W O R L D W I D E

wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2023 – 05:36 AM EDT

PDB ID	:	7KR8
Title	:	Dihydrodipicolinate synthase (DHDPS) from C.jejuni, H56A mutant with pyruvate bound in the active site
Authors	:	Saran, S.; Sanders, D.A.R.
Deposited on	:	2020-11-19
Resolution	:	2.12 Å(reported)

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

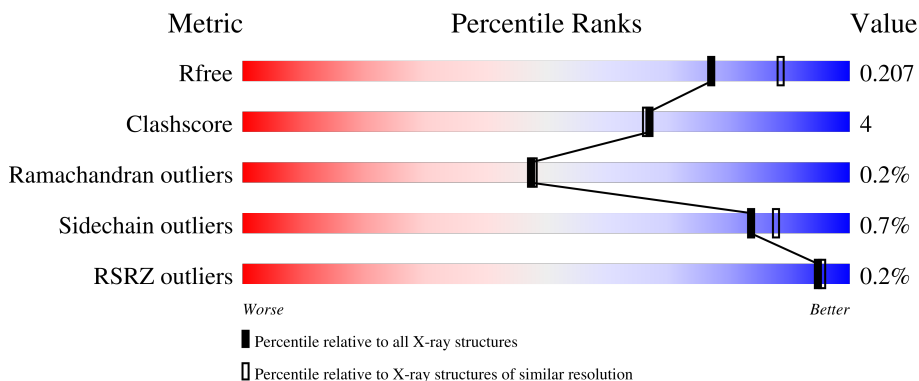|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.12 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	Percentile Ranks	Value
Rfree		0.207
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		0.7%
RSRZ outliers		0.2%

Worse　　　　　　　　　　　　　　　　　*Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	310	90%　　　　　　　5% · ·
1	B	310	87%　　　　　　　8%　5%
1	C	310	88%　　　　　　　7%　5%
1	D	310	84%　　　　　　　11%　5%
1	E	310	89%　　　　　　　6%　5%

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Mol	Chain	Length	Quality of chain
1	F	310	88%　　　　　　　　　　　7%　5%

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	EDO	F	301	-	-	X	-
3	PGE	D	308	-	-	X	-
3	PGE	F	303	-	-	X	-
6	PEG	B	306	-	-	-	X

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 14769 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 4-hydroxy-tetrahydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	1	0
			2292	1457	381	441	13			
1	B	296	Total	C	N	O	S	0	0	0
			2257	1435	372	437	13			
1	C	296	Total	C	N	O	S	0	0	0
			2259	1436	373	437	13			
1	D	296	Total	C	N	O	S	0	0	0
			2256	1434	372	437	13			
1	E	296	Total	C	N	O	S	0	0	0
			2258	1436	372	437	13			
1	F	296	Total	C	N	O	S	0	0	0
			2252	1431	371	437	13			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q9PPB4
A	-10	ARG	-	expression tag	UNP Q9PPB4
A	-9	GLY	-	expression tag	UNP Q9PPB4
A	-8	SER	-	expression tag	UNP Q9PPB4
A	-7	HIS	-	expression tag	UNP Q9PPB4
A	-6	HIS	-	expression tag	UNP Q9PPB4
A	-5	HIS	-	expression tag	UNP Q9PPB4
A	-4	HIS	-	expression tag	UNP Q9PPB4
A	-3	HIS	-	expression tag	UNP Q9PPB4
A	-2	HIS	-	expression tag	UNP Q9PPB4
A	-1	GLY	-	expression tag	UNP Q9PPB4
A	0	SER	-	expression tag	UNP Q9PPB4
A	56	ALA	HIS	engineered mutation	UNP Q9PPB4
B	-11	MET	-	expression tag	UNP Q9PPB4
B	-10	ARG	-	expression tag	UNP Q9PPB4
B	-9	GLY	-	expression tag	UNP Q9PPB4
B	-8	SER	-	expression tag	UNP Q9PPB4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	HIS	-	expression tag	UNP Q9PPB4
B	-6	HIS	-	expression tag	UNP Q9PPB4
B	-5	HIS	-	expression tag	UNP Q9PPB4
B	-4	HIS	-	expression tag	UNP Q9PPB4
B	-3	HIS	-	expression tag	UNP Q9PPB4
B	-2	HIS	-	expression tag	UNP Q9PPB4
B	-1	GLY	-	expression tag	UNP Q9PPB4
B	0	SER	-	expression tag	UNP Q9PPB4
B	56	ALA	HIS	engineered mutation	UNP Q9PPB4
C	-11	MET	-	expression tag	UNP Q9PPB4
C	-10	ARG	-	expression tag	UNP Q9PPB4
C	-9	GLY	-	expression tag	UNP Q9PPB4
C	-8	SER	-	expression tag	UNP Q9PPB4
C	-7	HIS	-	expression tag	UNP Q9PPB4
C	-6	HIS	-	expression tag	UNP Q9PPB4
C	-5	HIS	-	expression tag	UNP Q9PPB4
C	-4	HIS	-	expression tag	UNP Q9PPB4
C	-3	HIS	-	expression tag	UNP Q9PPB4
C	-2	HIS	-	expression tag	UNP Q9PPB4
C	-1	GLY	-	expression tag	UNP Q9PPB4
C	0	SER	-	expression tag	UNP Q9PPB4
C	56	ALA	HIS	engineered mutation	UNP Q9PPB4
D	-11	MET	-	expression tag	UNP Q9PPB4
D	-10	ARG	-	expression tag	UNP Q9PPB4
D	-9	GLY	-	expression tag	UNP Q9PPB4
D	-8	SER	-	expression tag	UNP Q9PPB4
D	-7	HIS	-	expression tag	UNP Q9PPB4
D	-6	HIS	-	expression tag	UNP Q9PPB4
D	-5	HIS	-	expression tag	UNP Q9PPB4
D	-4	HIS	-	expression tag	UNP Q9PPB4
D	-3	HIS	-	expression tag	UNP Q9PPB4
D	-2	HIS	-	expression tag	UNP Q9PPB4
D	-1	GLY	-	expression tag	UNP Q9PPB4
D	0	SER	-	expression tag	UNP Q9PPB4
D	56	ALA	HIS	engineered mutation	UNP Q9PPB4
E	-11	MET	-	expression tag	UNP Q9PPB4
E	-10	ARG	-	expression tag	UNP Q9PPB4
E	-9	GLY	-	expression tag	UNP Q9PPB4
E	-8	SER	-	expression tag	UNP Q9PPB4
E	-7	HIS	-	expression tag	UNP Q9PPB4
E	-6	HIS	-	expression tag	UNP Q9PPB4
E	-5	HIS	-	expression tag	UNP Q9PPB4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP Q9PPB4
E	-3	HIS	-	expression tag	UNP Q9PPB4
E	-2	HIS	-	expression tag	UNP Q9PPB4
E	-1	GLY	-	expression tag	UNP Q9PPB4
E	0	SER	-	expression tag	UNP Q9PPB4
E	56	ALA	HIS	engineered mutation	UNP Q9PPB4
F	-11	MET	-	expression tag	UNP Q9PPB4
F	-10	ARG	-	expression tag	UNP Q9PPB4
F	-9	GLY	-	expression tag	UNP Q9PPB4
F	-8	SER	-	expression tag	UNP Q9PPB4
F	-7	HIS	-	expression tag	UNP Q9PPB4
F	-6	HIS	-	expression tag	UNP Q9PPB4
F	-5	HIS	-	expression tag	UNP Q9PPB4
F	-4	HIS	-	expression tag	UNP Q9PPB4
F	-3	HIS	-	expression tag	UNP Q9PPB4
F	-2	HIS	-	expression tag	UNP Q9PPB4
F	-1	GLY	-	expression tag	UNP Q9PPB4
F	0	SER	-	expression tag	UNP Q9PPB4
F	56	ALA	HIS	engineered mutation	UNP Q9PPB4

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$) (labeled as "Ligand of Interest" by depositor).

EDO

O2
OH

C1

C2

HO
O1
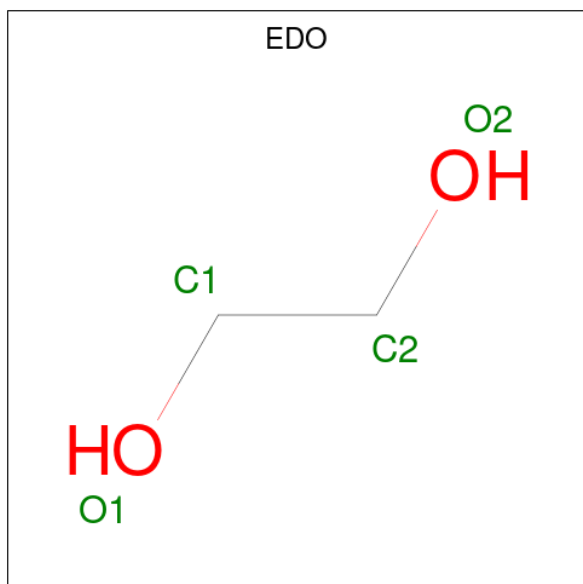
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0
2	E	1	Total 4	C 2	O 2	0	0
2	F	1	Total 4	C 2	O 2	0	0

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$) (labeled as "Ligand of Interest" by depositor).

PGE
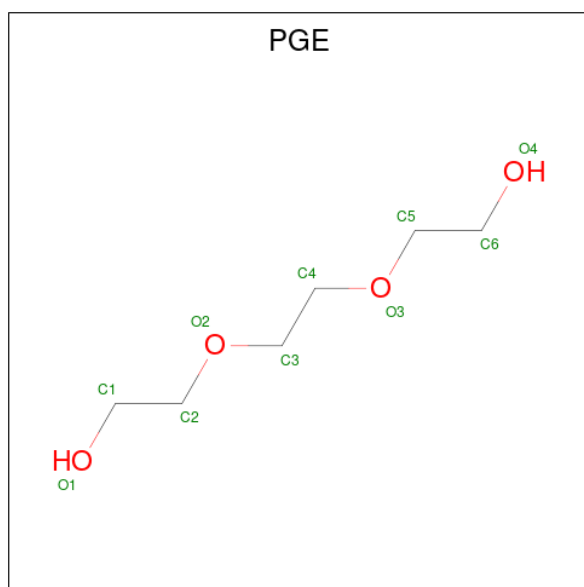
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 10	C 6	O 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total 10	C 6	O 4	0	0
3	C	1	Total 10	C 6	O 4	0	0
3	D	1	Total 10	C 6	O 4	0	0
3	D	1	Total 10	C 6	O 4	0	0
3	F	1	Total 10	C 6	O 4	0	0
3	F	1	Total 9	C 6	O 3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).

ACT

OXT
O⁻

C

CH3

O

O
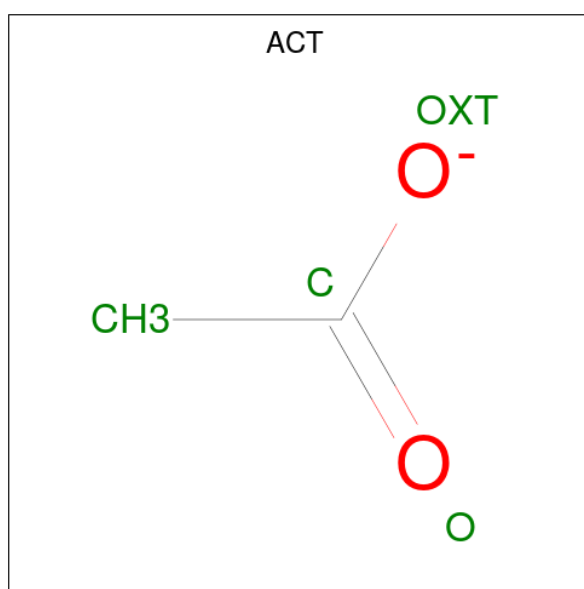
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Mg 1	0	0
5	C	1	Total 1	Mg 1	0	0
5	D	3	Total 3	Mg 3	0	0
5	E	2	Total 2	Mg 2	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).
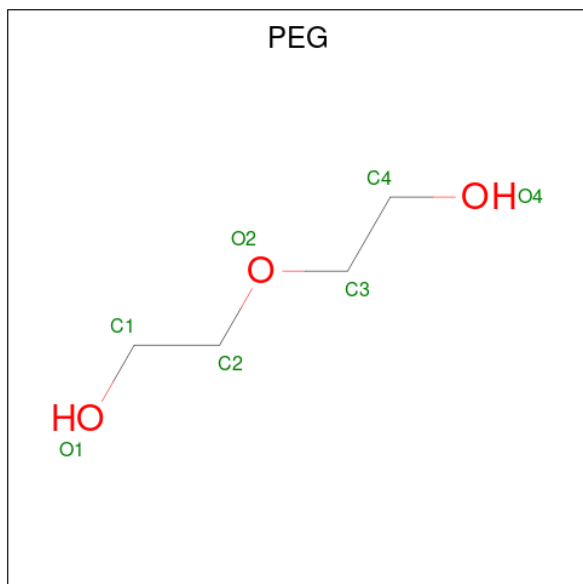
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total 7	C 4	O 3	0	0
6	B	1	Total 7	C 4	O 3	0	0
6	C	1	Total 7	C 4	O 3	0	0
6	D	1	Total 7	C 4	O 3	0	0
6	F	1	Total 7	C 4	O 3	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	185	Total 185	O 185	0	0
7	B	175	Total 175	O 175	0	0
7	C	150	Total 150	O 150	0	0
7	D	168	Total 168	O 168	0	0
7	E	162	Total 162	O 162	0	0
7	F	164	Total 164	O 164	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain A:

- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain B:
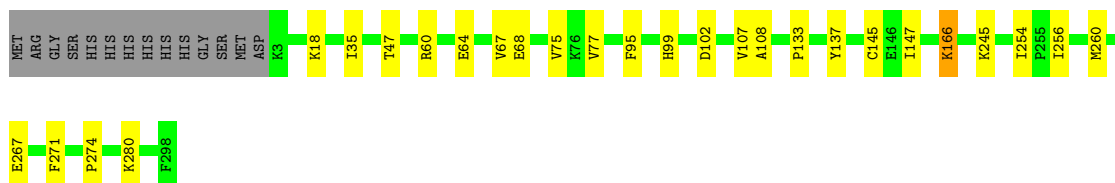
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain C:
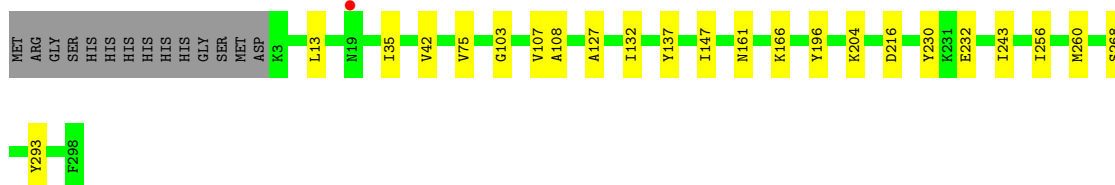
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain D:

• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain E:

• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	84.93Å 231.65Å 200.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.74 – 2.12 45.94 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.74-2.12) 94.2 (45.94-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.91 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.173 , 0.209 0.172 , 0.207	Depositor DCC
R_{free} test set	5587 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	28.7	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.0	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	14769	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: EDO, MG, PGE, PEG, ACT, KPI

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	0.33	0/2316	0.50	0/3131
1	B	0.45	0/2280	0.53	0/3088
1	C	0.41	0/2282	0.52	0/3090
1	D	0.44	0/2279	0.52	0/3087
1	E	0.38	0/2281	0.52	0/3089
1	F	0.40	0/2275	0.51	0/3083
All	All	0.40	0/13713	0.52	0/18568

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
1	B	0	1
1	D	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	KPI	Mainchain
1	B	166	KPI	Mainchain
1	D	166	KPI	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2292	0	2326	12	0
1	B	2257	0	2267	24	0
1	C	2259	0	2275	13	0
1	D	2256	0	2265	26	0
1	E	2258	0	2269	15	0
1	F	2252	0	2255	22	0
2	A	8	0	12	0	0
2	B	4	0	6	0	0
2	C	12	0	18	0	0
2	D	12	0	18	2	0
2	E	4	0	6	2	0
2	F	4	0	6	4	0
3	A	10	0	14	1	0
3	B	10	0	14	0	0
3	C	10	0	14	0	0
3	D	20	0	28	6	0
3	F	19	0	25	7	0
4	A	8	0	6	0	0
4	B	4	0	3	0	0
4	C	8	0	6	0	0
4	D	8	0	6	0	0
4	E	8	0	6	1	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	3	0	0	0	0
5	E	2	0	0	0	0
6	B	14	0	20	0	0
6	C	7	0	10	1	0
6	D	7	0	10	0	0
6	F	7	0	10	0	0
7	A	185	0	0	0	0
7	B	175	0	0	1	0
7	C	150	0	0	0	0
7	D	168	0	0	4	0
7	E	162	0	0	3	0
7	F	164	0	0	2	0
All	All	14769	0	13895	109	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 109 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:95:PHE:CE2	1:B:99:HIS:CE1	2.42	1.07
1:D:294:LYS:NZ	3:D:308:PGE:H32	1.73	1.01
1:B:60:ARG:HG3	1:B:95:PHE:CZ	2.03	0.94
1:D:294:LYS:NZ	3:D:308:PGE:H1	1.87	0.89
1:D:294:LYS:HZ2	3:D:308:PGE:H32	1.32	0.89

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	295/310 (95%)	288 (98%)	7 (2%)	0	100	100
1	B	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
1	C	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
1	D	293/310 (94%)	282 (96%)	8 (3%)	3 (1%)	15	10
1	E	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
1	F	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
All	All	1760/1860 (95%)	1714 (97%)	43 (2%)	3 (0%)	47	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	270	GLU
1	D	268	SER
1	D	273	LEU

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	249/259 (96%)	243 (98%)	6 (2%)	49	52
1	B	242/259 (93%)	241 (100%)	1 (0%)	91	94
1	C	243/259 (94%)	242 (100%)	1 (0%)	91	94
1	D	242/259 (93%)	241 (100%)	1 (0%)	91	94
1	E	242/259 (93%)	242 (100%)	0	100	100
1	F	241/259 (93%)	240 (100%)	1 (0%)	91	94
All	All	1459/1554 (94%)	1449 (99%)	10 (1%)	84	88

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	268	SER
1	D	18	LYS
1	F	281	GLU
1	A	280	LYS
1	A	281	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	161	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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	#$|Z| > 2$
1	KPI	A	166	1	11,13,14	1.48	1 (9%)	10,15,17	3.26	5 (50%)
1	KPI	D	166	1	11,13,14	1.48	2 (18%)	10,15,17	3.02	5 (50%)
1	KPI	C	166	1	11,13,14	0.83	0	10,15,17	3.25	4 (40%)
1	KPI	B	166	1	11,13,14	1.46	1 (9%)	10,15,17	3.21	4 (40%)
1	KPI	F	166	1	11,13,14	0.83	0	10,15,17	3.23	4 (40%)
1	KPI	E	166	1	11,13,14	1.79	2 (18%)	10,15,17	3.65	5 (50%)

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
1	KPI	A	166	1	-	0/13/14/16	-
1	KPI	D	166	1	-	0/13/14/16	-
1	KPI	C	166	1	-	0/13/14/16	-
1	KPI	B	166	1	-	4/13/14/16	-
1	KPI	F	166	1	-	1/13/14/16	-
1	KPI	E	166	1	-	0/13/14/16	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	166	KPI	O2-CX2	5.12	1.36	1.22
1	A	166	KPI	O-C	4.12	1.36	1.19
1	B	166	KPI	O-C	4.11	1.36	1.19
1	D	166	KPI	O-C	4.10	1.36	1.19
1	E	166	KPI	O1-CX2	-2.30	1.23	1.30

The worst 5 of 27 bond angle outliers are listed below:

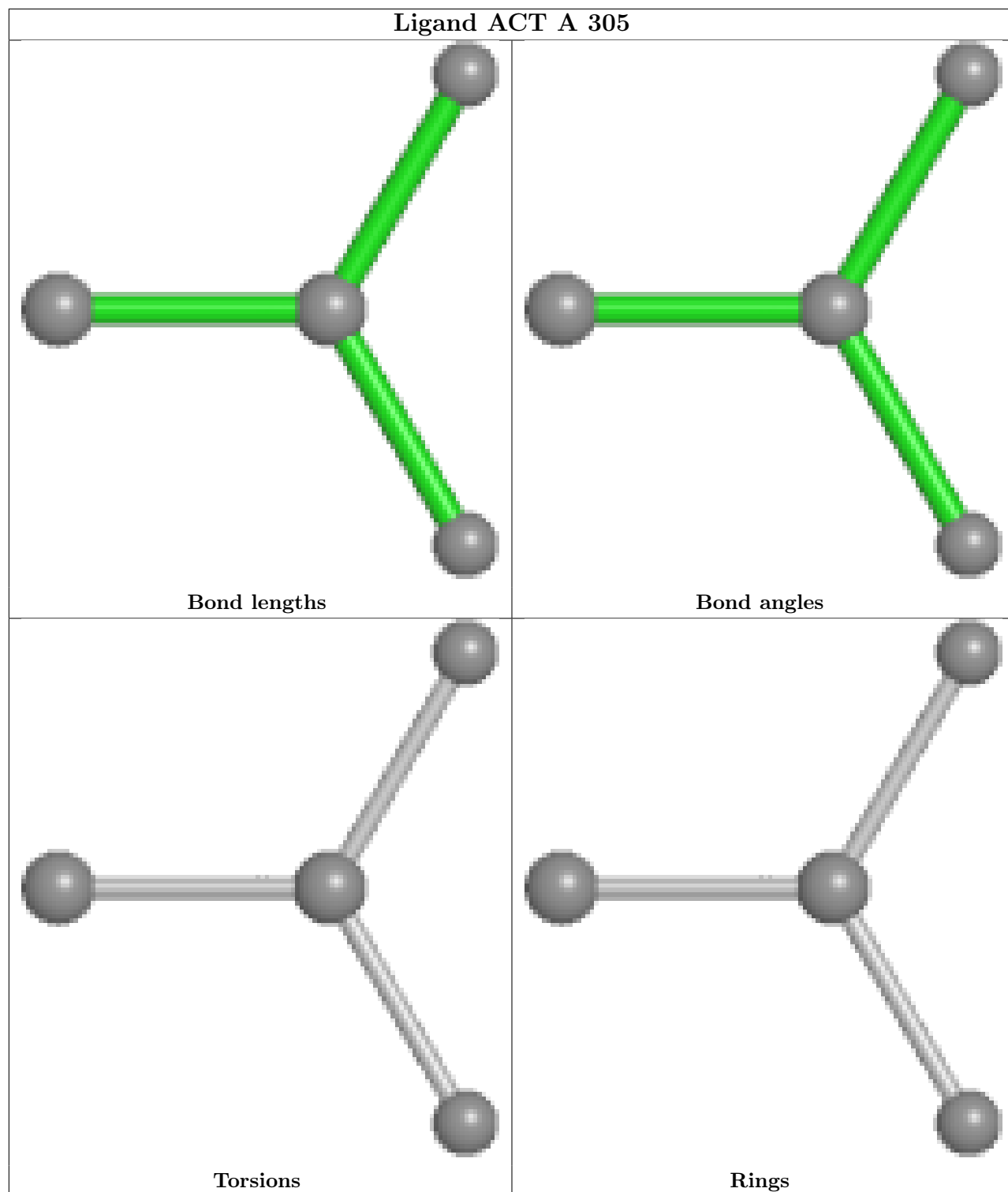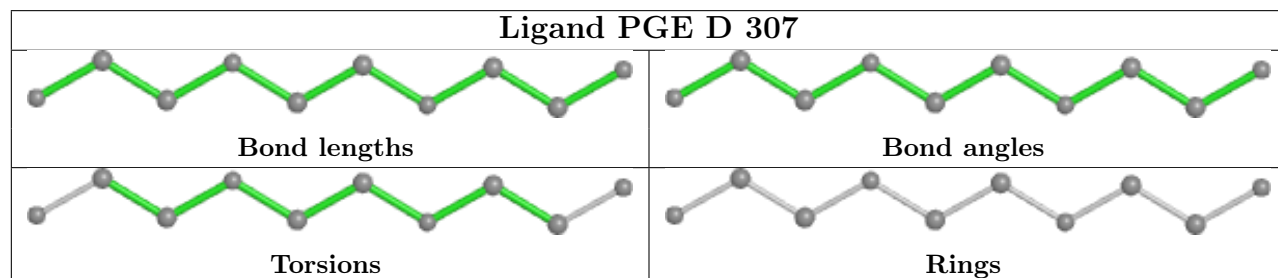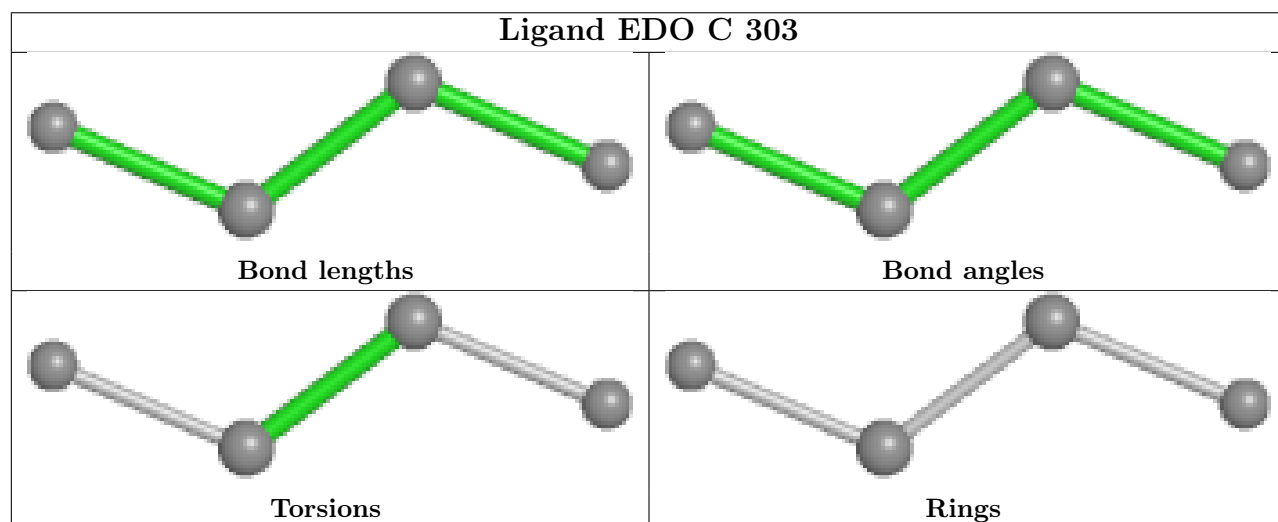| Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	166	KPI	C1-CX1-CX2	-7.46	110.91	118.17
1	A	166	KPI	C1-CX1-CX2	-7.32	111.06	118.17

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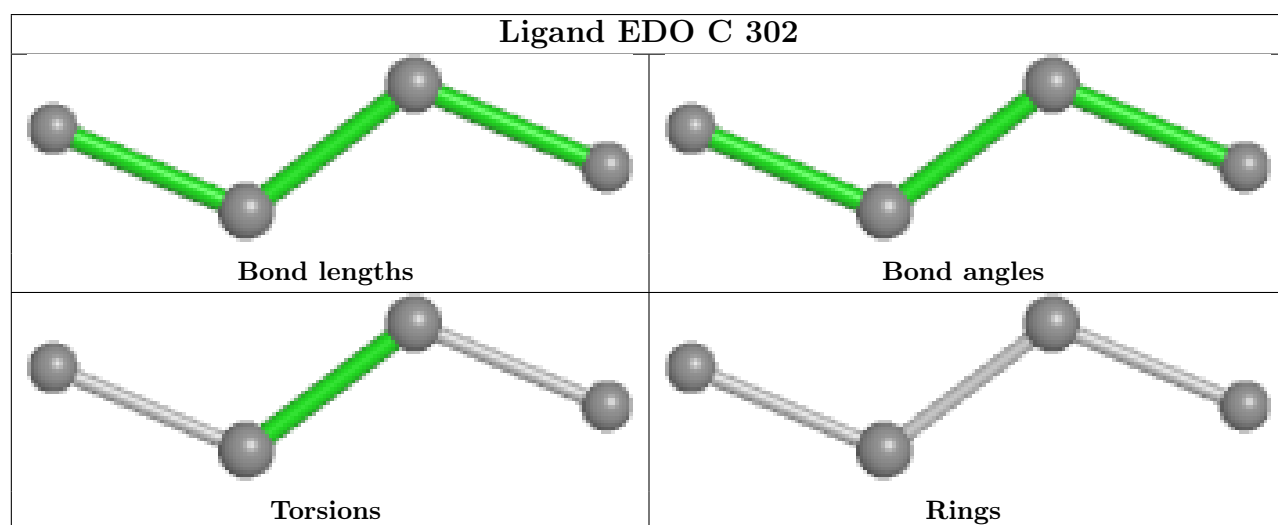| Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	166	KPI	C1-CX1-CX2	-7.18	111.19	118.17
1	E	166	KPI	C1-CX1-CX2	-7.10	111.27	118.17
1	B	166	KPI	C1-CX1-CX2	-7.07	111.30	118.17

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	166	KPI	NZ-CX1-CX2-O1
1	B	166	KPI	NZ-CX1-CX2-O2
1	B	166	KPI	C1-CX1-CX2-O1
1	B	166	KPI	C1-CX1-CX2-O2
1	F	166	KPI	NZ-CX1-CX2-O1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 39 ligands modelled in this entry, 7 are monoatomic - leaving 32 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	EDO	A	302	-	3,3,3	0.45	0	2,2,2	0.33	0
2	EDO	F	301	-	3,3,3	0.45	0	2,2,2	0.27	0
4	ACT	A	305	-	3,3,3	1.30	0	3,3,3	1.37	0
4	ACT	C	307	-	3,3,3	1.28	0	3,3,3	1.37	0
3	PGE	D	307	-	9,9,9	0.31	0	8,8,8	0.25	0
2	EDO	D	306	-	3,3,3	0.45	0	2,2,2	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	EDO	C	302	-	3,3,3	0.45	0	2,2,2	0.39	0
2	EDO	C	303	-	3,3,3	0.45	0	2,2,2	0.32	0
3	PGE	A	303	-	9,9,9	0.29	0	8,8,8	0.41	0
3	PGE	B	303	-	9,9,9	0.31	0	8,8,8	0.25	0
3	PGE	C	305	-	9,9,9	0.30	0	8,8,8	0.30	0
2	EDO	B	302	-	3,3,3	0.45	0	2,2,2	0.32	0
4	ACT	D	309	-	3,3,3	1.29	0	3,3,3	1.38	0
6	PEG	B	305	-	6,6,6	0.48	0	5,5,5	0.25	0
6	PEG	F	304	-	6,6,6	0.49	0	5,5,5	0.30	0
2	EDO	C	304	-	3,3,3	0.46	0	2,2,2	0.28	0
4	ACT	B	304	-	3,3,3	1.30	0	3,3,3	1.37	0
4	ACT	E	305	-	3,3,3	1.30	0	3,3,3	1.52	0
4	ACT	A	304	-	3,3,3	1.30	0	3,3,3	1.53	0
4	ACT	C	306	-	3,3,3	1.30	0	3,3,3	1.38	0
2	EDO	E	303	-	3,3,3	0.43	0	2,2,2	0.33	0
3	PGE	F	303	-	8,8,9	0.45	0	7,7,8	0.30	0
4	ACT	E	304	-	3,3,3	1.18	0	3,3,3	1.43	0
2	EDO	A	301	-	3,3,3	0.47	0	2,2,2	0.31	0
3	PGE	D	308	-	9,9,9	0.35	0	8,8,8	0.30	0
2	EDO	D	305	-	3,3,3	0.45	0	2,2,2	0.32	0
6	PEG	D	311	-	6,6,6	0.48	0	5,5,5	0.33	0
3	PGE	F	302	-	9,9,9	0.29	0	8,8,8	0.34	0
6	PEG	C	308	-	6,6,6	0.49	0	5,5,5	0.25	0
4	ACT	D	310	-	3,3,3	1.29	0	3,3,3	1.38	0
6	PEG	B	306	-	6,6,6	0.49	0	5,5,5	0.31	0
2	EDO	D	304	-	3,3,3	0.46	0	2,2,2	0.34	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
2	EDO	A	302	-	-	1/1/1/1	-
2	EDO	F	301	-	-	1/1/1/1	-
3	PGE	D	307	-	-	0/7/7/7	-
2	EDO	D	306	-	-	0/1/1/1	-
2	EDO	C	302	-	-	0/1/1/1	-
2	EDO	C	303	-	-	0/1/1/1	-
3	PGE	A	303	-	-	<mark>2/7/7/7</mark>	-
3	PGE	B	303	-	-	<mark>3/7/7/7</mark>	-
3	PGE	C	305	-	-	1/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	302	-	-	0/1/1/1	-
6	PEG	B	305	-	-	2/4/4/4	-
6	PEG	F	304	-	-	2/4/4/4	-
2	EDO	C	304	-	-	0/1/1/1	-
2	EDO	E	303	-	-	1/1/1/1	-
3	PGE	F	303	-	-	4/6/6/7	-
2	EDO	A	301	-	-	0/1/1/1	-
3	PGE	D	308	-	-	5/7/7/7	-
2	EDO	D	305	-	-	1/1/1/1	-
6	PEG	D	311	-	-	2/4/4/4	-
3	PGE	F	302	-	-	3/7/7/7	-
6	PEG	C	308	-	-	3/4/4/4	-
6	PEG	B	306	-	-	2/4/4/4	-
2	EDO	D	304	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	308	PGE	O2-C3-C4-O3
3	F	303	PGE	O3-C5-C6-O4
3	F	303	PGE	O2-C3-C4-O3
6	C	308	PEG	O1-C1-C2-O2
6	C	308	PEG	O2-C3-C4-O4

There are no ring outliers.

9 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	EDO	4	0
2	D	306	EDO	2	0
3	A	303	PGE	1	0
4	E	305	ACT	1	0
2	E	303	EDO	2	0
3	F	303	PGE	6	0
3	D	308	PGE	6	0
3	F	302	PGE	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	308	PEG	1	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 EDO A 302

Bond lengths   Bond angles

Torsions   Rings

Ligand EDO F 301

Bond lengths   Bond angles

Torsions   Rings

Ligand ACT A 305

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT C 307

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE D 307

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO D 306

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO C 302

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO C 303

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE A 303

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE B 303

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE C 305

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO B 302

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT D 309

Bond lengths

Bond angles

Torsions

Rings

Ligand PEG B 305

Bond lengths

Bond angles

Torsions

Rings

Ligand PEG F 304

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO C 304

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT B 304

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT E 305

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT A 304

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT C 306

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO E 303

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE F 303

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT E 304

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO A 301

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE D 308

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO D 305

Bond lengths

Bond angles

Torsions

Rings

Ligand PEG D 311

Bond lengths

Bond angles

Torsions

Rings

Ligand PGE F 302

Bond lengths

Bond angles

Torsions

Rings

Ligand PEG C 308

Bond lengths

Bond angles

Torsions

Rings

Ligand ACT D 310

Bond lengths

Bond angles

Torsions

Rings

Ligand PEG B 306

Bond lengths

Bond angles

Torsions

Rings

Ligand EDO D 304

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	296/310 (95%)	-0.42	1 (0%)	94	95	22, 30, 50, 76	0
1	B	295/310 (95%)	-0.50	0	100	100	21, 31, 48, 67	0
1	C	295/310 (95%)	-0.48	1 (0%)	94	95	22, 29, 47, 60	0
1	D	295/310 (95%)	-0.44	0	100	100	21, 30, 47, 60	0
1	E	295/310 (95%)	-0.40	1 (0%)	94	95	21, 30, 50, 70	0
1	F	295/310 (95%)	-0.44	0	100	100	23, 31, 49, 68	0
All	All	1771/1860 (95%)	-0.45	3 (0%)	95	95	21, 30, 49, 76	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	19	ASN	2.4
1	A	145	CYS	2.4
1	E	281	GLU	2.2

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

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
1	KPI	E	166	14/15	0.93	0.13	21,26,33,33	0
1	KPI	B	166	14/15	0.95	0.10	24,27,42,42	0
1	KPI	F	166	14/15	0.95	0.12	24,29,34,34	0
1	KPI	A	166	14/15	0.96	0.12	23,28,37,38	0
1	KPI	D	166	14/15	0.96	0.11	20,25,32,35	0
1	KPI	C	166	14/15	0.97	0.11	25,28,34,35	0

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
6	PEG	B	306	7/7	0.58	0.46	77,81,86,86	0
4	ACT	E	304	4/4	0.63	0.25	82,82,83,84	0
6	PEG	D	311	7/7	0.65	0.29	64,65,68,70	0
2	EDO	D	304	4/4	0.67	0.21	57,58,60,61	0
5	MG	D	302	1/1	0.70	0.07	38,38,38,38	0
5	MG	D	303	1/1	0.73	0.18	44,44,44,44	0
3	PGE	F	303	9/10	0.74	0.18	48,51,54,55	0
2	EDO	A	302	4/4	0.75	0.18	66,66,67,68	0
2	EDO	F	301	4/4	0.79	0.24	73,73,73,74	0
3	PGE	D	308	10/10	0.79	0.17	62,66,71,72	0
4	ACT	C	307	4/4	0.80	0.20	63,64,64,65	0
3	PGE	B	303	10/10	0.80	0.20	44,49,55,55	0
2	EDO	D	305	4/4	0.84	0.19	68,68,69,69	0
4	ACT	E	305	4/4	0.84	0.17	54,57,59,60	0
2	EDO	B	302	4/4	0.85	0.16	60,60,61,63	0
4	ACT	B	304	4/4	0.85	0.13	66,68,68,69	0
3	PGE	A	303	10/10	0.85	0.25	67,71,74,76	0
5	MG	E	302	1/1	0.85	0.11	53,53,53,53	0
4	ACT	D	309	4/4	0.85	0.28	56,57,59,62	0
6	PEG	C	308	7/7	0.85	0.16	59,64,69,70	0
3	PGE	F	302	10/10	0.85	0.22	54,65,71,71	0
6	PEG	B	305	7/7	0.88	0.22	59,60,62,63	0
4	ACT	A	305	4/4	0.88	0.15	57,60,60,62	0
2	EDO	C	303	4/4	0.88	0.20	44,46,49,51	0
2	EDO	D	306	4/4	0.88	0.38	61,62,64,65	0
2	EDO	C	304	4/4	0.89	0.34	54,54,56,56	0
4	ACT	C	306	4/4	0.89	0.20	64,65,65,66	0
4	ACT	D	310	4/4	0.89	0.19	53,54,54,55	0
6	PEG	F	304	7/7	0.89	0.19	56,57,59,61	0
5	MG	C	301	1/1	0.90	0.25	54,54,54,54	0
2	EDO	E	303	4/4	0.91	0.16	47,49,50,52	0
2	EDO	C	302	4/4	0.91	0.14	50,52,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
3	PGE	C	305	10/10	0.91	0.14	48,50,53,53	0
3	PGE	D	307	10/10	0.91	0.14	37,44,50,51	0
5	MG	E	301	1/1	0.95	0.07	50,50,50,50	0
4	ACT	A	304	4/4	0.96	0.20	44,46,48,50	0
2	EDO	A	301	4/4	0.96	0.11	25,26,27,28	0
5	MG	D	301	1/1	0.96	0.07	36,36,36,36	0
5	MG	B	301	1/1	0.98	0.11	42,42,42,42	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 PEG B 306:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
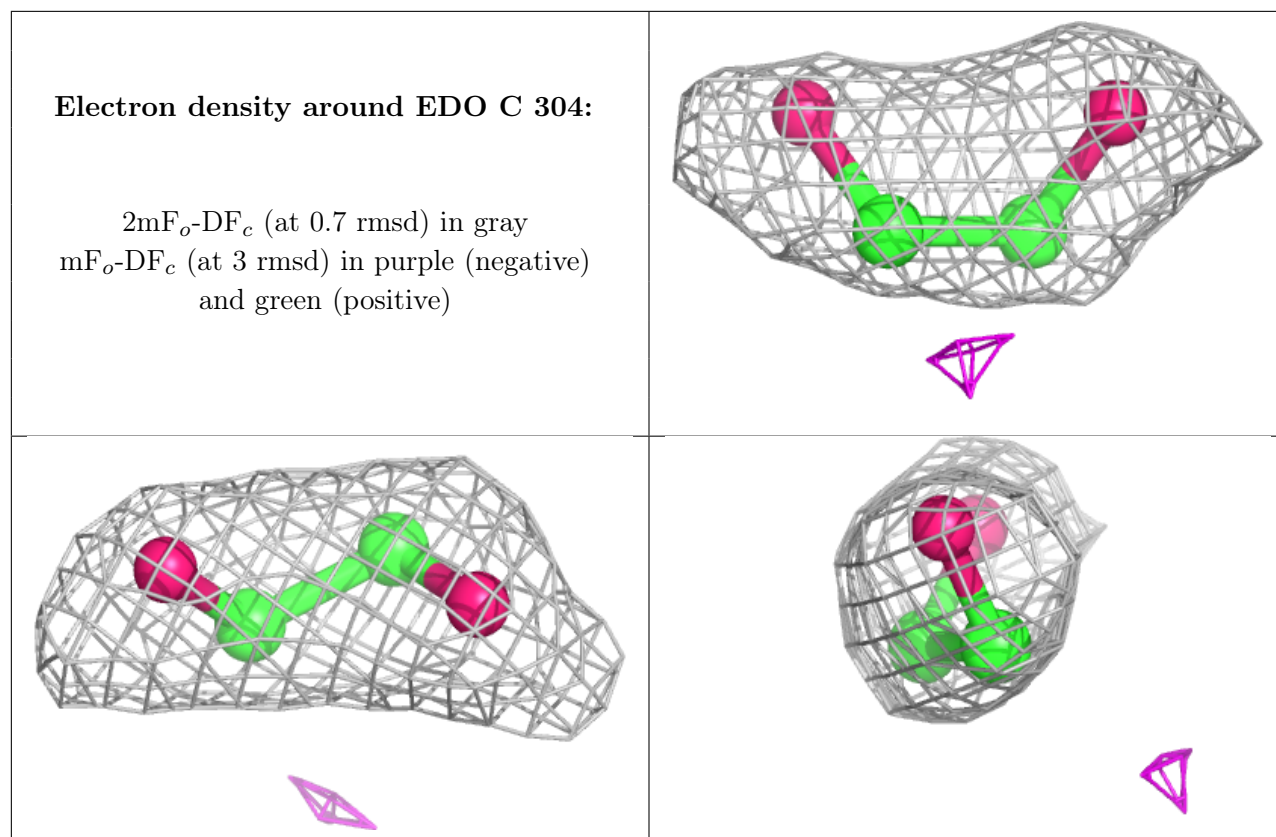and green (positive)
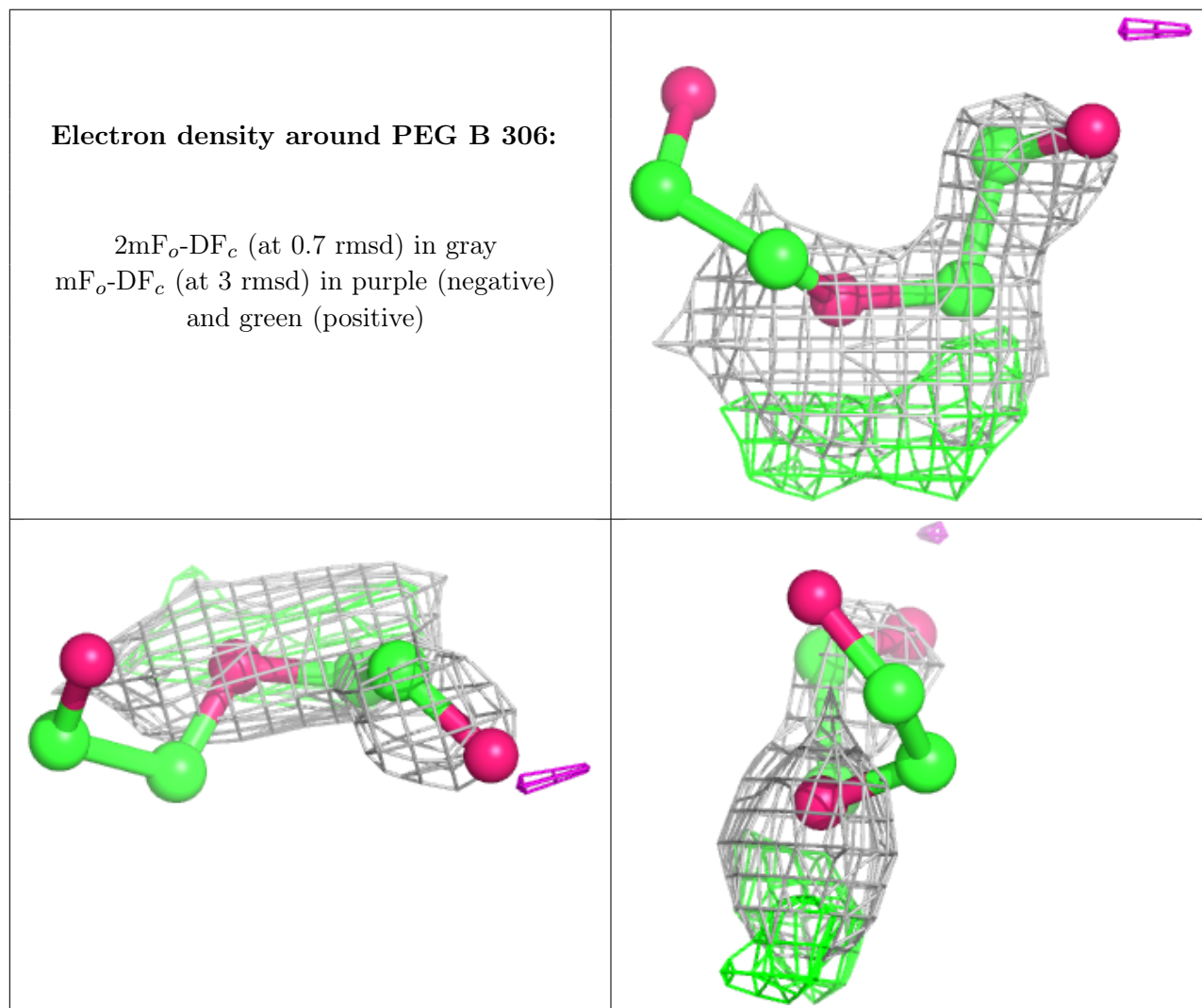
Electron density around ACT E 304:

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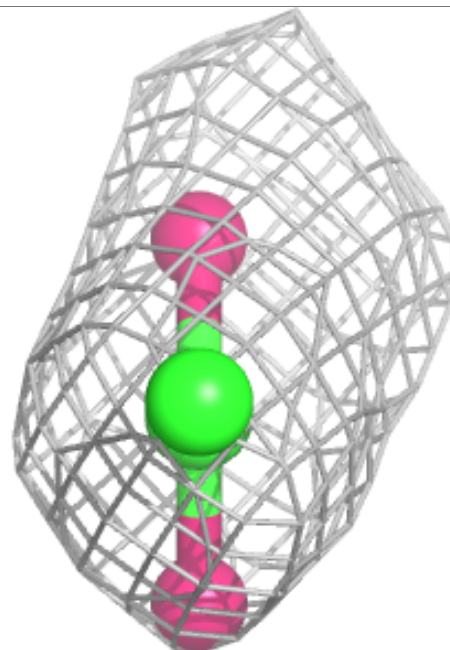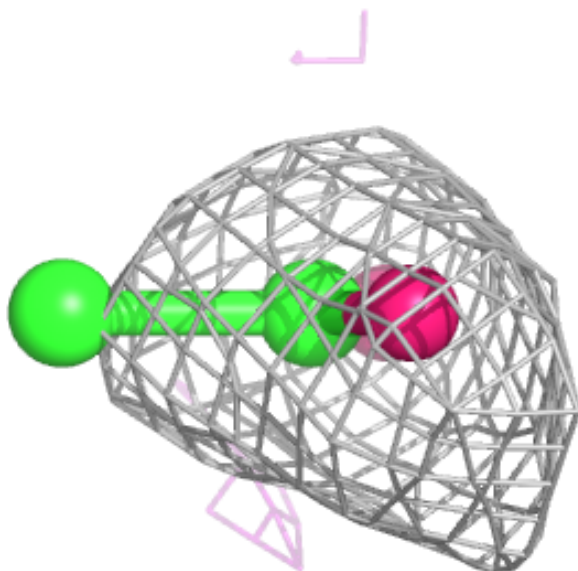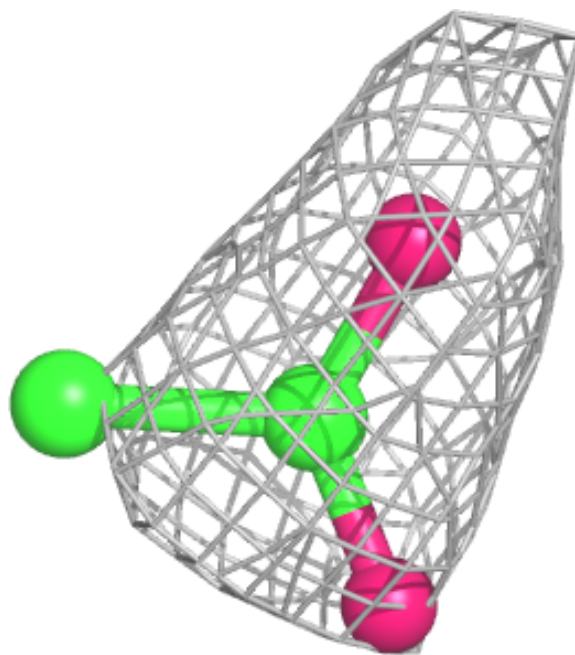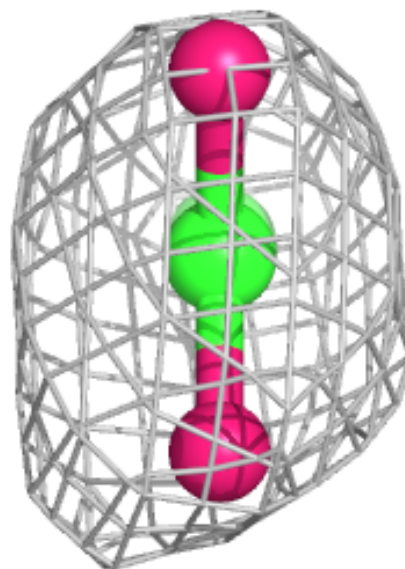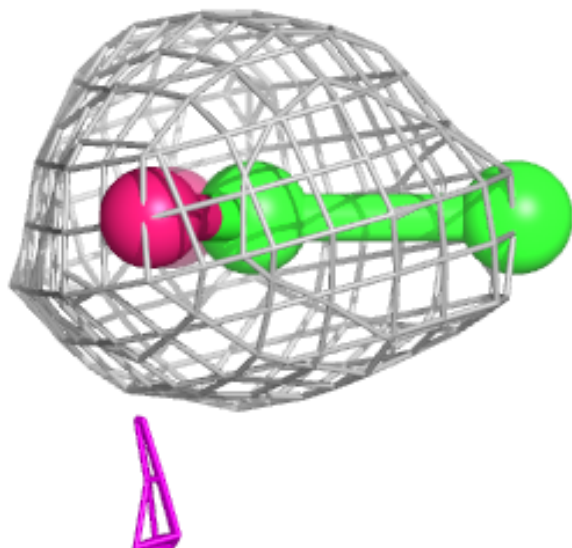mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around PEG D 311:

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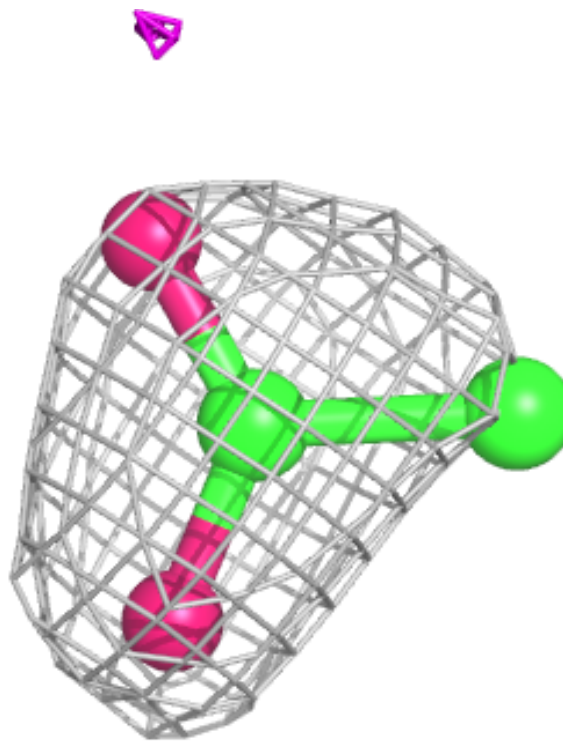and green (positive)

Electron density around EDO D 304:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
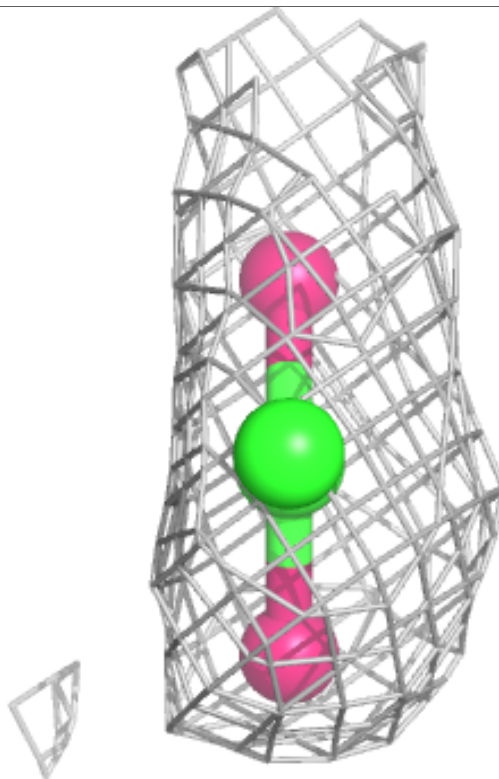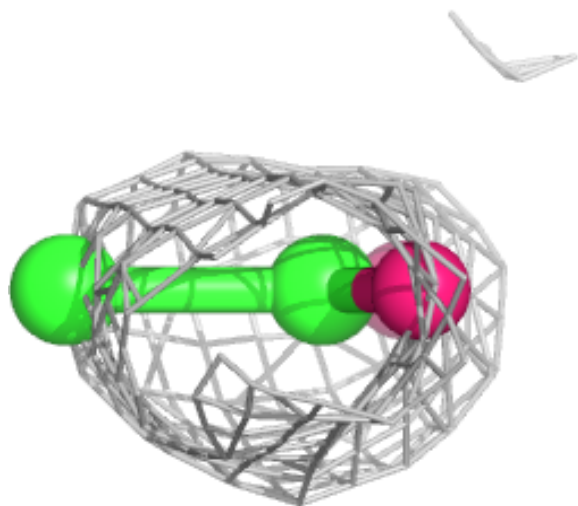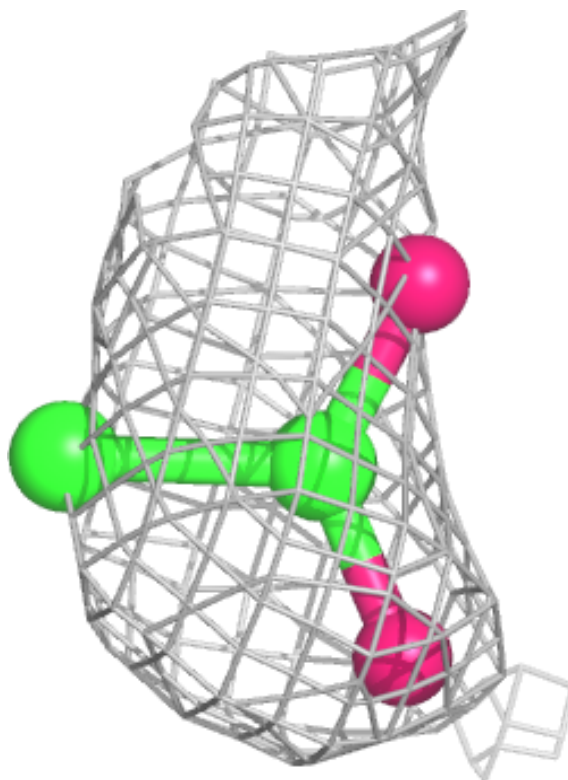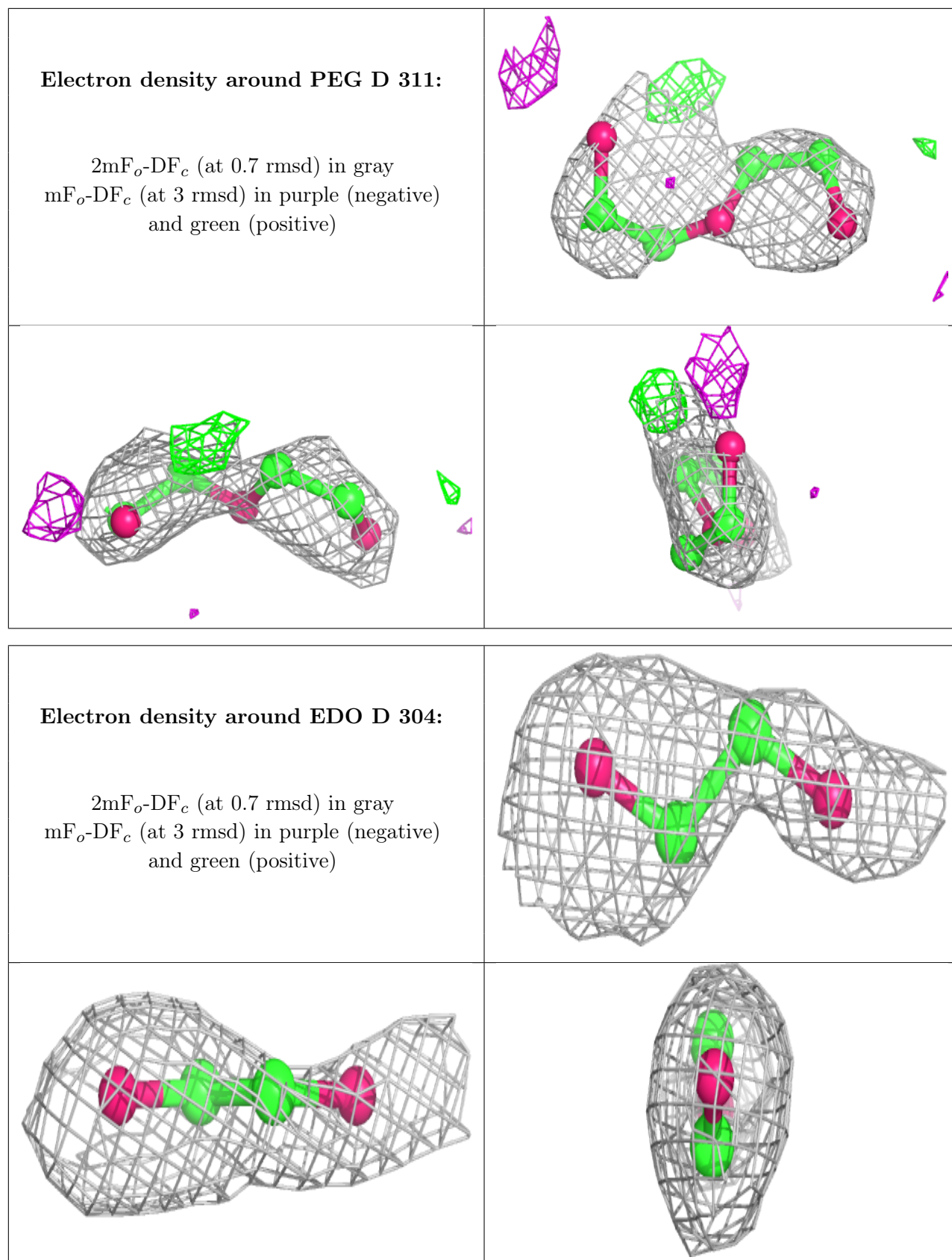
Electron density around MG D 302:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
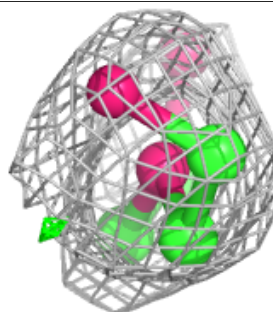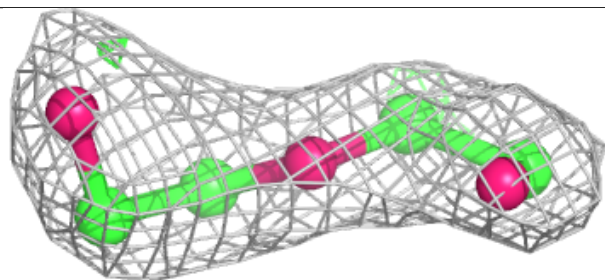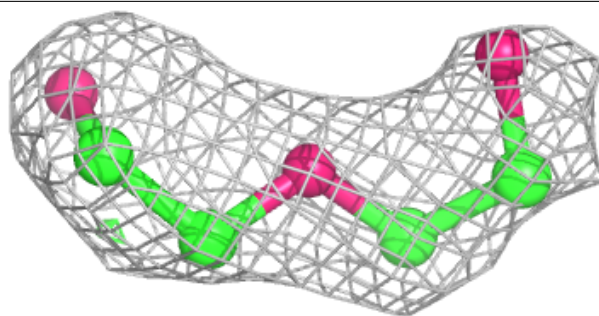and green (positive)
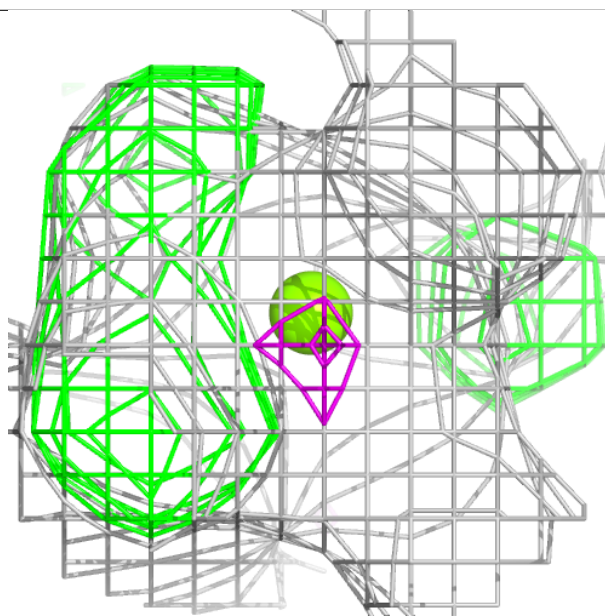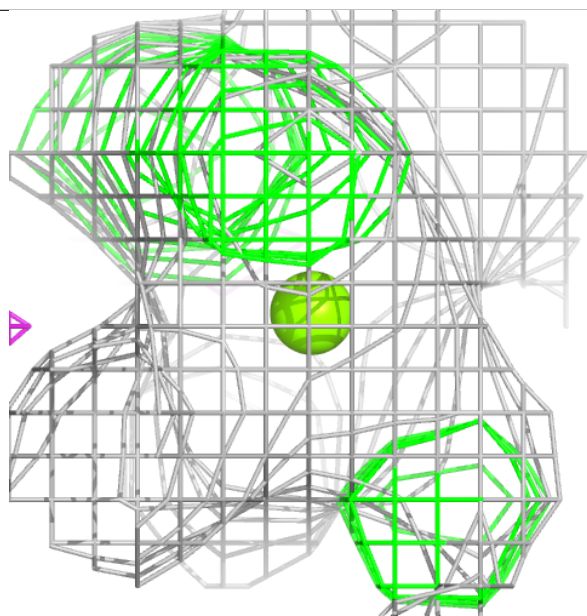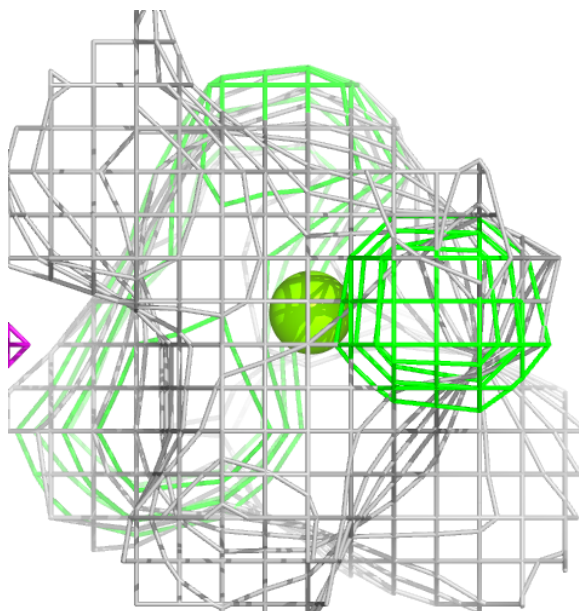
Electron density around MG D 303:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
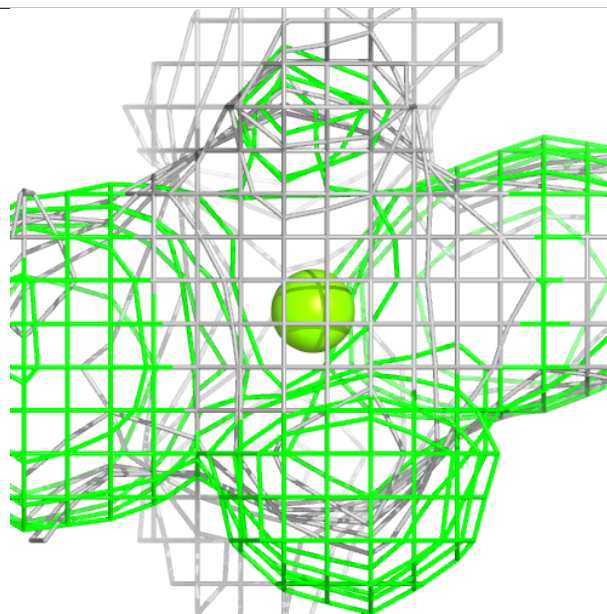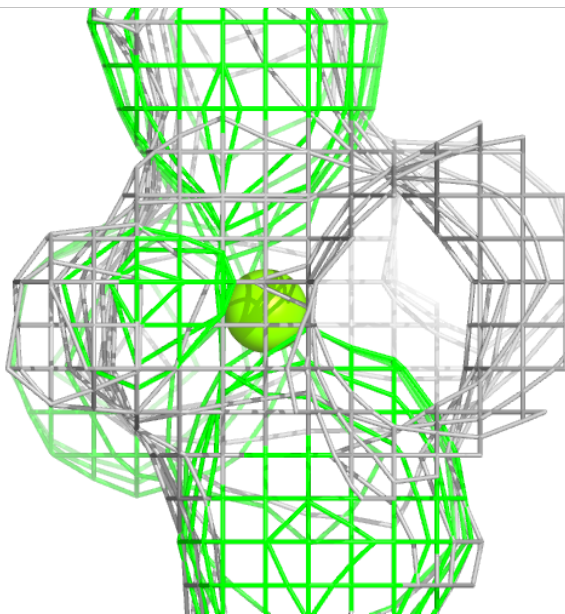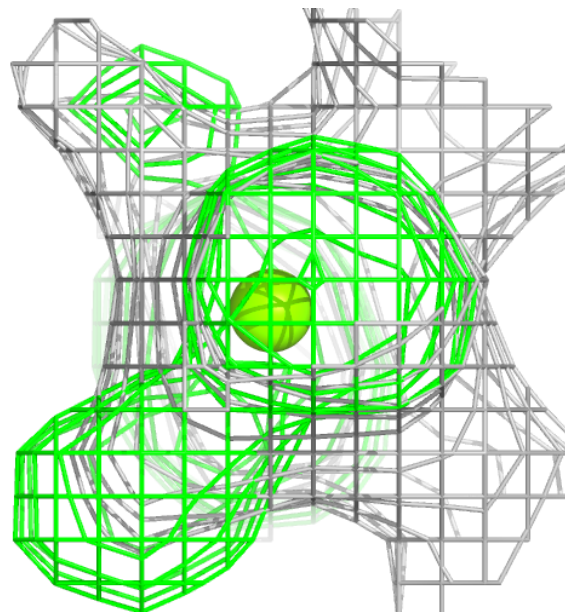
Electron density around PGE F 303:

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

Electron density around EDO A 302:

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

Electron density around EDO F 301:

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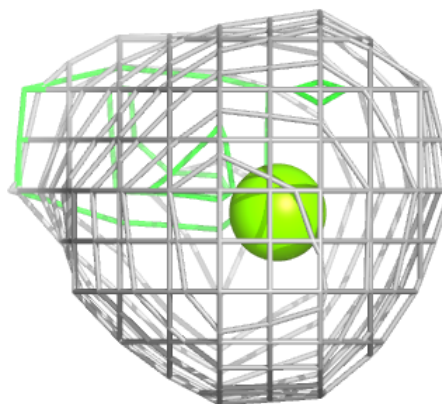$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
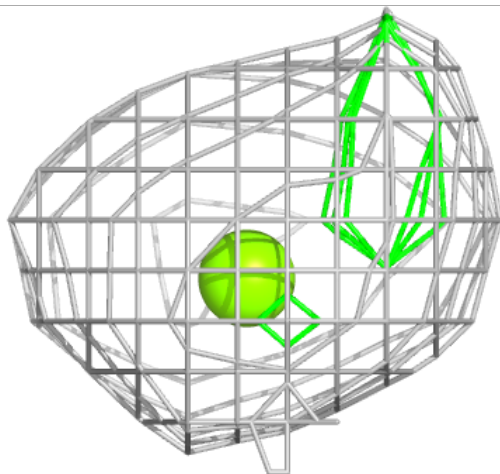and green (positive)

Electron density around PGE D 308:

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

Electron density around ACT C 307:

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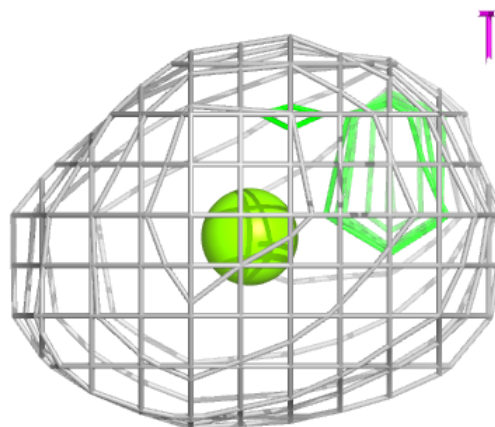and green (positive)

Electron density around PGE B 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 EDO D 305:

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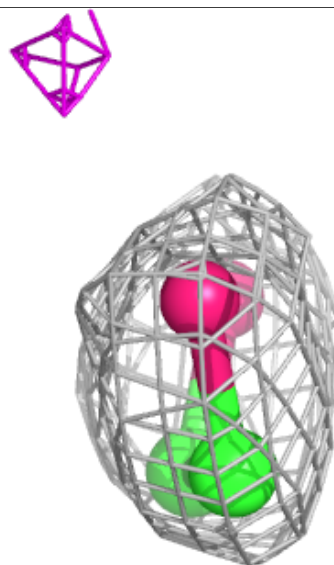mF_o-DF_c (at 3 rmsd) in purple (negative)
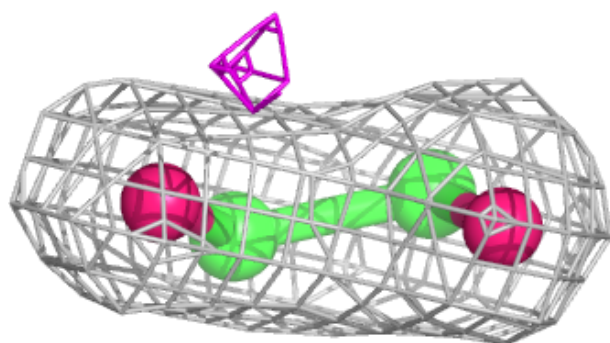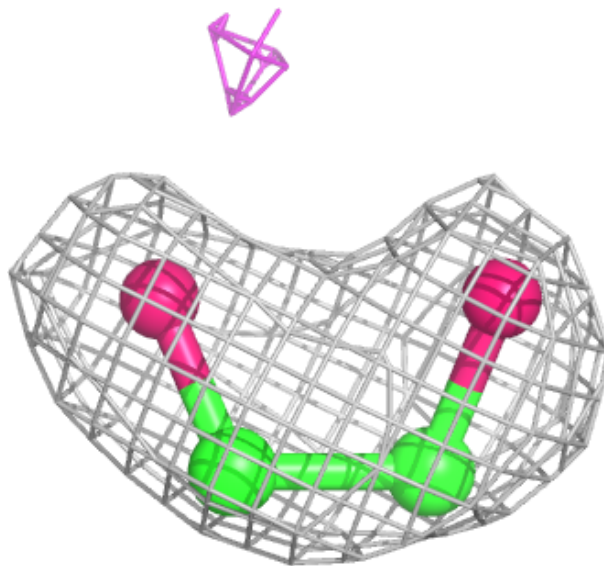and green (positive)

Electron density around ACT E 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 EDO B 302:

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

Electron density around ACT B 304:

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

Electron density around PGE A 303:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
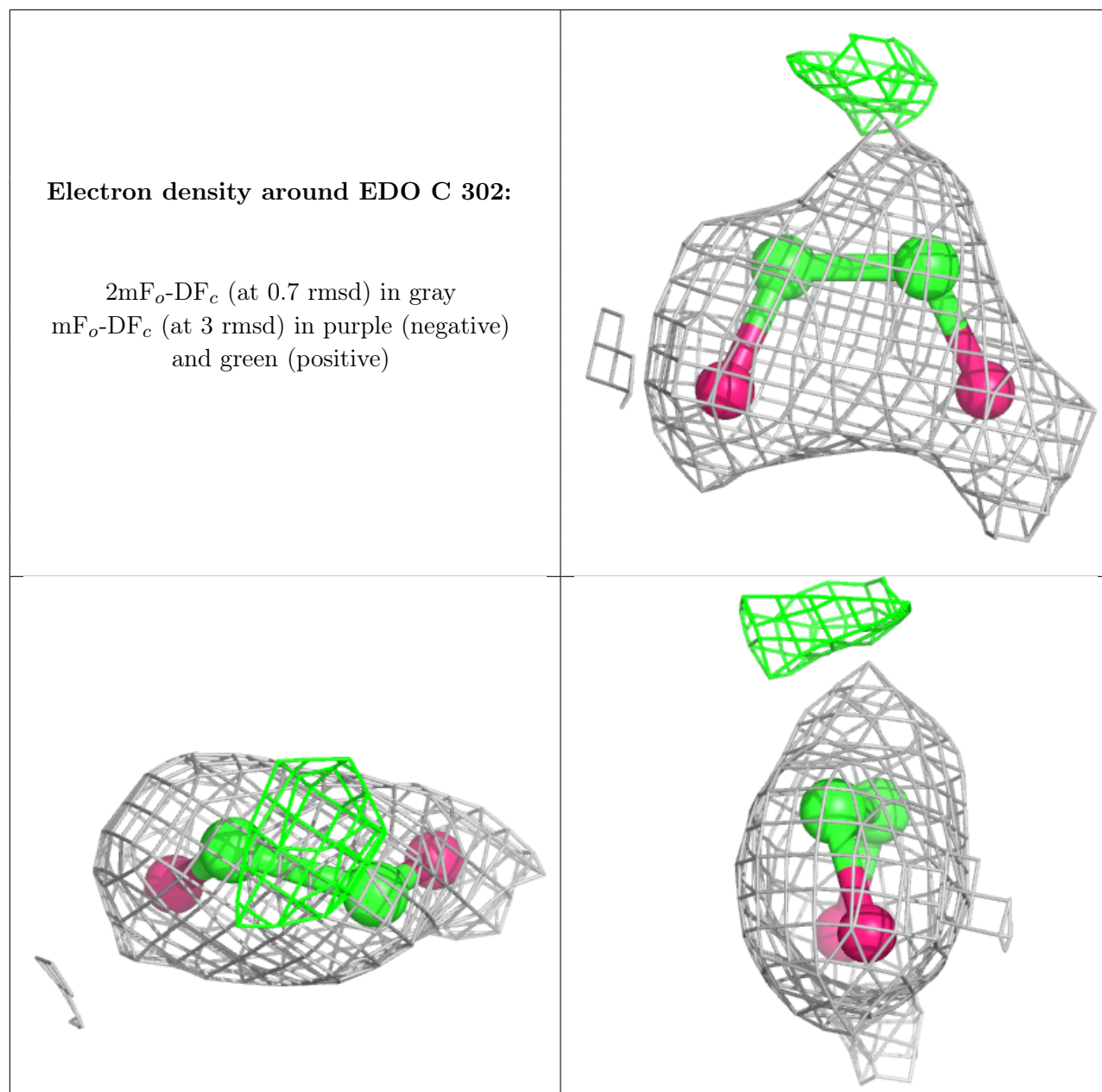and green (positive)
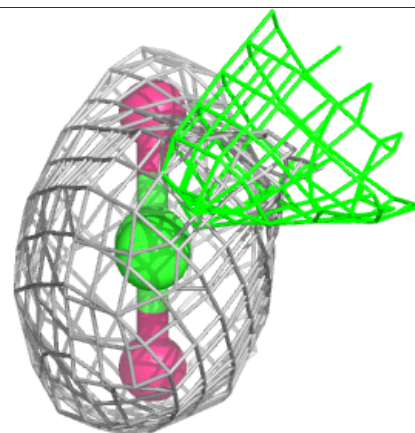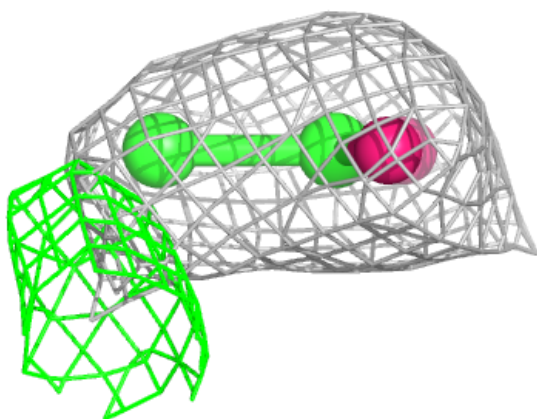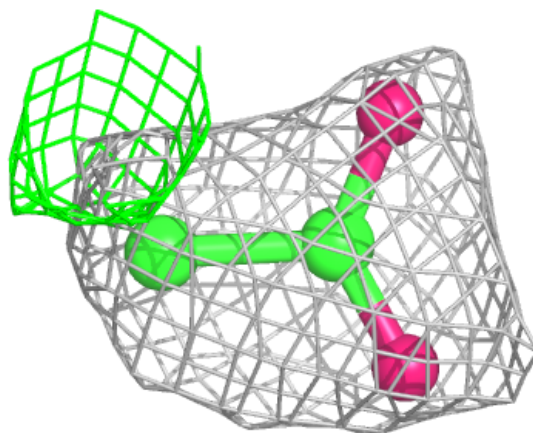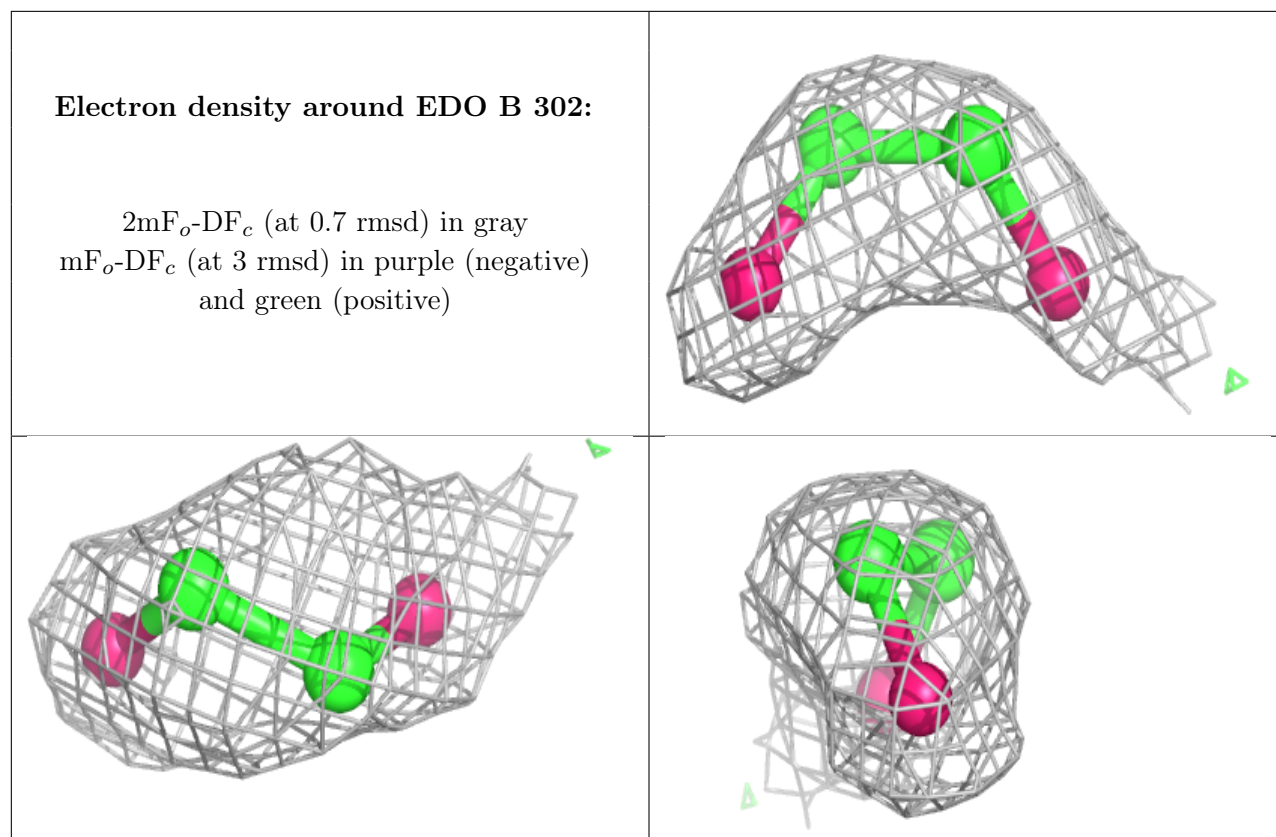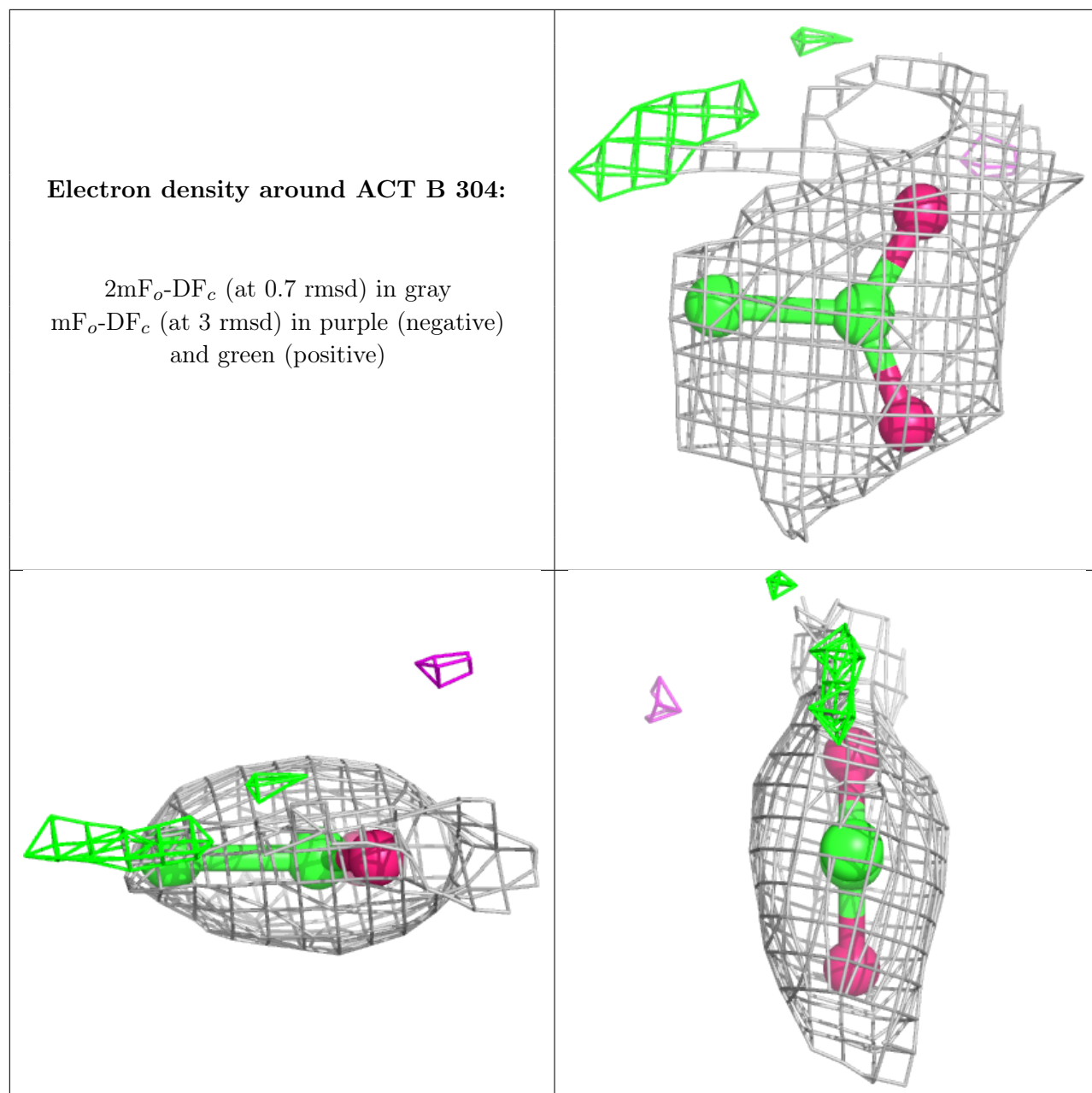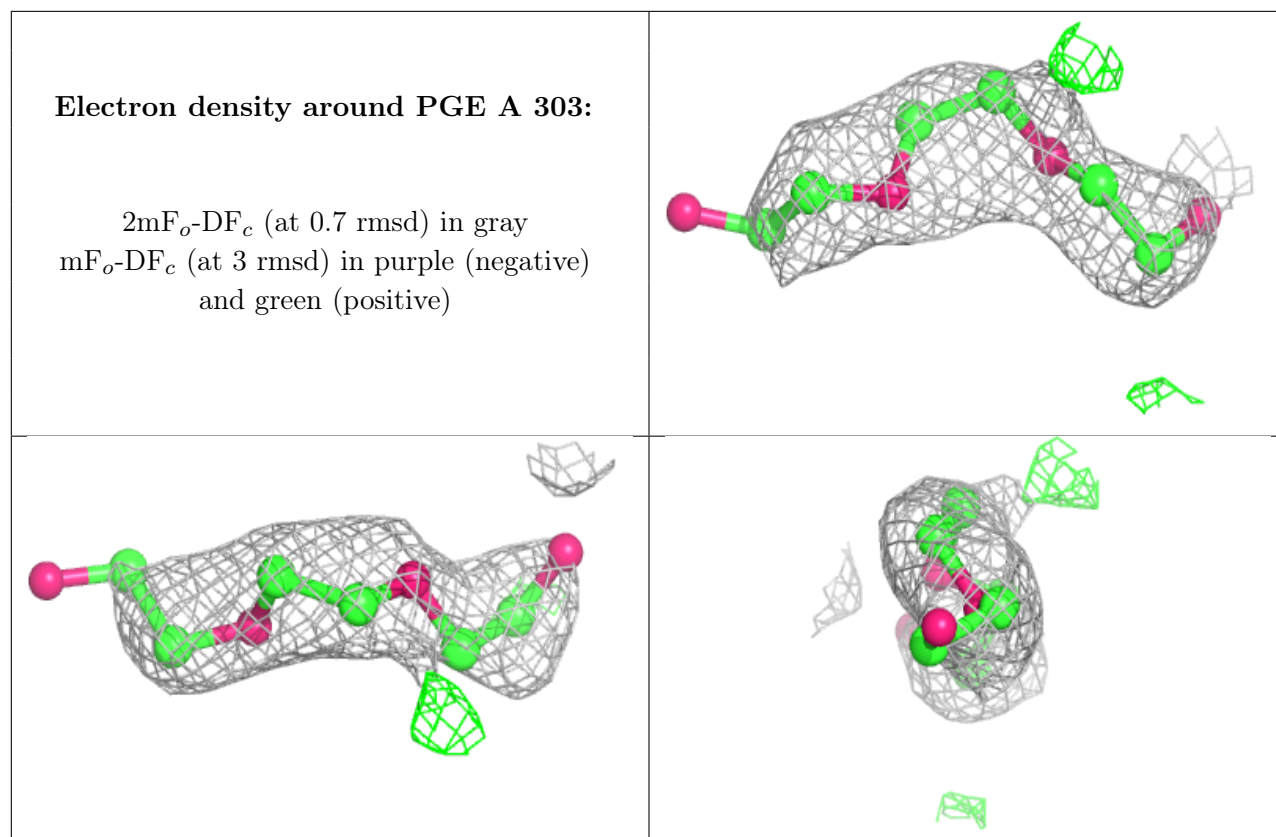
Electron density around MG E 302:

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

Electron density around ACT D 309:

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

Electron density around PEG C 308:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
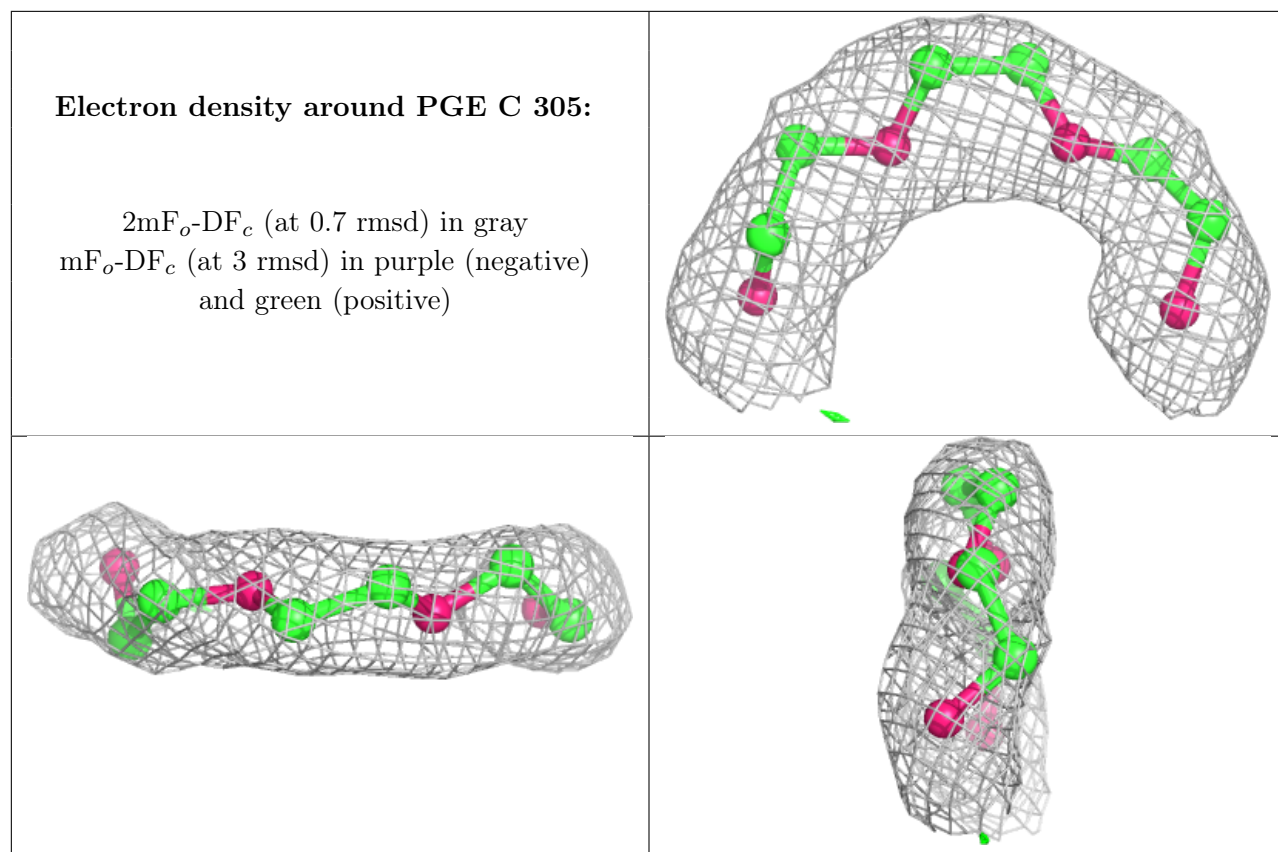$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
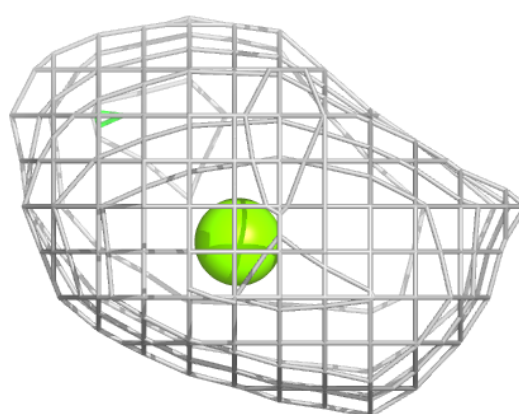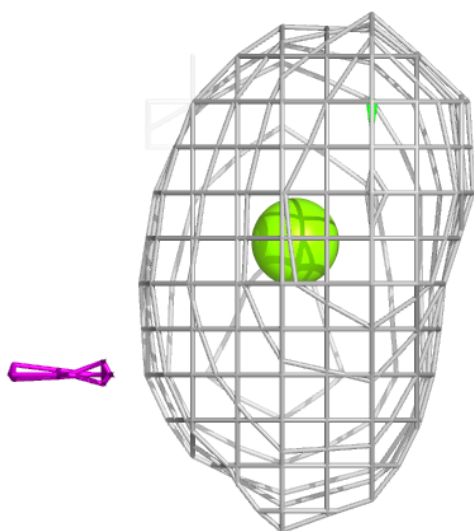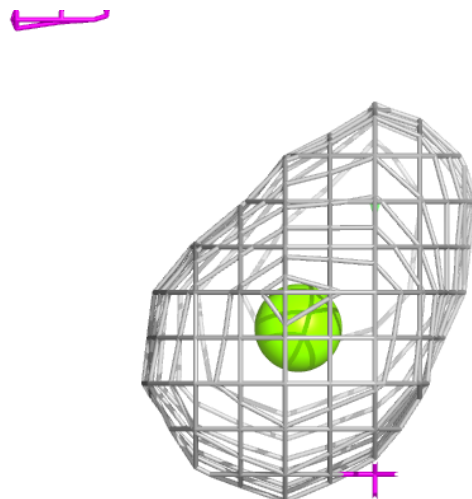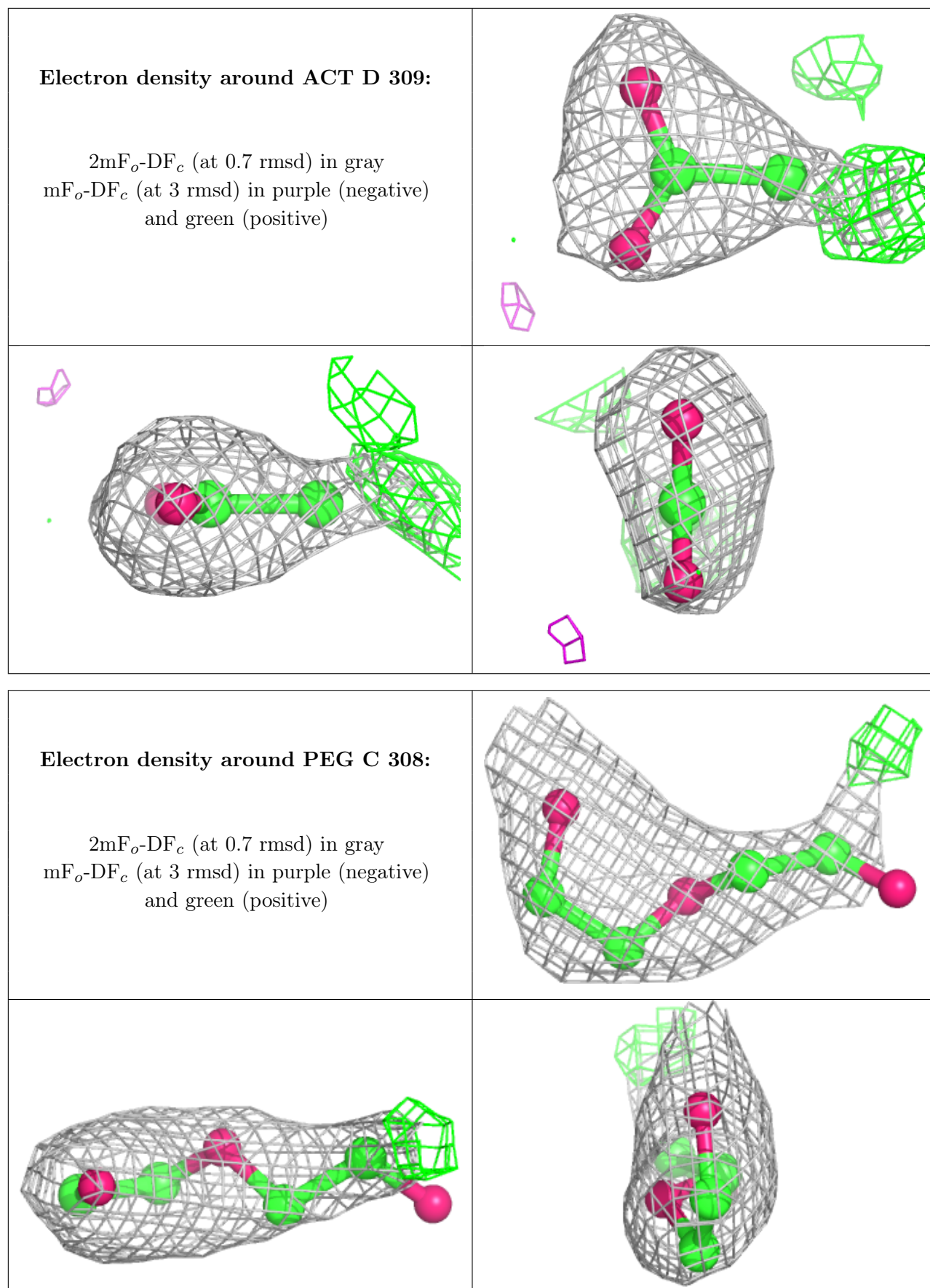
Electron density around PGE F 302:

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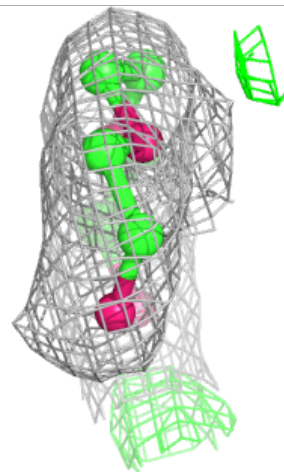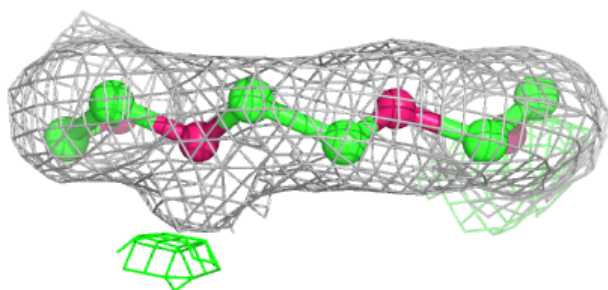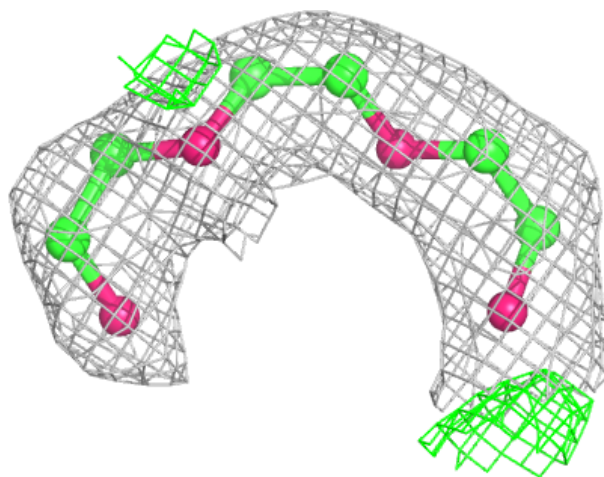mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around PEG B 305:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
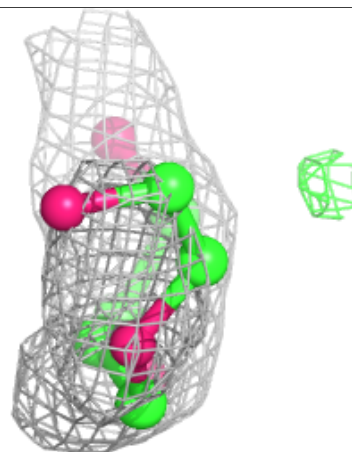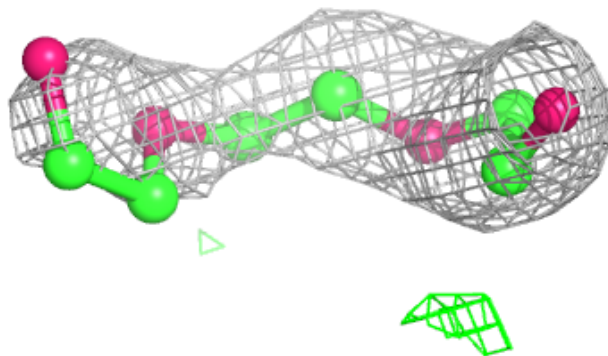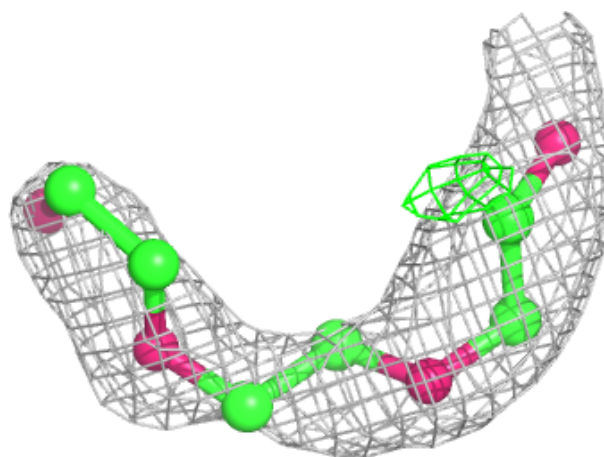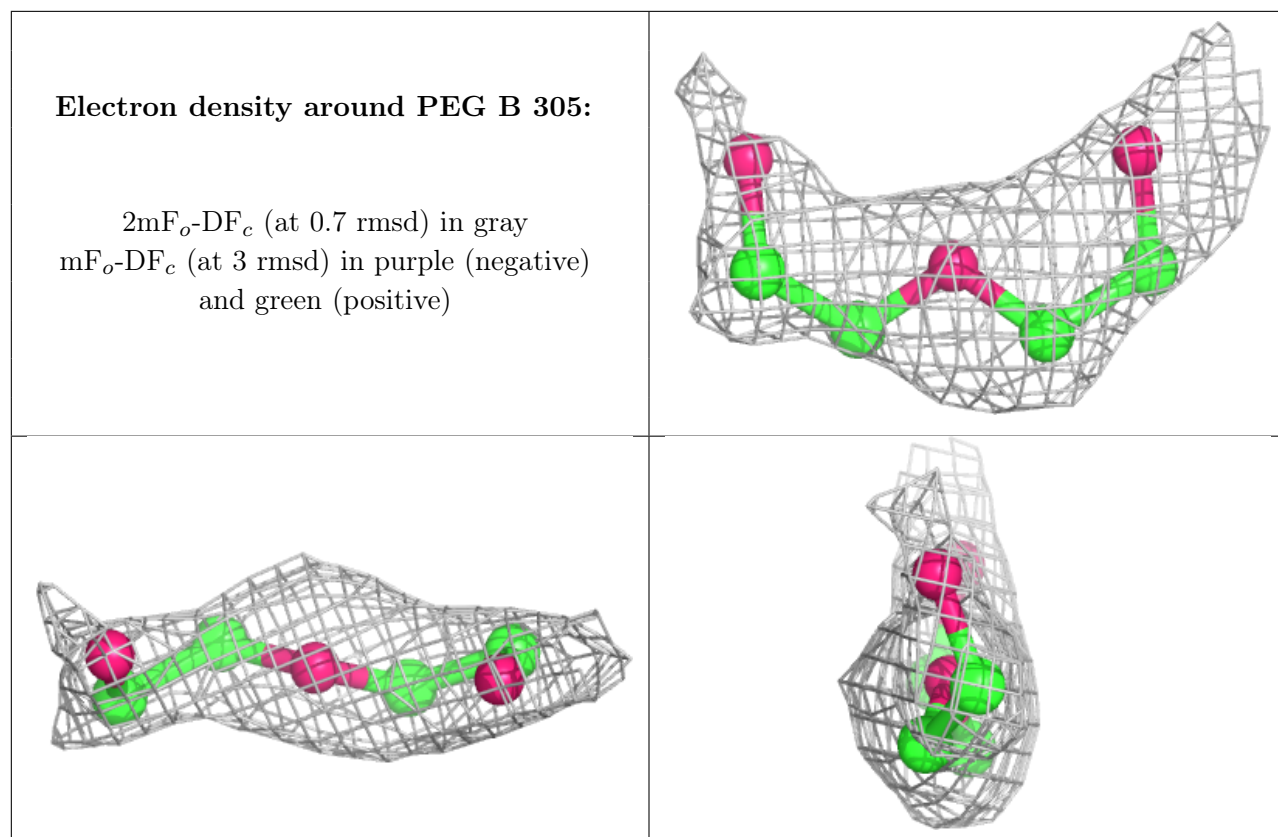
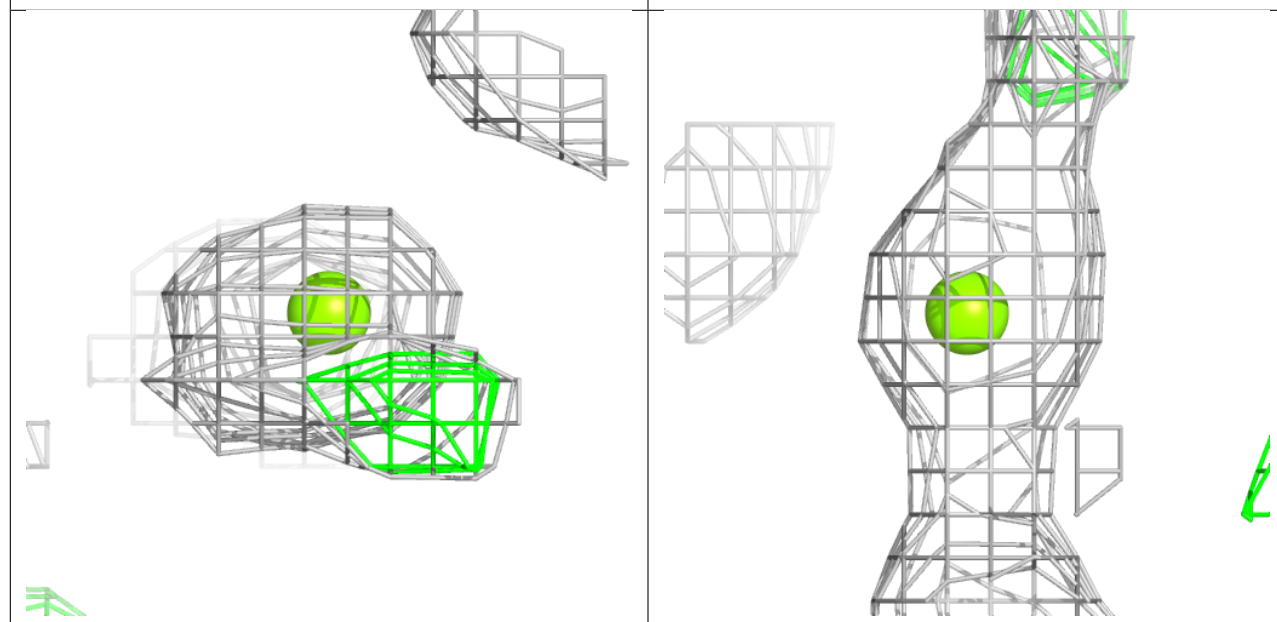**Electron density around ACT A 305:**

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

Electron density around EDO C 303:

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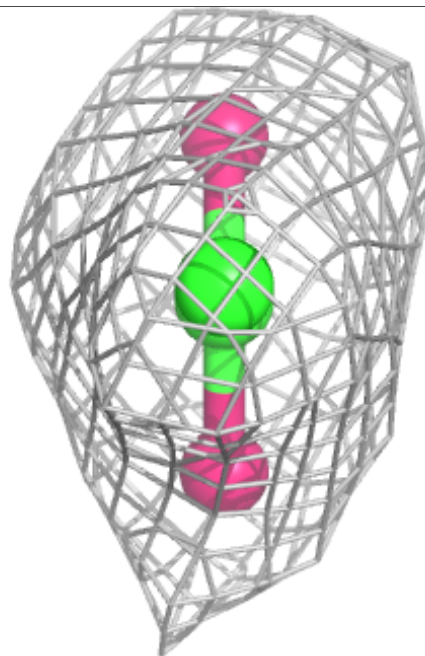and green (positive)

Electron density around EDO D 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 EDO C 304:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
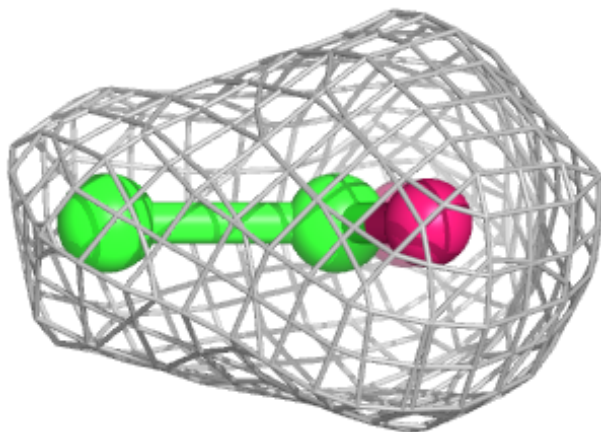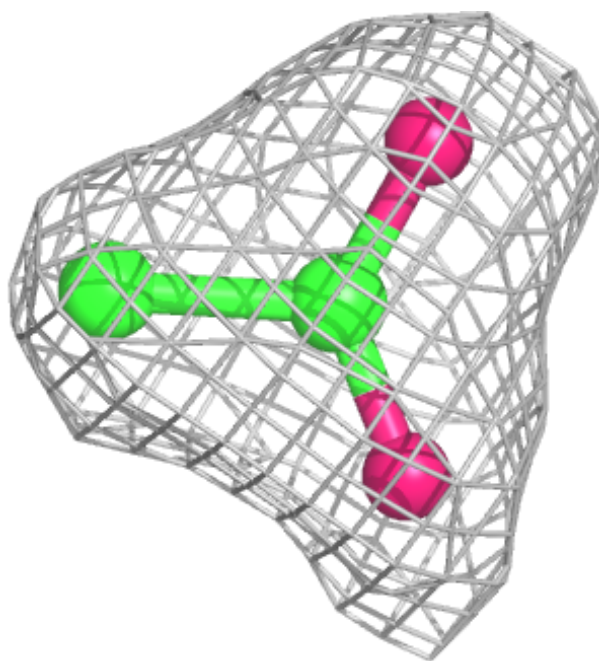and green (positive)
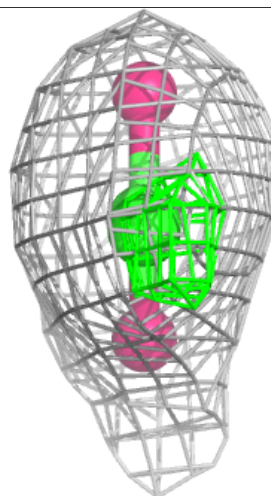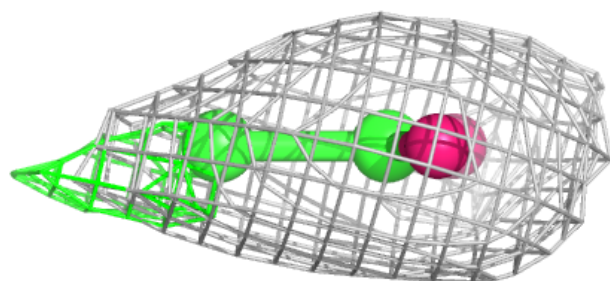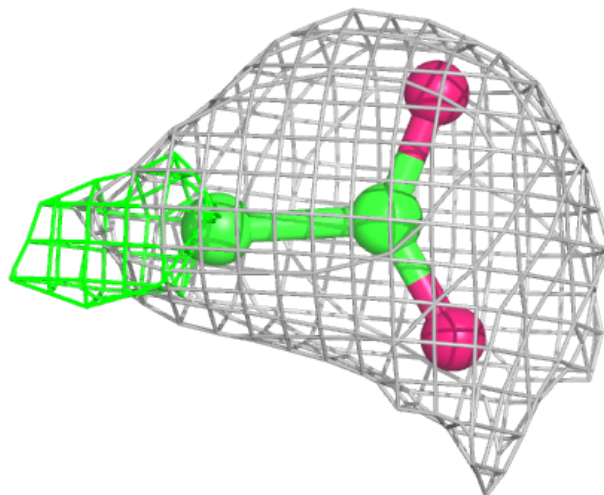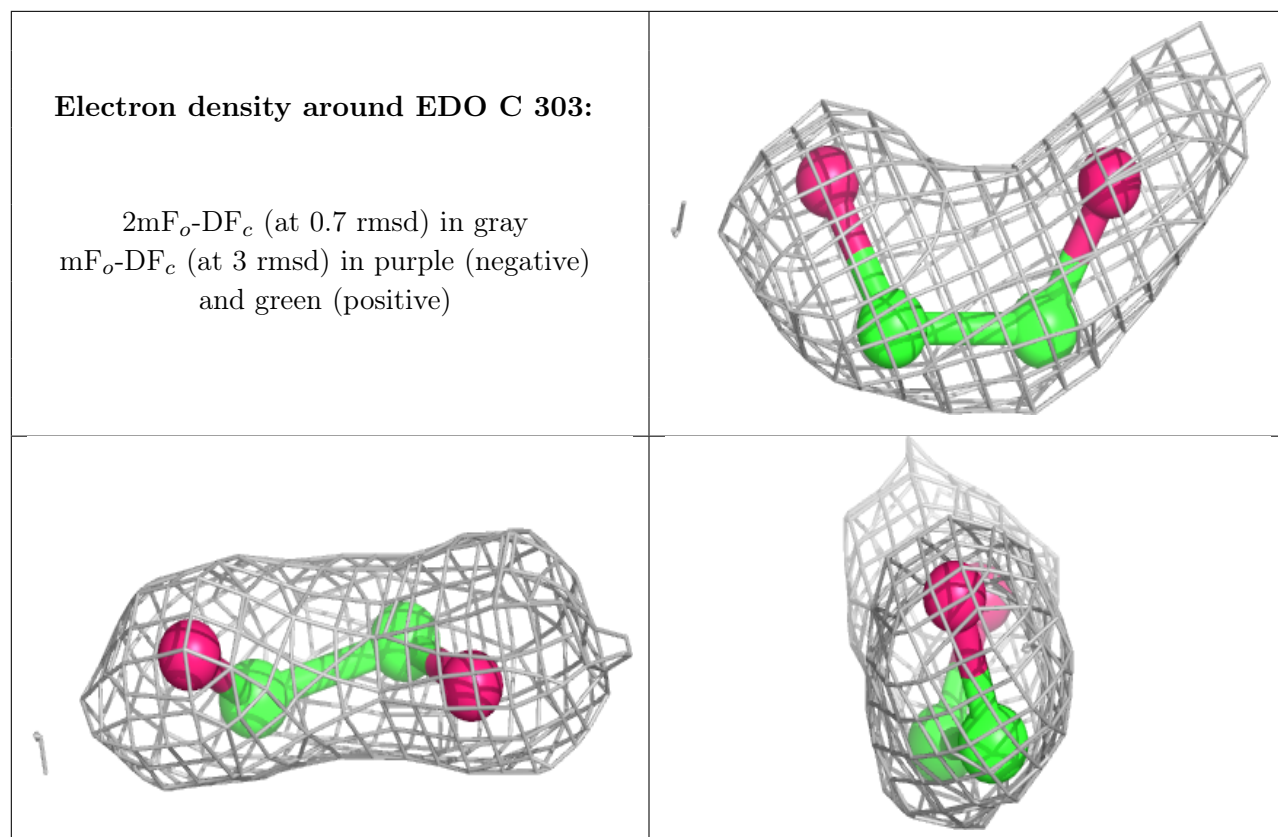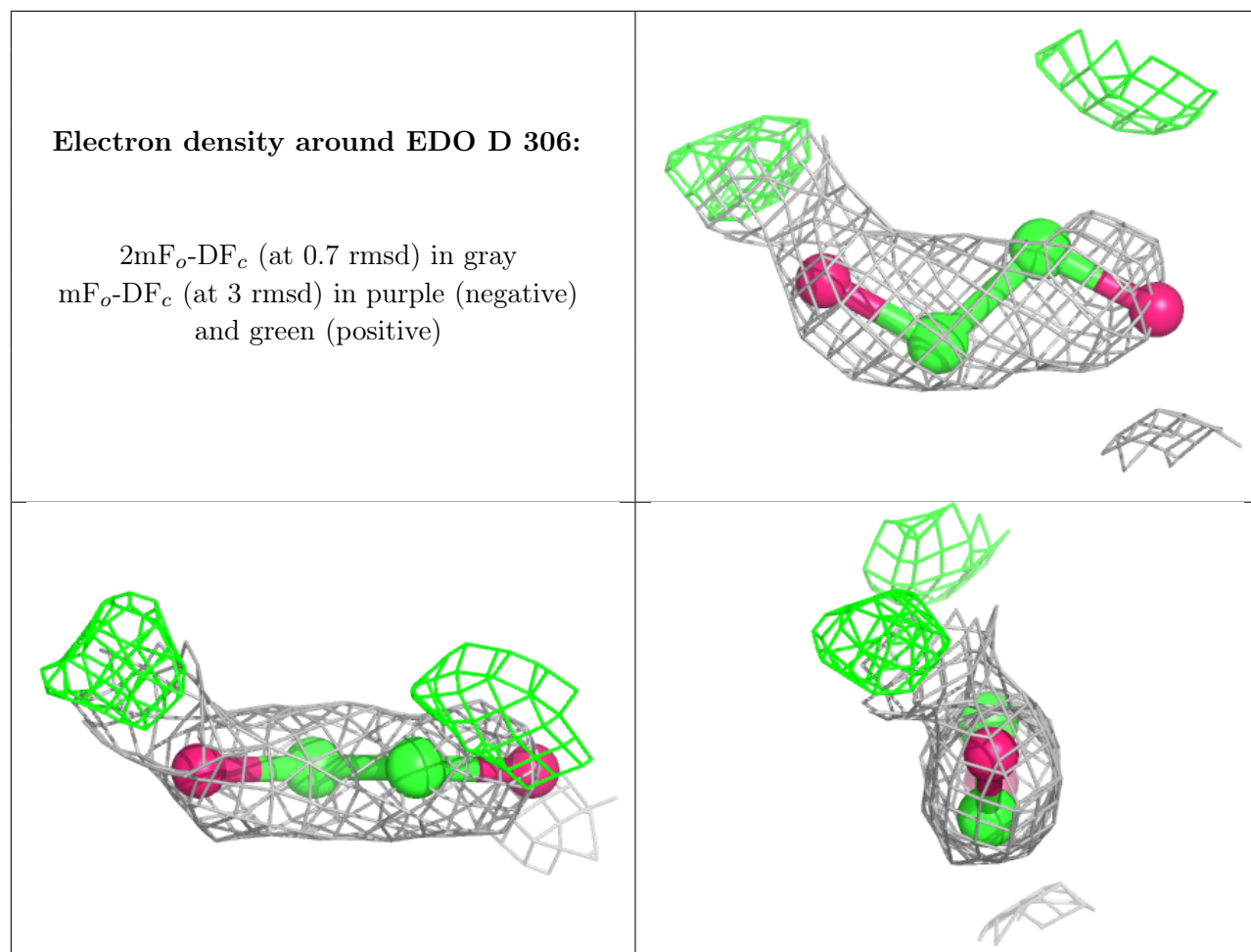
Electron density around ACT C 306:

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

Electron density around ACT D 310:

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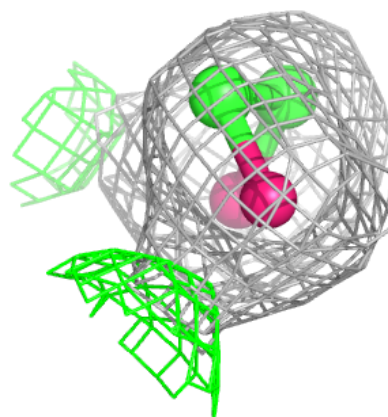and green (positive)

Electron density around PEG F 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 MG C 301:

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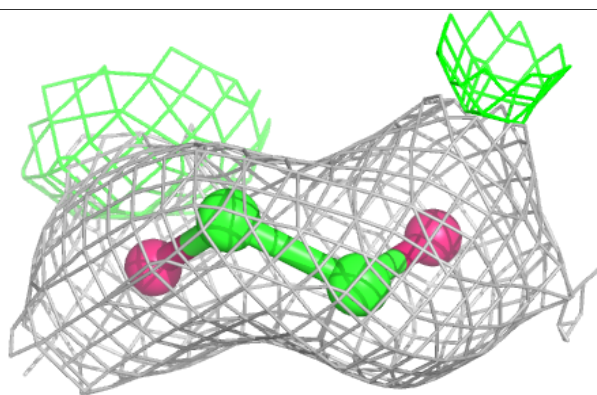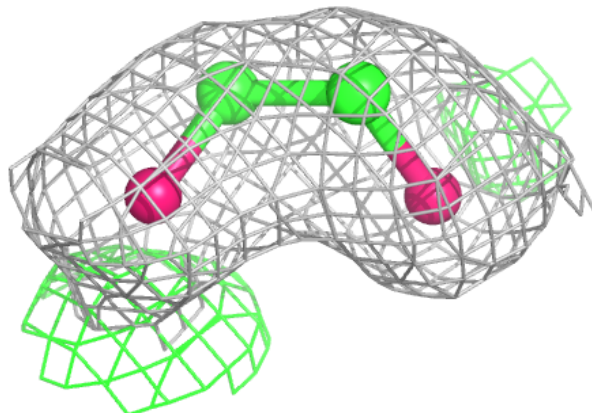and green (positive)

Electron density around EDO E 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 EDO C 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 PGE C 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 PGE D 307:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
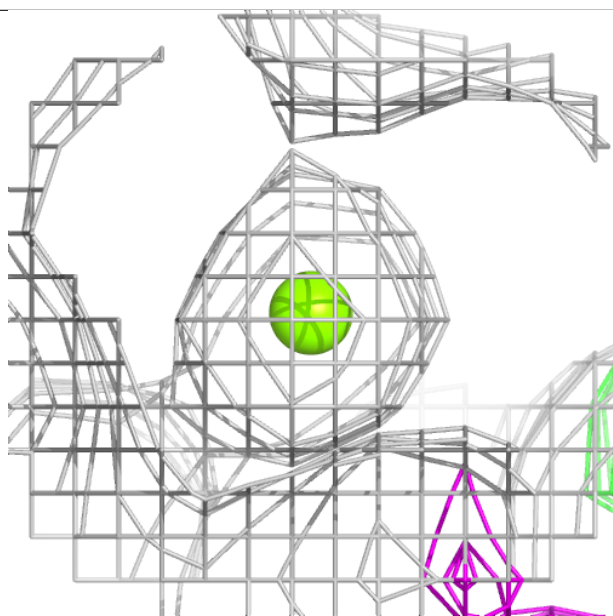mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around MG E 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 ACT 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)

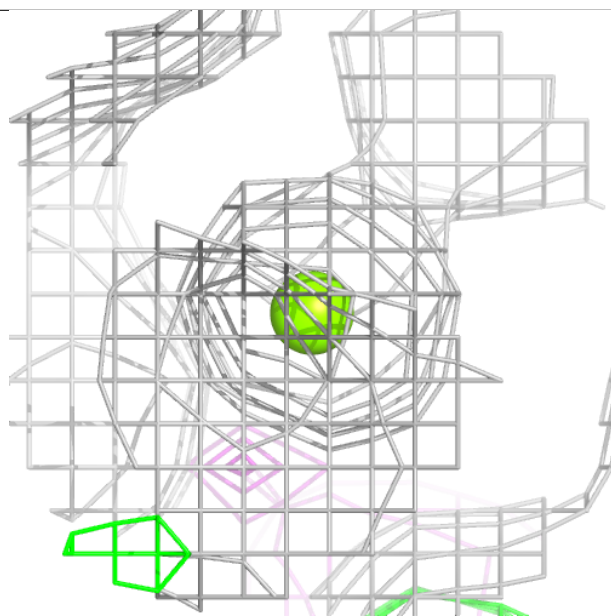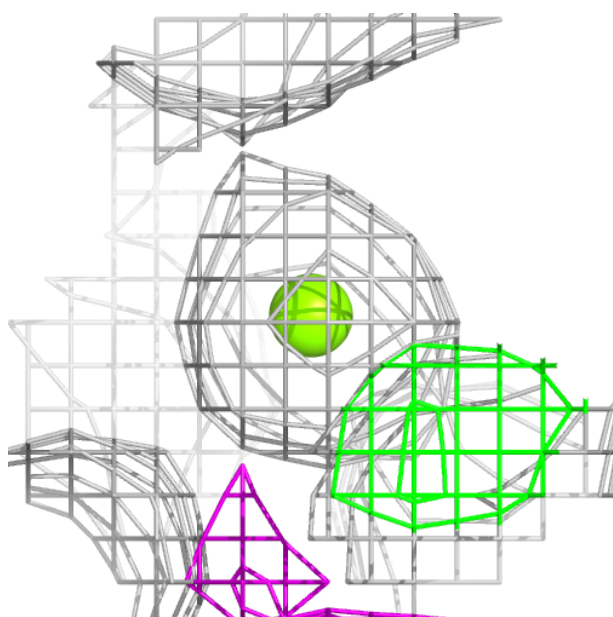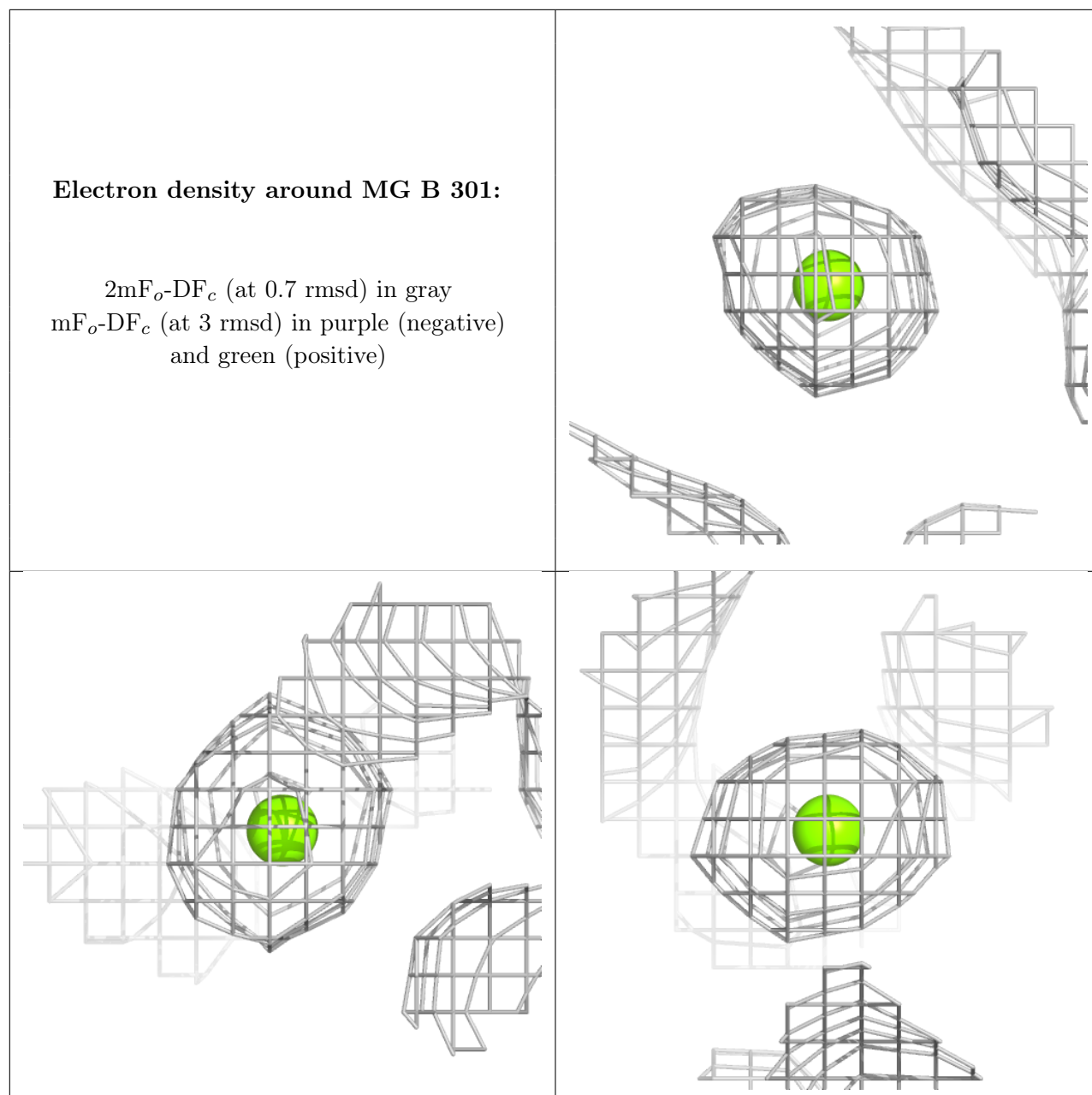**Electron density around EDO A 301:**

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

Electron density around MG D 301:

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

Electron density around MG 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)

6.5 Other polymers ⓘ

There are no such residues in this entry.