,54,60,62	1
7	MG	B	1504	1/1	0.98	0.07	27,27,27,27	0
7	MG	A	1503	1/1	0.98	0.05	19,19,19,19	0
7	MG	B	1502	1/1	0.98	0.04	31,31,31,31	0
7	MG	B	1503	1/1	0.98	0.07	26,26,26,26	0
8	CL	B	1505	1/1	0.99	0.11	47,47,47,47	0
7	MG	A	1504	1/1	1.00	0.09	8,8,8,8	0

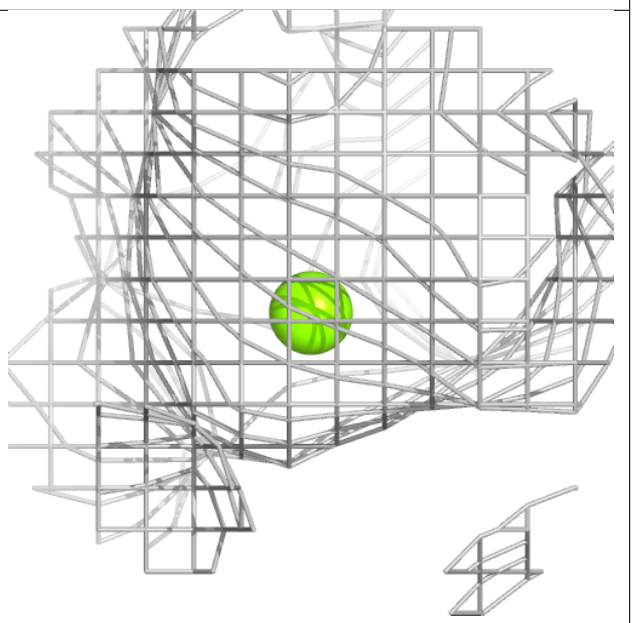
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around MG A 1505:

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

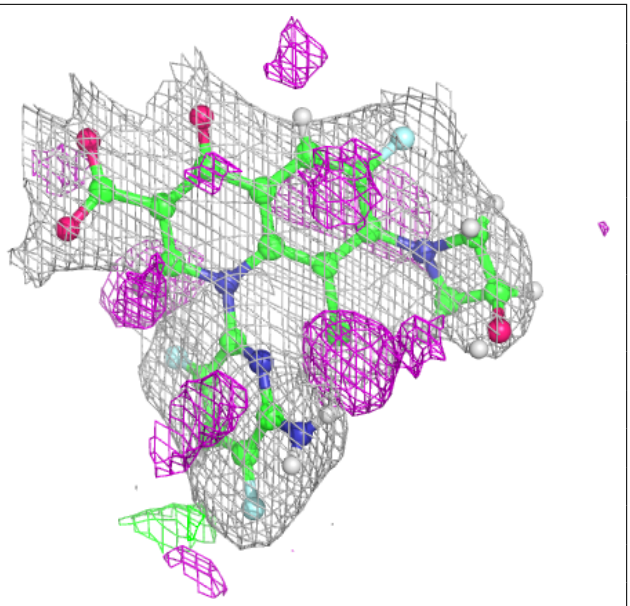


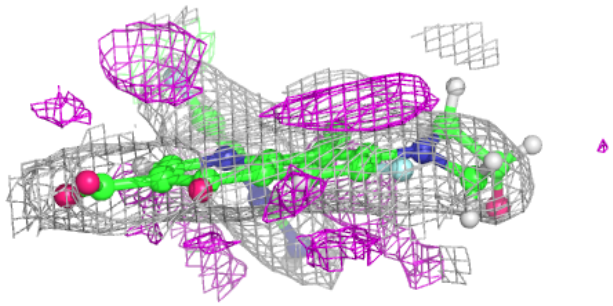


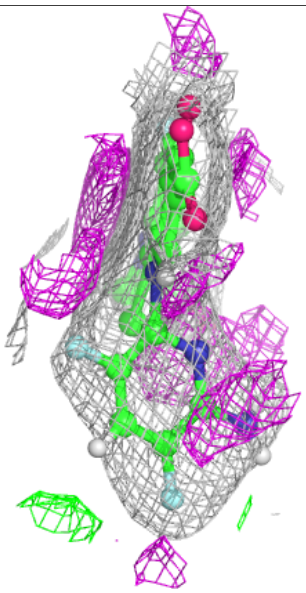


Electron density around TE9 F 101:

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

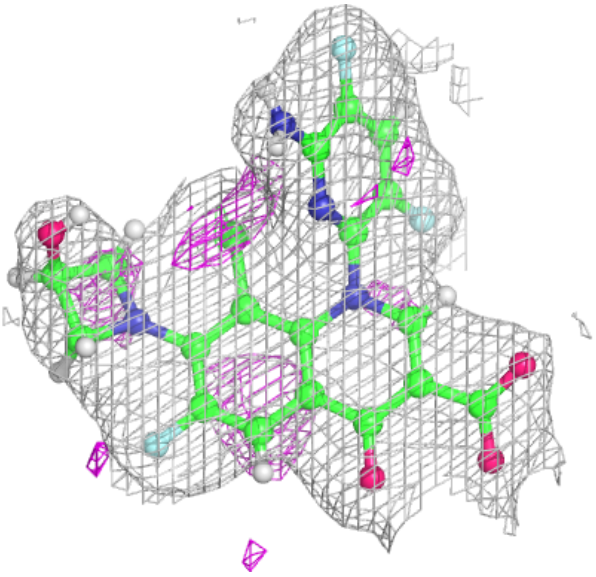


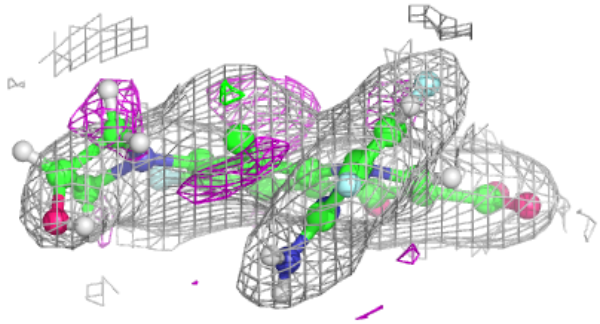


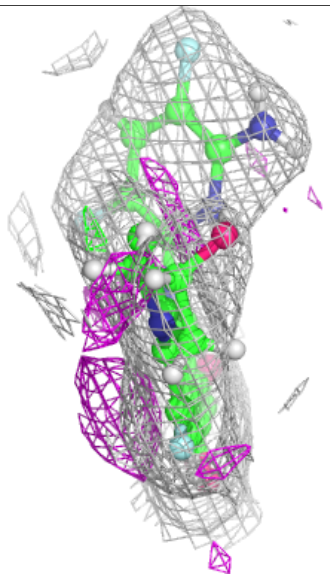


Electron density around TE9 H 101:

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

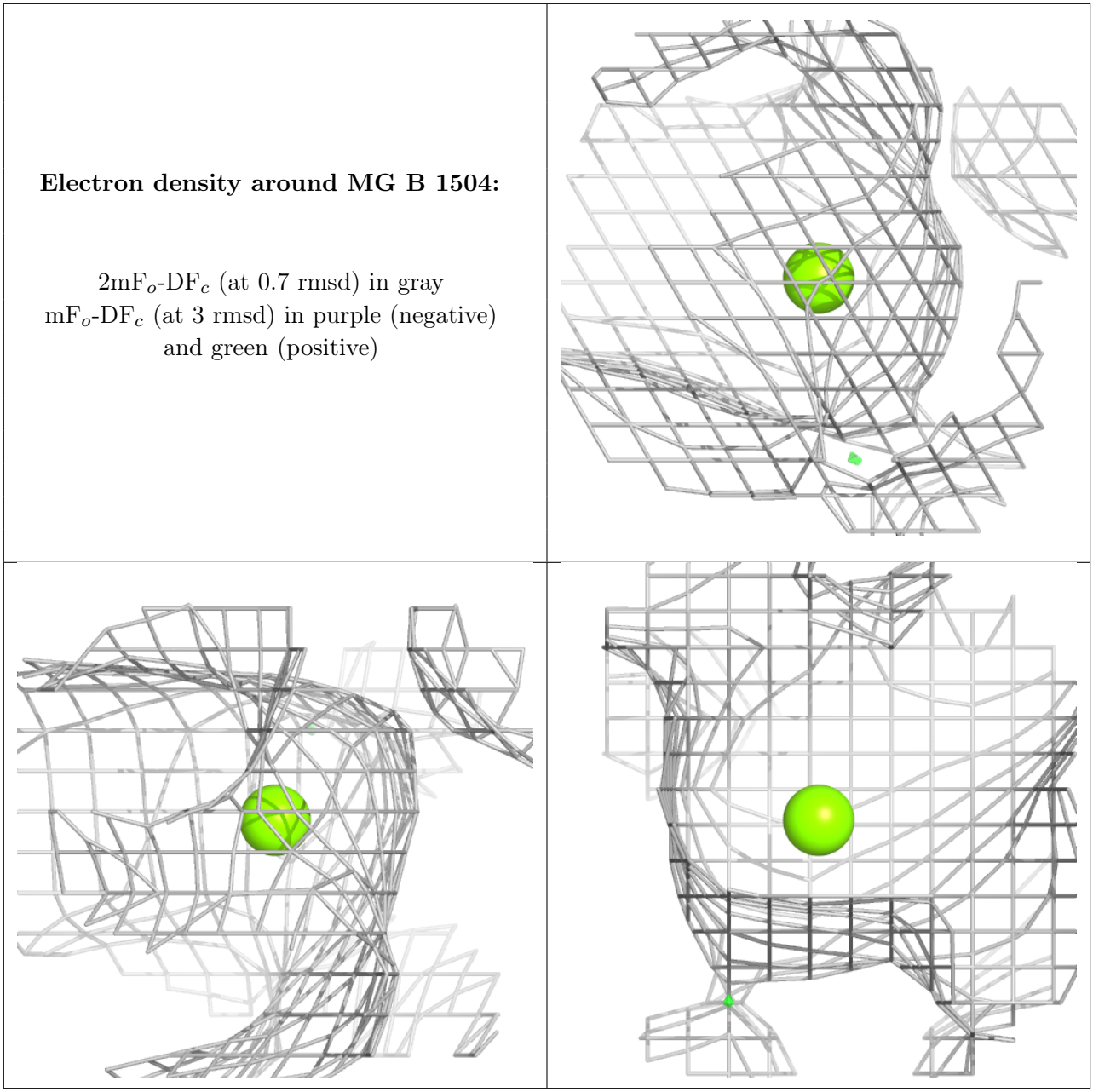






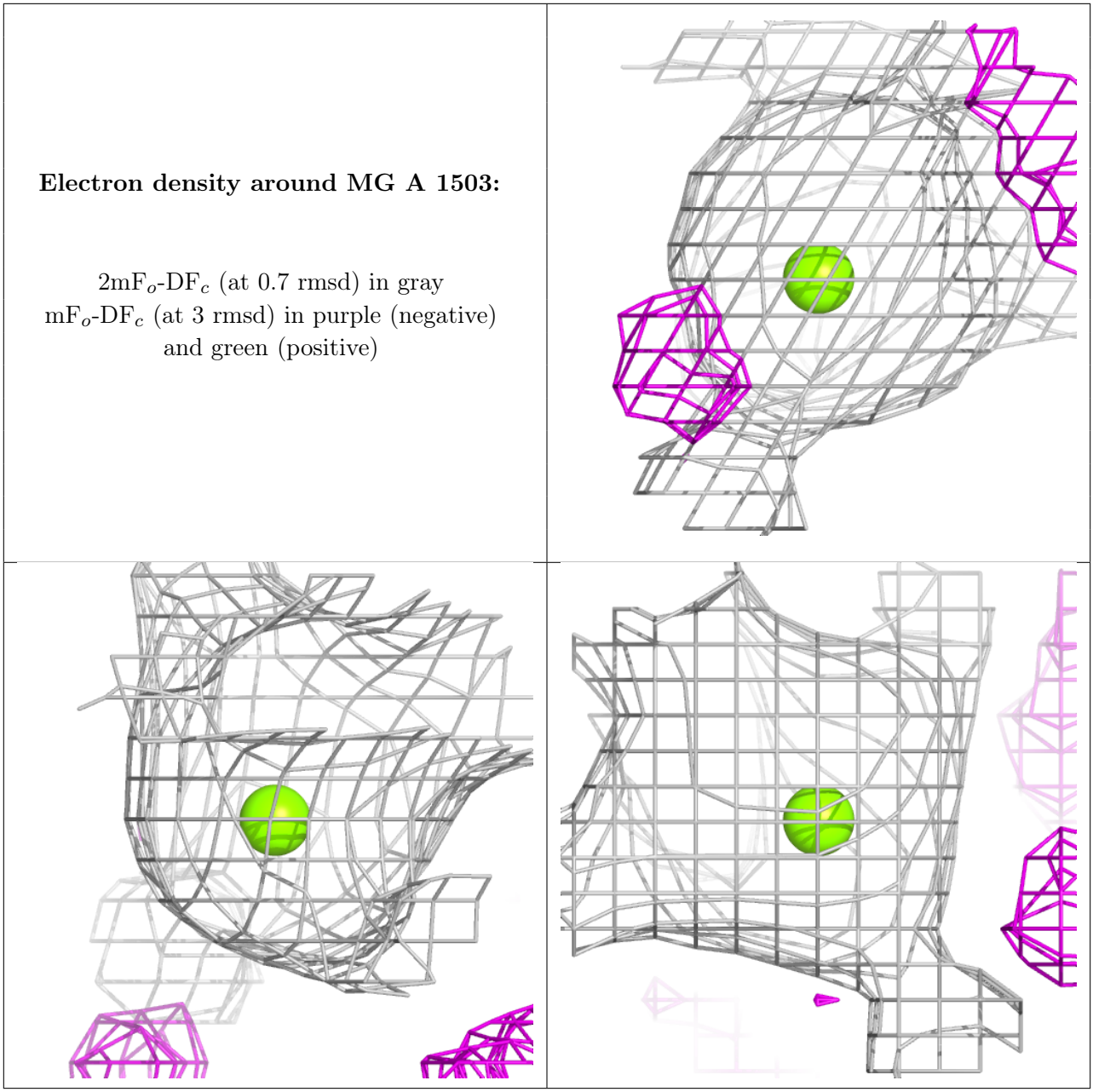
Electron density around MG B 1504:

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



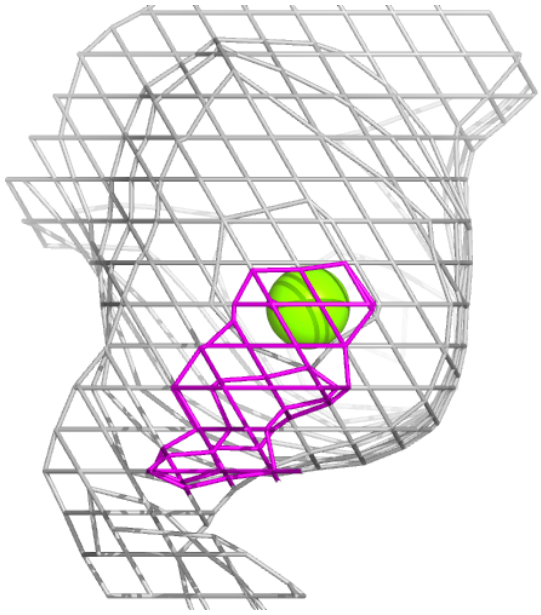
Electron density around MG A 1503:

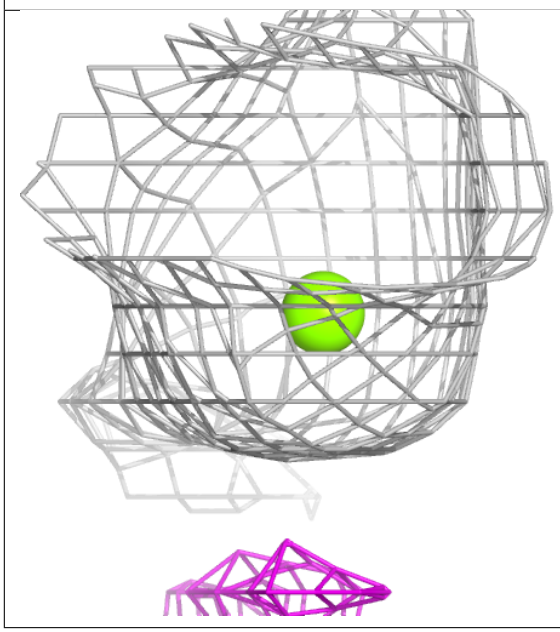
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

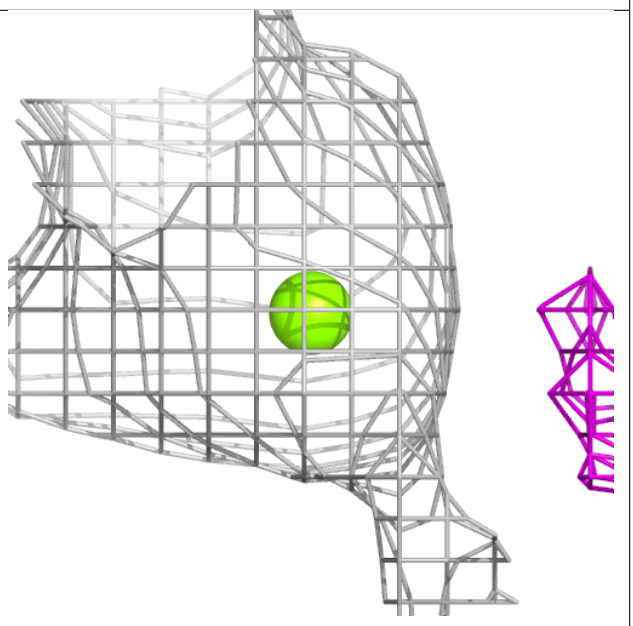


Electron density around MG B 1502:

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

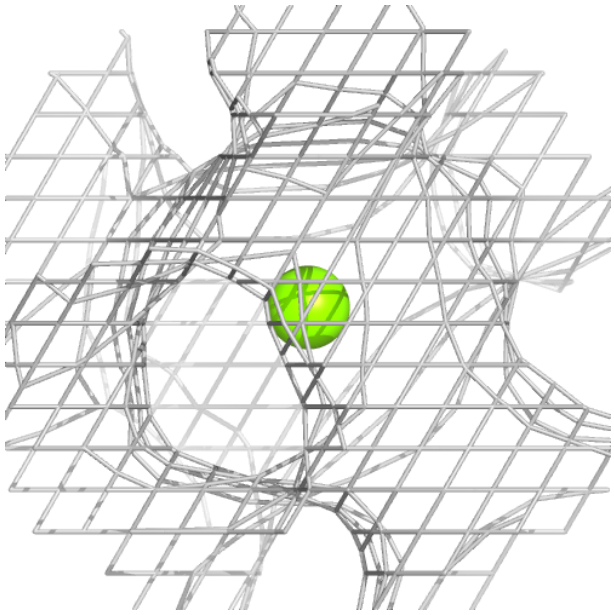


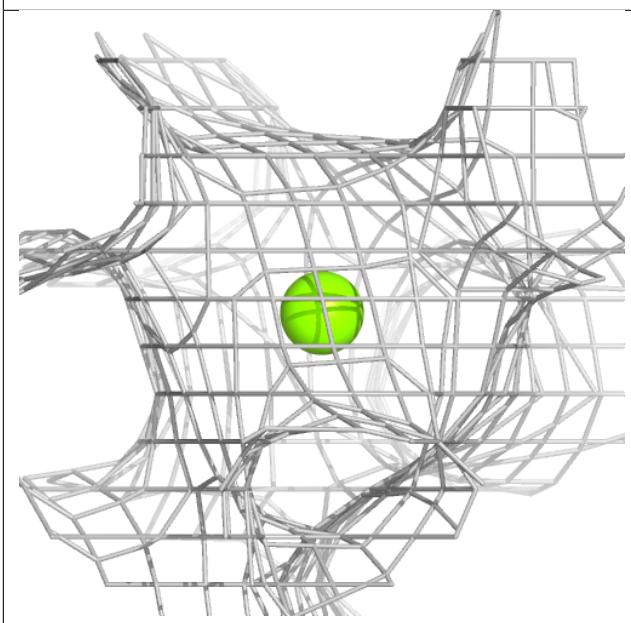


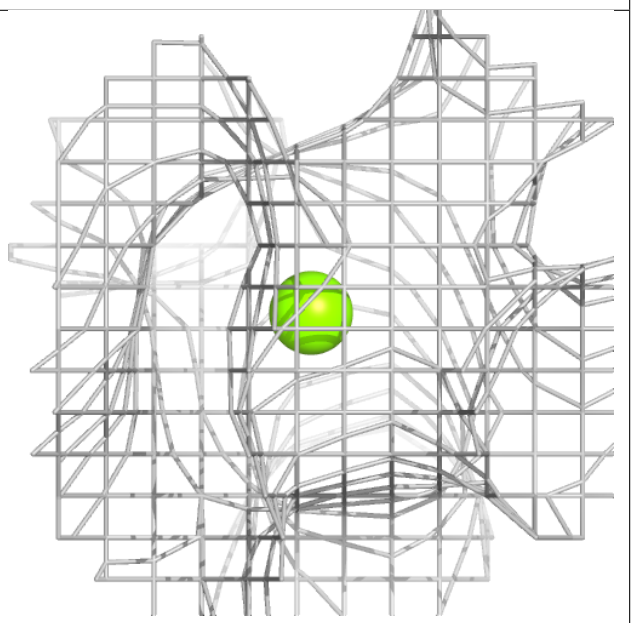


Electron density around MG B 1503:

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

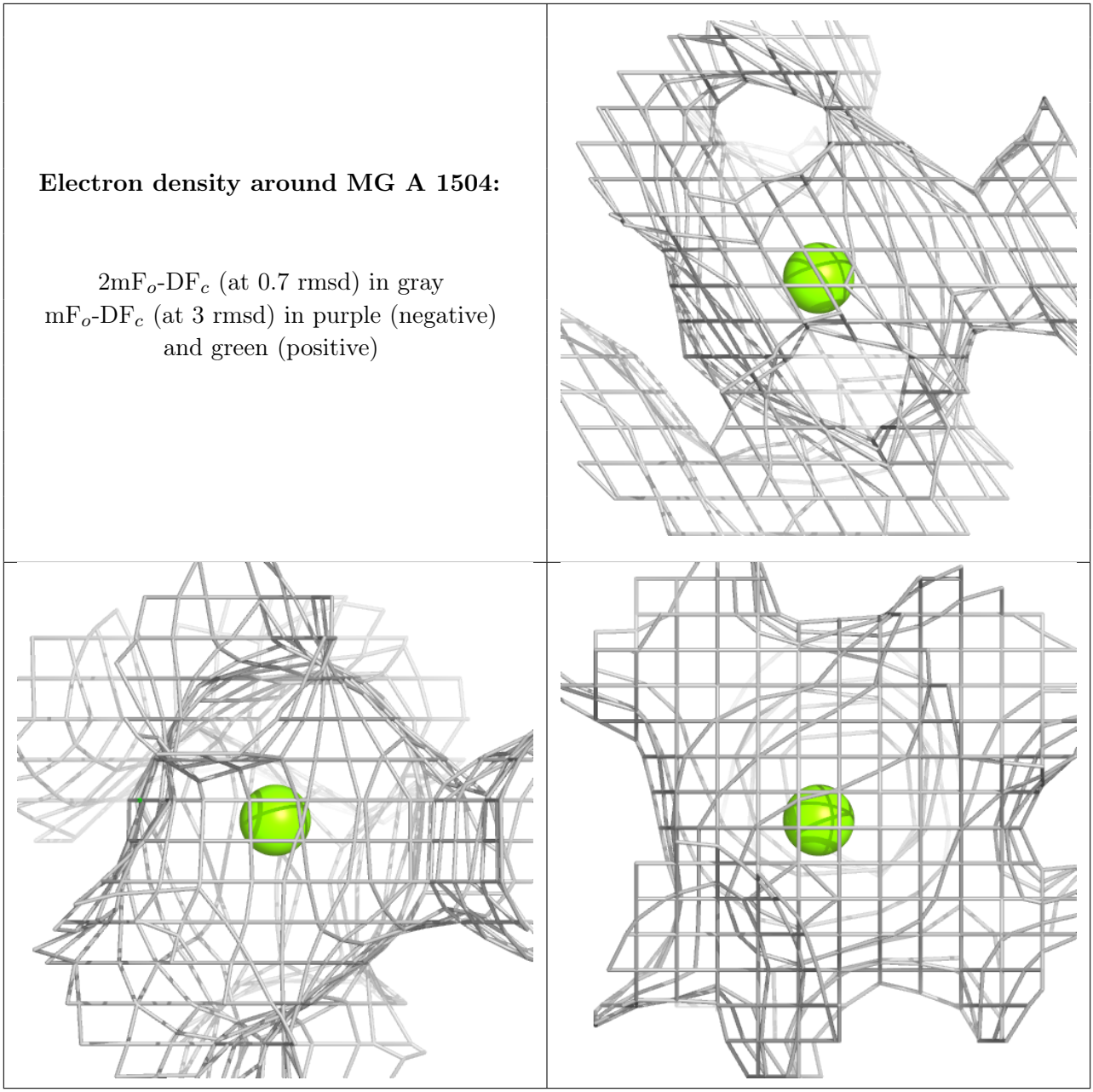






Electron density around MG A 1504:

$2mF_o$-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.