



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2025 – 04:25 PM JST

PDB ID : 8YZY / pdb\_00008zyz  
Title : STC SydA mutant - W297Y  
Authors : Fan, A.; Fan, S.; Wu, M.  
Deposited on : 2024-04-08  
Resolution : 1.73 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

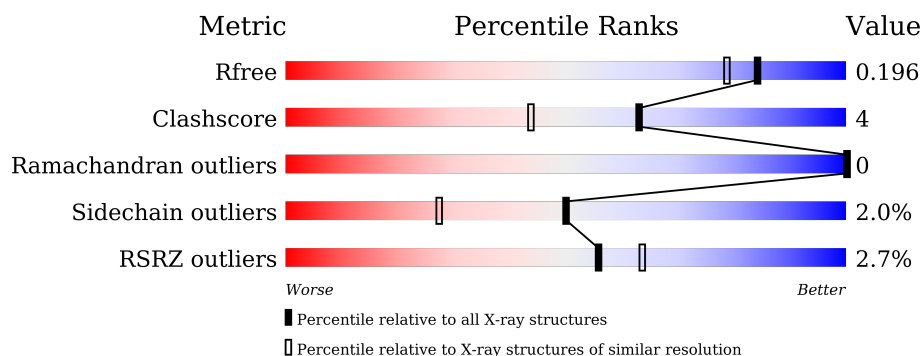
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.73 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))
$R_{free}$	164625	1043 (1.74-1.74)
Clashscore	180529	1119 (1.74-1.74)
Ramachandran outliers	177936	1112 (1.74-1.74)
Sidechain outliers	177891	1112 (1.74-1.74)
RSRZ outliers	164620	1043 (1.74-1.74)

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  $\geq 3$ , 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	307	<div> <div>91%</div> <div>8% .</div> </div>
1	B	307	<div> <div>2%</div> <div>91%</div> <div>8% .</div> </div>
1	C	307	<div> <div>2%</div> <div>87%</div> <div>12% .</div> </div>
1	D	307	<div> <div>6%</div> <div>87%</div> <div>11% ..</div> </div>

## 2 Entry composition [i](#)

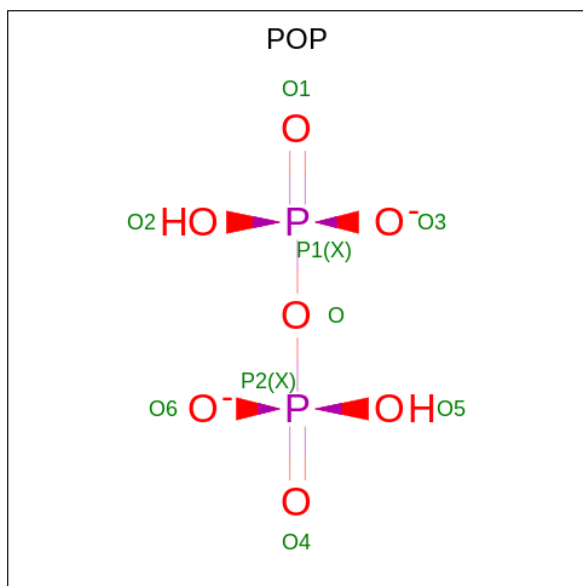
There are 4 unique types of molecules in this entry. The entry contains 10817 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SydA mutant W297Y.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	1	0
			2474	1604	405	457	8			
1	B	305	Total	C	N	O	S	0	0	0
			2476	1605	405	459	7			
1	C	305	Total	C	N	O	S	0	1	0
			2482	1608	406	460	8			
1	D	305	Total	C	N	O	S	0	0	0
			2478	1607	405	459	7			

- Molecule 2 is PYROPHOSPHATE 2- (CCD ID: POP) (formula:  $\text{H}_2\text{O}_7\text{P}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			9	7	2		
2	B	1	Total	O	P	0	0
			9	7	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	P	0	0
			9	7	2		
2	D	1	Total	O	P	0	0
			9	7	2		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	263	Total	O	0	0
			263	263		
4	B	225	Total	O	0	0
			225	225		
4	C	203	Total	O	0	0
			203	203		
4	D	172	Total	O	0	0
			172	172		

### 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.

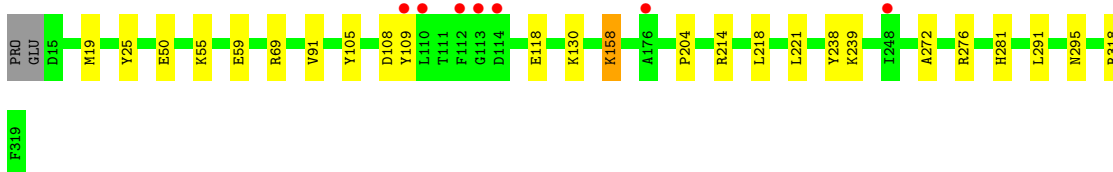
#### • Molecule 1: SydA mutant W297Y

Chain A: 




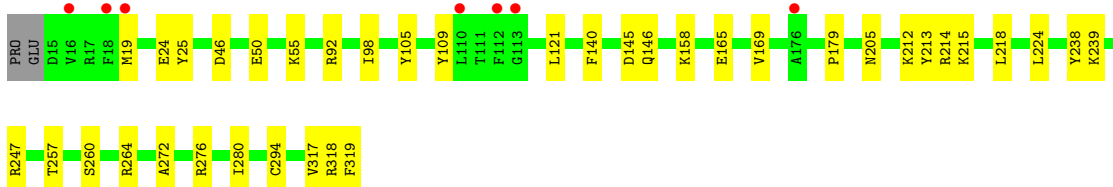
#### • Molecule 1: SydA mutant W297Y

Chain B: 




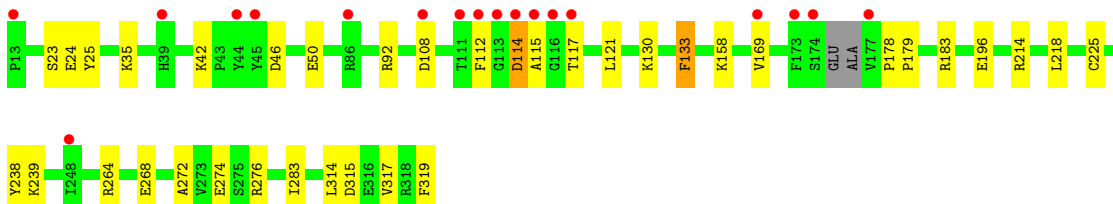
#### • Molecule 1: SydA mutant W297Y

Chain C: 



#### • Molecule 1: SydA mutant W297Y

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.89Å 127.64Å 89.14Å 90.00° 93.47° 90.00°	Depositor
Resolution (Å)	27.30 – 1.73 27.30 – 1.73	Depositor EDS
% Data completeness (in resolution range)	94.2 (27.30-1.73) 94.2 (27.30-1.73)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 1.74Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.155 , 0.192 0.161 , 0.196	Depositor DCC
$R_{free}$ test set	119860 reflections (1.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.4	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 43.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10817	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, POP

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	0.57	0/2541	0.71	0/3458
1	B	0.54	0/2543	0.69	0/3461
1	C	0.52	0/2549	0.66	0/3469
1	D	0.51	0/2545	0.67	0/3462
All	All	0.54	0/10178	0.68	0/13850

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	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	2474	0	2423	17	1
1	B	2476	0	2423	14	0
1	C	2482	0	2427	25	1
1	D	2478	0	2426	23	0
2	A	9	0	0	0	0
2	B	9	0	0	0	0
2	C	9	0	0	0	0
2	D	9	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	263	0	0	7	1
4	B	225	0	0	2	1
4	C	203	0	0	5	0
4	D	172	0	0	2	0
All	All	10817	0	9699	76	2

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:ALA:HA	1:D:130:LYS:HD2	1.35	1.05
1:D:46:ASP:OD2	1:D:92:ARG:NH1	2.15	0.80
1:B:69:ARG:NH1	1:B:108:ASP:OD2	2.22	0.73
1:D:35:LYS:NZ	1:D:274:GLU:OE1	2.19	0.73
1:C:146:GLN:NE2	4:C:502:HOH:O	2.24	0.68
1:B:50:GLU:H	1:B:50:GLU:CD	1.97	0.68
1:D:264:ARG:O	1:D:268:GLU:HG3	1.96	0.65
1:D:92:ARG:NH2	4:D:501:HOH:O	2.29	0.65
1:C:50:GLU:H	1:C:50:GLU:CD	2.02	0.63
1:C:214:ARG:HG2	1:C:218:LEU:HD13	1.80	0.62
1:C:146:GLN:NE2	4:C:505:HOH:O	2.33	0.61
1:A:224:LEU:HG	1:A:280:ILE:HD12	1.82	0.60
1:C:260:SER:OG	1:C:264:ARG:HD2	2.00	0.60
1:C:25:TYR:CE2	1:C:238:TYR:HB2	2.37	0.60
1:C:105:TYR:O	1:C:109:TYR:HB3	2.03	0.59
1:A:264:ARG:NH1	4:A:502:HOH:O	2.36	0.58
1:B:318:ARG:NH1	4:B:501:HOH:O	2.37	0.57
1:A:16:VAL:HG23	1:A:17:ARG:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:TYR:O	1:B:109:TYR:HB3	2.06	0.56
1:D:114:ASP:O	1:D:117:THR:OG1	2.14	0.53
1:B:214:ARG:HG2	1:B:218:LEU:HD22	1.91	0.53
1:A:35:LYS:HE3	4:A:715:HOH:O	2.07	0.53
1:D:214:ARG:HG2	1:D:218:LEU:HD13	1.90	0.53
1:D:112:PHE:HB3	1:D:115:ALA:CB	2.40	0.52
1:C:214:ARG:O	1:C:218:LEU:HB2	2.11	0.51
1:C:247:ARG:NE	4:C:507:HOH:O	2.41	0.51
1:C:260:SER:OG	1:C:264:ARG:NH1	2.39	0.51
1:C:145:ASP:HB3	1:D:121:LEU:HD11	1.92	0.51
1:B:25:TYR:CE2	1:B:238:TYR:HB2	2.47	0.49
1:C:50:GLU:CD	1:C:50:GLU:N	2.65	0.49
1:D:112:PHE:CE2	1:D:133:PHE:HE2	2.31	0.48
1:B:218:LEU:HD12	1:B:221:LEU:CD1	2.44	0.48
1:B:91:VAL:HG21	1:B:204:PRO:HB3	1.96	0.48
1:D:112:PHE:HB3	1:D:115:ALA:HB3	1.96	0.47
1:A:55:LYS:HE3	4:A:606:HOH:O	2.15	0.47
1:C:146:GLN:CD	4:C:505:HOH:O	2.53	0.47
1:A:180:ASP:HB2	4:A:591:HOH:O	2.14	0.46
1:B:281:HIS:ND1	1:B:291:LEU:HD11	2.30	0.46
1:A:279:GLU:HG3	4:B:520:HOH:O	2.15	0.46
1:B:281:HIS:HE1	1:B:295:ASN:OD1	1.98	0.46
1:A:224:LEU:HG	1:A:280:ILE:CD1	2.45	0.46
1:D:317:VAL:HG23	1:D:319:PHE:HD2	1.79	0.46
1:C:212:LYS:HE2	1:C:213:TYR:CE1	2.51	0.46
1:D:112:PHE:CE2	1:D:133:PHE:CE2	3.04	0.46
1:C:179:PRO:O	1:C:257:THR:O	2.34	0.45
1:C:214:ARG:NE	1:D:169:VAL:HG23	2.32	0.45
1:B:55:LYS:NZ	1:B:59:GLU:OE2	2.50	0.44
1:D:108:ASP:HB3	1:D:112:PHE:CD2	2.53	0.44
1:C:317:VAL:HG23	1:C:319:PHE:HD2	1.83	0.44
1:A:112:PHE:HB2	4:A:664:HOH:O	2.18	0.44
1:A:17:ARG:HG2	1:A:261:SER:HA	1.99	0.44
1:D:42:LYS:HA	1:D:42:LYS:HD3	1.90	0.43
1:A:27:ALA:O	1:A:31:ARG:HG2	2.19	0.43
1:B:118:GLU:OE2	1:B:130:LYS:HE3	2.19	0.43
1:D:283:ILE:HD13	1:D:283:ILE:HG21	1.77	0.43
1:D:178:PRO:HA	1:D:179:PRO:HD2	1.90	0.43
1:C:46:ASP:OD2	1:C:92:ARG:NH1	2.46	0.42
1:C:165:GLU:O	1:C:169:VAL:HG13	2.19	0.42
1:D:272:ALA:O	1:D:276:ARG:HG2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:ASP:OD1	1:D:315:ASP:N	2.52	0.42
1:A:55:LYS:O	1:A:59:GLU:HG3	2.19	0.42
1:C:224:LEU:HD21	1:C:294[B]:CYS:SG	2.60	0.42
1:C:280:ILE:HG21	1:C:294[B]:CYS:SG	2.60	0.42
1:D:196:GLU:HG3	1:D:225:CYS:SG	2.59	0.42
1:A:25:TYR:CE2	1:A:238:TYR:HB2	2.55	0.41
1:C:272:ALA:O	1:C:276:ARG:HG2	2.20	0.41
1:D:25:TYR:CE2	1:D:238:TYR:HB2	2.55	0.41
1:D:314:LEU:HB2	4:D:520:HOH:O	2.19	0.41
1:B:272:ALA:O	1:B:276:ARG:HG2	2.20	0.41
1:A:105:TYR:O	1:A:109:TYR:HB3	2.21	0.41
1:A:307:ARG:NH1	4:A:508:HOH:O	2.48	0.41
1:C:205:ASN:ND2	4:C:511:HOH:O	2.46	0.41
1:A:158:LYS:HB2	1:B:158:LYS:HB2	2.03	0.41
1:A:215:LYS:HE3	4:A:583:HOH:O	2.20	0.40
1:C:121:LEU:HD23	1:C:121:LEU:HA	1.89	0.40
1:C:98:ILE:HB	1:C:140:PHE:CZ	2.57	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:709:HOH:O	4:B:548:HOH:O[1_455]	1.72	0.48
1:A:264:ARG:NH2	1:C:24:GLU:OE2[2_555]	2.14	0.06

## 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	303/307 (99%)	301 (99%)	2 (1%)	0	100	100
1	B	303/307 (99%)	302 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	304/307 (99%)	302 (99%)	2 (1%)	0	100	100
1	D	301/307 (98%)	295 (98%)	6 (2%)	0	100	100
All	All	1211/1228 (99%)	1200 (99%)	11 (1%)	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	267/269 (99%)	263 (98%)	4 (2%)	60	42
1	B	267/269 (99%)	264 (99%)	3 (1%)	70	55
1	C	268/269 (100%)	262 (98%)	6 (2%)	47	23
1	D	268/269 (100%)	260 (97%)	8 (3%)	36	13
All	All	1070/1076 (99%)	1049 (98%)	21 (2%)	50	27

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ARG
1	A	158	LYS
1	A	239	LYS
1	A	318	ARG
1	B	19	MET
1	B	158	LYS
1	B	239	LYS
1	C	19	MET
1	C	55	LYS
1	C	158	LYS
1	C	215	LYS
1	C	239	LYS
1	C	318	ARG
1	D	23	SER

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Mol	Chain	Res	Type
1	D	24	GLU
1	D	50	GLU
1	D	114	ASP
1	D	133	PHE
1	D	158	LYS
1	D	183	ARG
1	D	239	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	39	HIS
1	B	281	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 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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
2	POP	D	401	3	6,8,8	0.75	0	13,13,13	1.24	2 (15%)
2	POP	A	401	3	6,8,8	0.98	0	13,13,13	1.08	1 (7%)
2	POP	B	401	3	6,8,8	0.61	0	13,13,13	1.36	2 (15%)
2	POP	C	401	3	6,8,8	0.93	0	13,13,13	1.40	2 (15%)

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
2	POP	D	401	3	-	0/6/6/6	-
2	POP	A	401	3	-	0/6/6/6	-
2	POP	B	401	3	-	0/6/6/6	-
2	POP	C	401	3	-	0/6/6/6	-

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	POP	P2-O-P1	-3.89	119.46	132.83
2	B	401	POP	P2-O-P1	-3.02	122.46	132.83
2	A	401	POP	P2-O-P1	-2.85	123.04	132.83
2	D	401	POP	O5-P2-O	2.28	112.28	104.64
2	B	401	POP	O2-P1-O	2.24	112.15	104.64
2	D	401	POP	P2-O-P1	-2.19	125.30	132.83
2	C	401	POP	O3-P1-O	2.14	111.82	104.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	304/307 (99%)	-0.32	1 (0%) 90 93	10, 25, 47, 70	1 (0%)
1	B	305/307 (99%)	-0.27	7 (2%) 61 67	14, 25, 53, 84	0
1	C	305/307 (99%)	-0.11	7 (2%) 61 67	14, 30, 54, 78	1 (0%)
1	D	305/307 (99%)	0.02	18 (5%) 29 36	15, 30, 62, 98	0
All	All	1219/1228 (99%)	-0.17	33 (2%) 56 63	10, 27, 54, 98	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	112	PHE	7.5
1	A	16	VAL	4.8
1	D	115	ALA	4.3
1	B	110	LEU	4.1
1	D	45	TYR	3.6
1	C	112	PHE	3.5
1	D	44	TYR	3.1
1	D	117	THR	3.1
1	D	13	PRO	3.1
1	D	86	ARG	3.0
1	B	112	PHE	3.0
1	D	114	ASP	2.9
1	D	169	VAL	2.7
1	D	111	THR	2.6
1	B	109	TYR	2.6
1	D	173	PHE	2.5
1	B	248	ILE	2.5
1	C	110	LEU	2.5
1	C	176	ALA	2.4
1	B	113	GLY	2.4
1	B	114	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	108	ASP	2.4
1	D	177	VAL	2.4
1	C	113	GLY	2.4
1	D	248	ILE	2.3
1	D	174	SER	2.2
1	C	16	VAL	2.2
1	D	39	HIS	2.2
1	C	18	PHE	2.1
1	C	19	MET	2.1
1	D	113	GLY	2.1
1	D	116	GLY	2.0
1	B	176	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	POP	D	401	9/9	0.95	0.07	23,27,29,33	0
3	MG	D	403	1/1	0.95	0.06	29,29,29,29	0
3	MG	C	403	1/1	0.96	0.05	25,25,25,25	0
3	MG	B	403	1/1	0.96	0.04	22,22,22,22	0
3	MG	A	403	1/1	0.98	0.03	16,16,16,16	0
3	MG	A	402	1/1	0.98	0.04	22,22,22,22	0
3	MG	B	402	1/1	0.99	0.05	17,17,17,17	0
2	POP	A	401	9/9	0.99	0.04	15,17,19,21	0
3	MG	C	402	1/1	0.99	0.03	18,18,18,18	0
2	POP	B	401	9/9	0.99	0.03	17,18,20,22	0
3	MG	D	402	1/1	0.99	0.03	22,22,22,22	0

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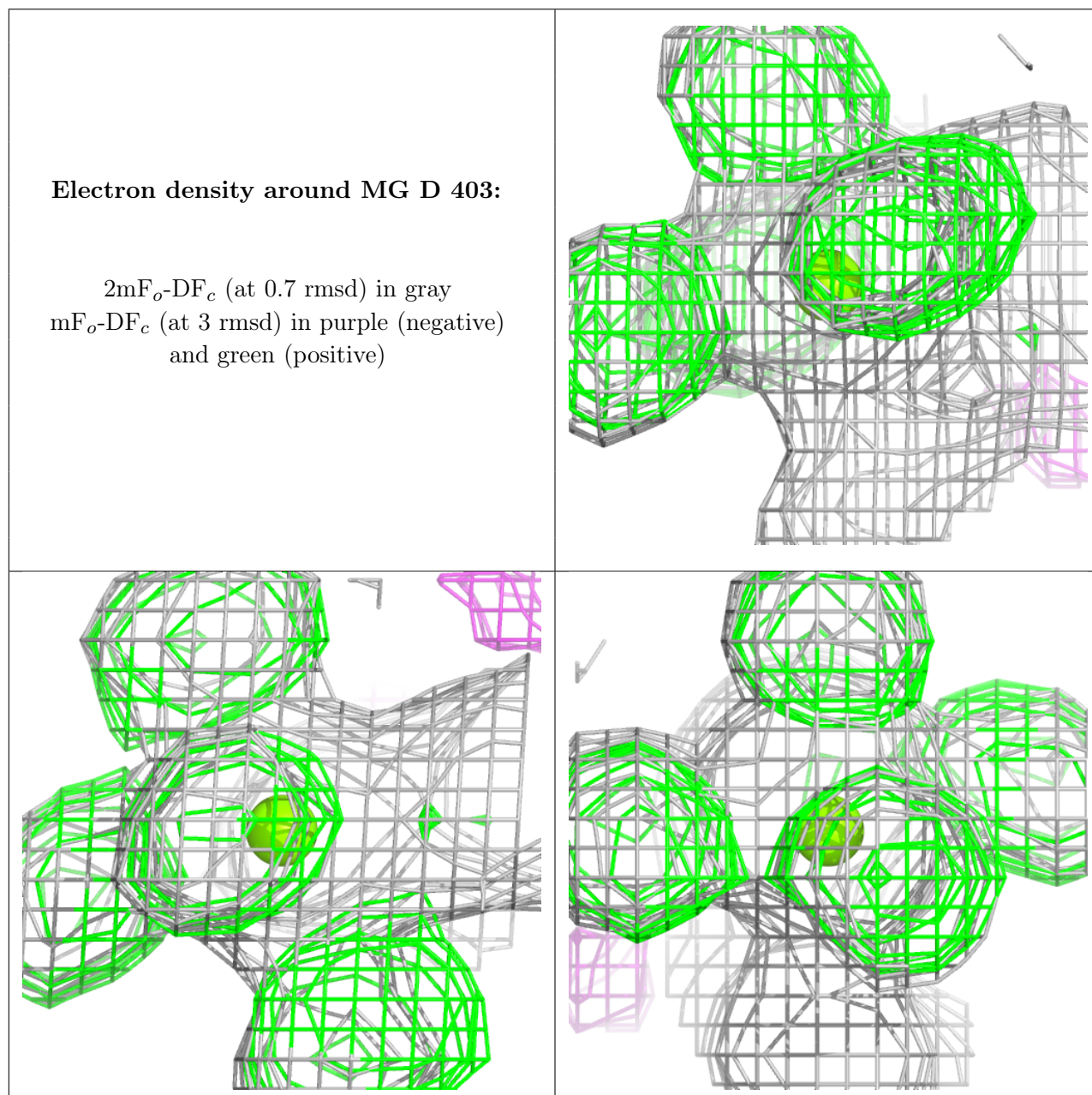
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	POP	C	401	9/9	0.99	0.04	16,19,21,22	0

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.

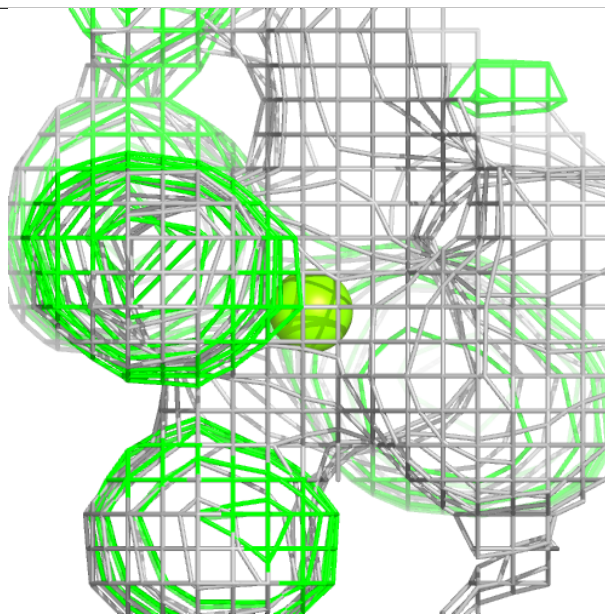
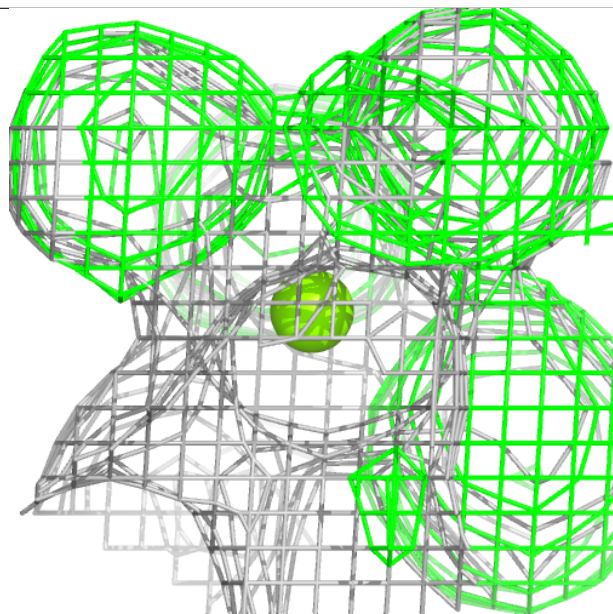
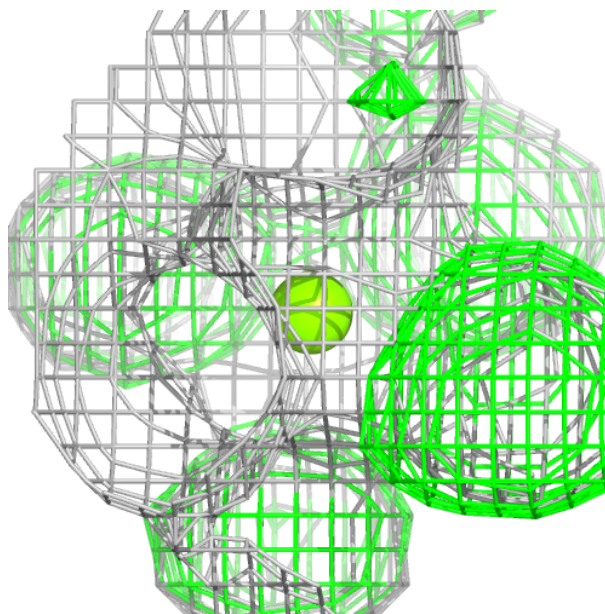
**Electron density around MG D 403:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



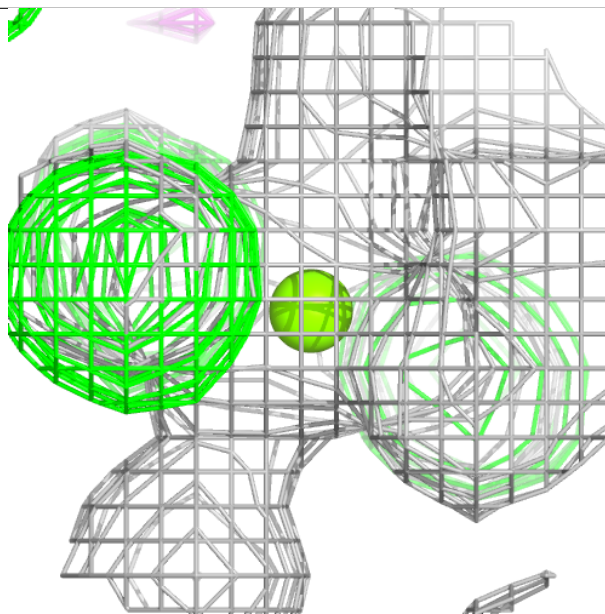
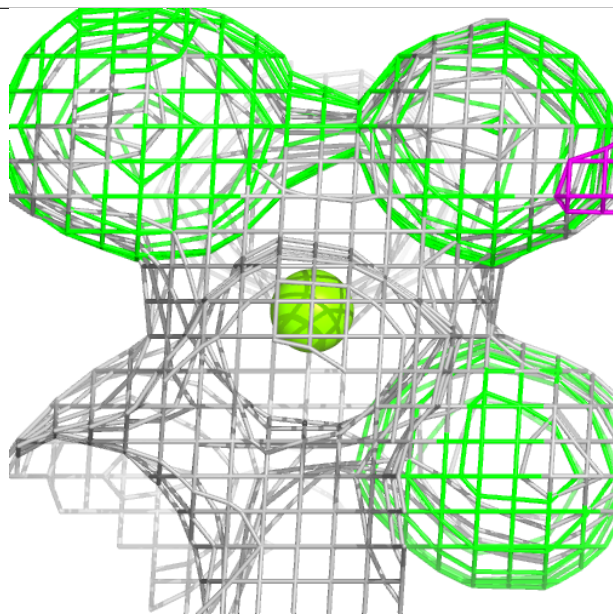
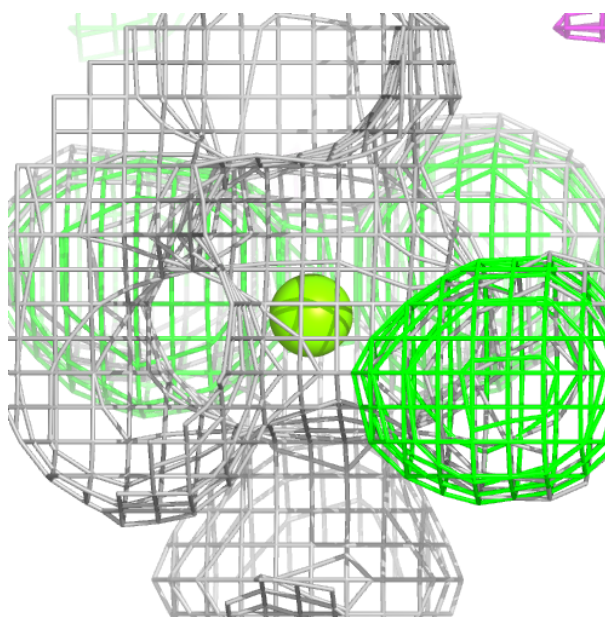
**Electron density around MG C 403:**

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



**Electron density around MG B 403:**

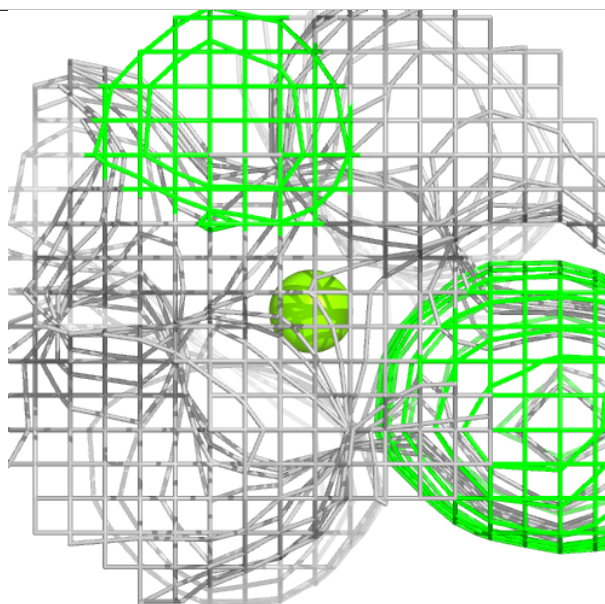
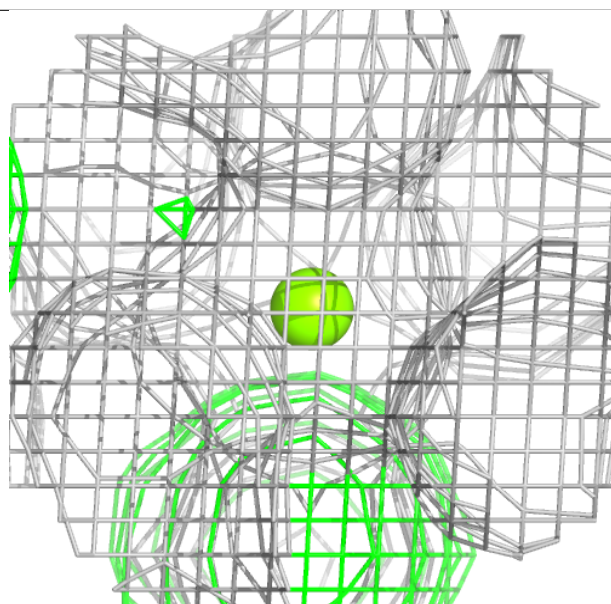
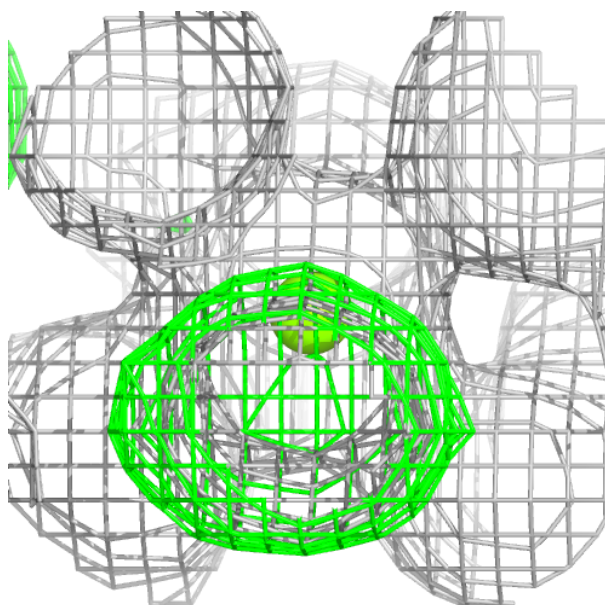
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





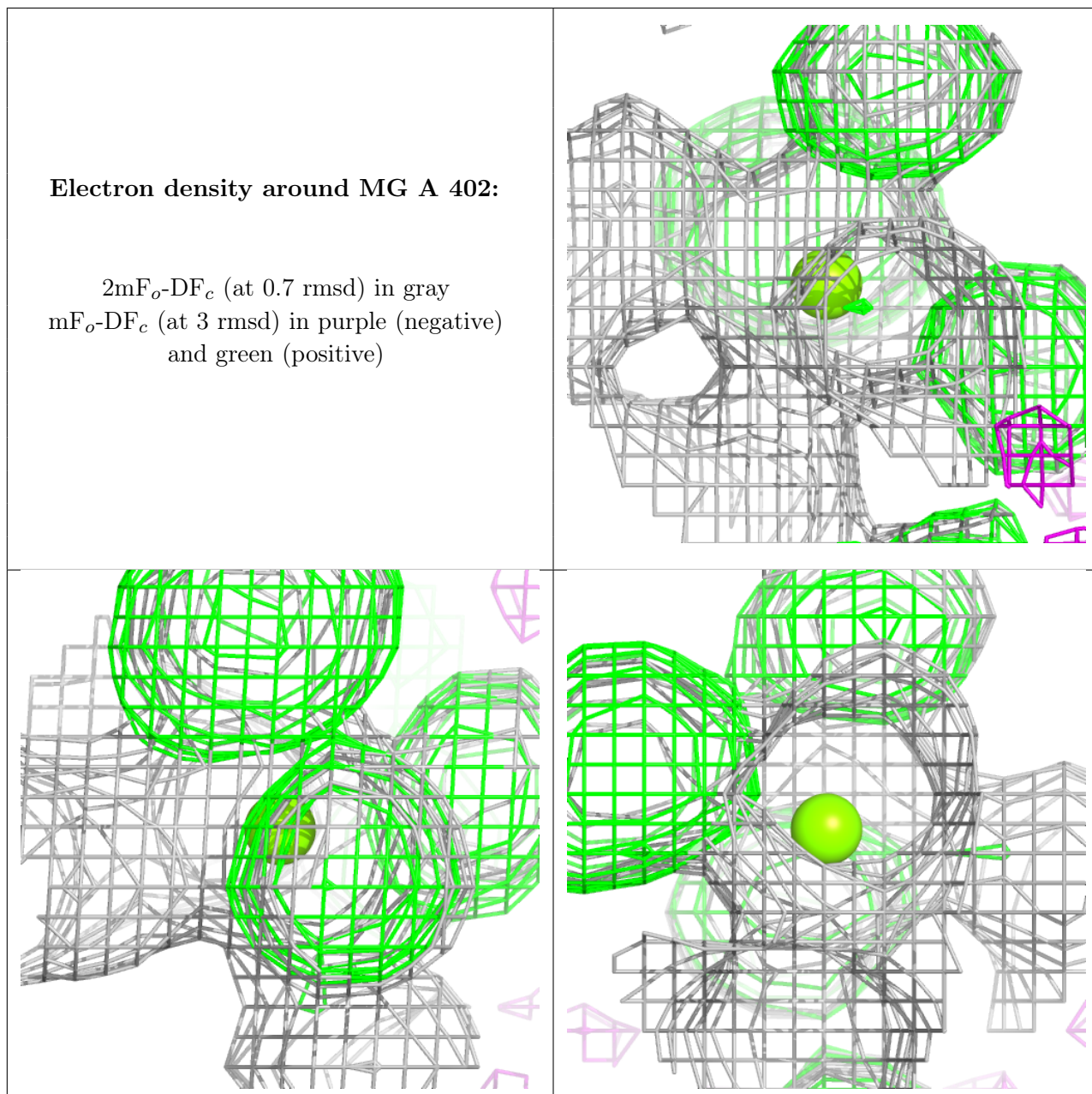
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



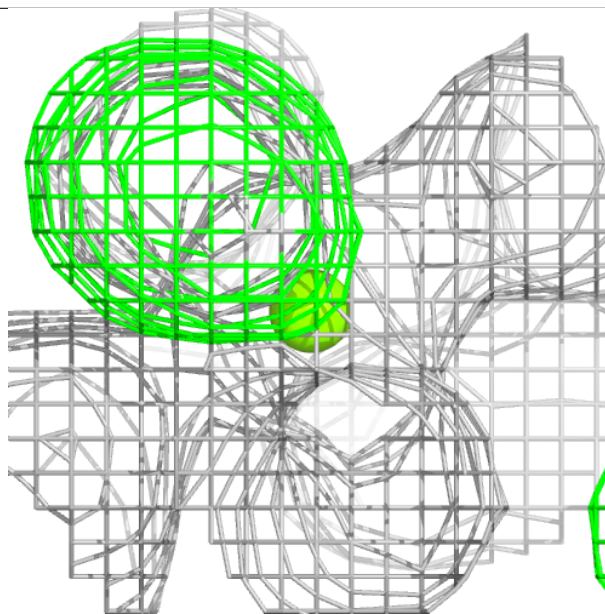
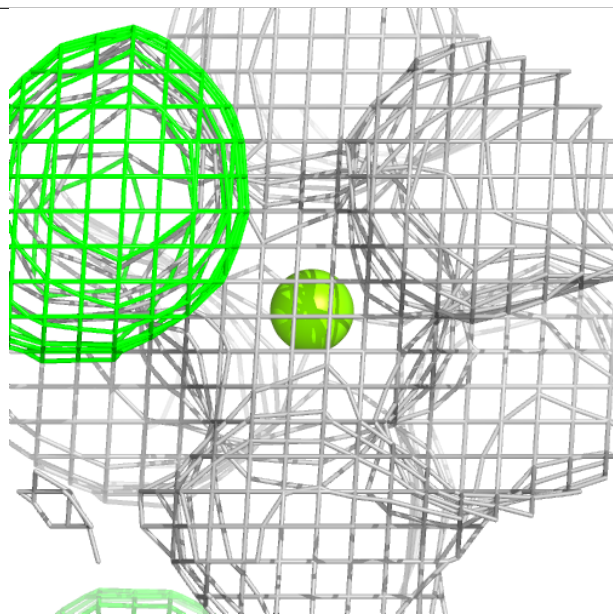
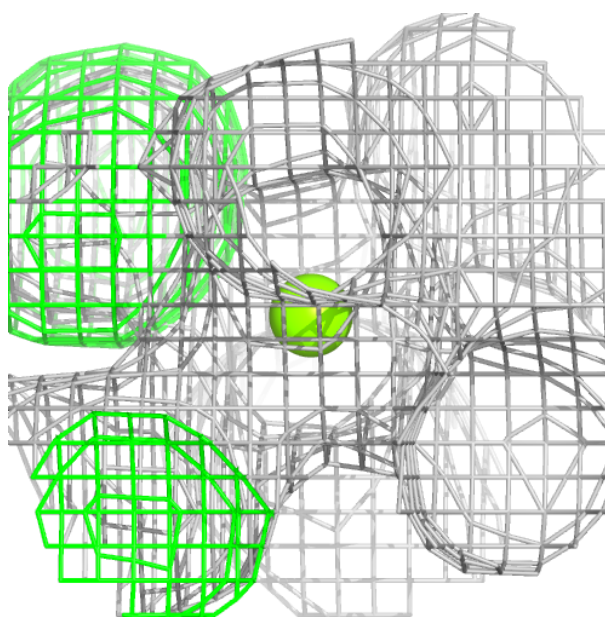
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and green (positive)



**Electron density around MG B 402:**

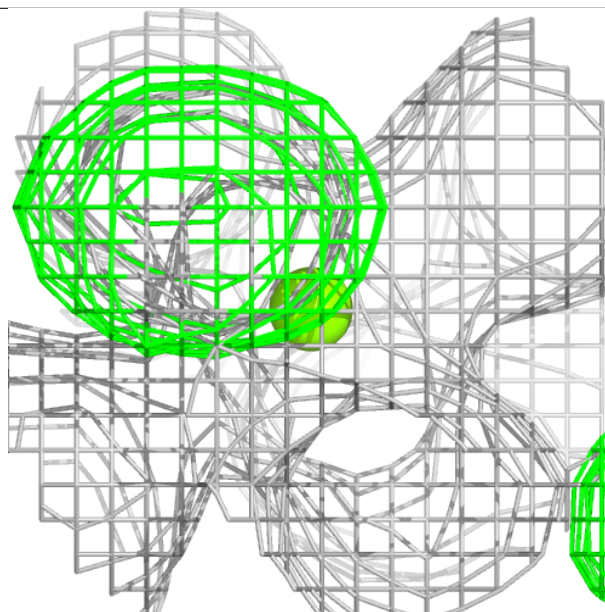
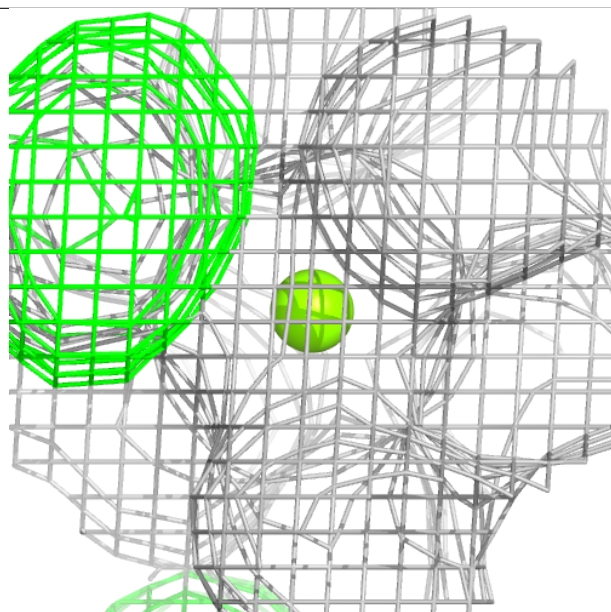
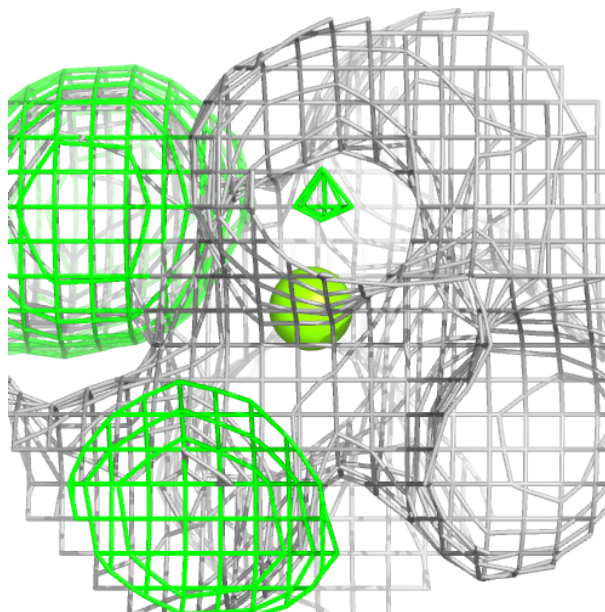
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





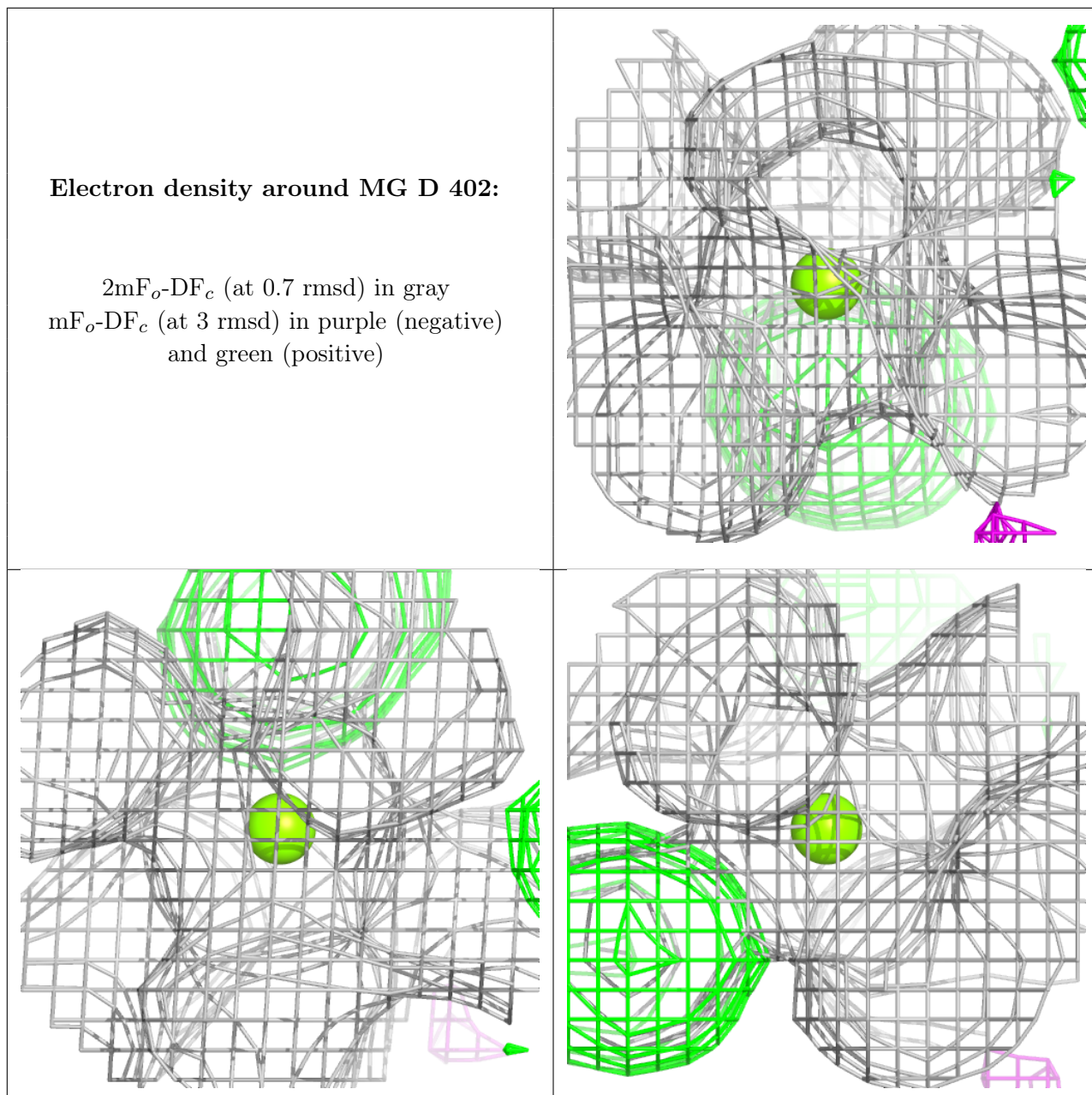
**Electron density around MG C 402:**

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



**Electron density around MG D 402:**

$2mF_o-DF_c$  (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.