Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 03:06 PM EDT

PDB ID	:	7KOC
Title	:	Dihydrodipicolinate synthase (DHDPS) from C.jejuni, E88Q mutant with pyruvate bound in the active site
Authors	:	Saran, S.; Sanders, D.A.R.
Deposited on	:	2020-11-08
Resolution	:	2.06 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

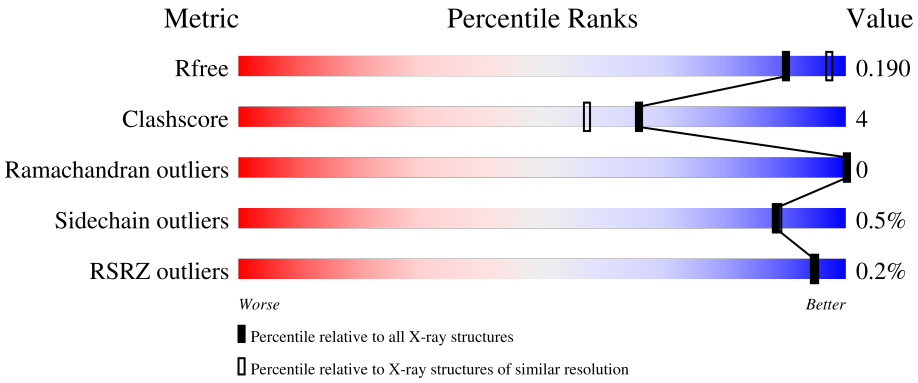
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	84% 12% 5%
1	B	310	90% 5% 5%
1	C	310	89% 6% 5%
1	D	310	86% 9% 5%
1	E	310	% 87% 9% 5%

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Mol	Chain	Length	Quality of chain
1	F	310	91% 5% 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
4	EDO	A	304	-	-	X	-
5	ACT	A	305	-	-	X	-
5	ACT	F	302	-	-	X	-
6	PEG	C	304	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 14920 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	296	Total	C	N	O	S	0	1	0
			2278	1447	380	438	13			
1	B	296	Total	C	N	O	S	0	0	0
			2264	1440	376	435	13			
1	C	296	Total	C	N	O	S	0	1	0
			2273	1445	380	435	13			
1	D	296	Total	C	N	O	S	0	0	0
			2268	1442	377	436	13			
1	E	296	Total	C	N	O	S	0	0	0
			2261	1437	375	436	13			
1	F	296	Total	C	N	O	S	0	0	0
			2268	1442	376	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	88	GLN	GLU	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	88	GLN	GLU	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	88	GLN	GLU	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	88	GLN	GLU	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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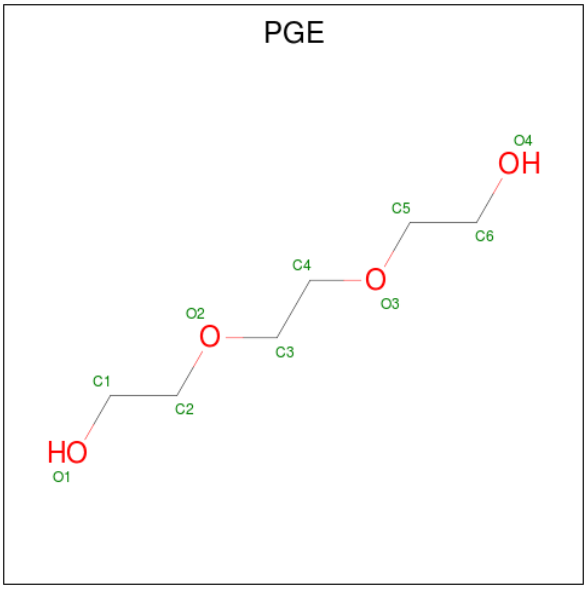
Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP Q9PPB4
E	-3	HIS	-	expression tag	UNP Q9PPB4
E	-2	HIS	-	expression tag	UNP Q9PPB4
E	-1	GLY	-	expression tag	UNP Q9PPB4
E	0	SER	-	expression tag	UNP Q9PPB4
E	88	GLN	GLU	engineered mutation	UNP Q9PPB4
F	-11	MET	-	expression tag	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	88	GLN	GLU	engineered mutation	UNP Q9PPB4

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$) (labeled as "Ligand of Interest" by depositor).



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

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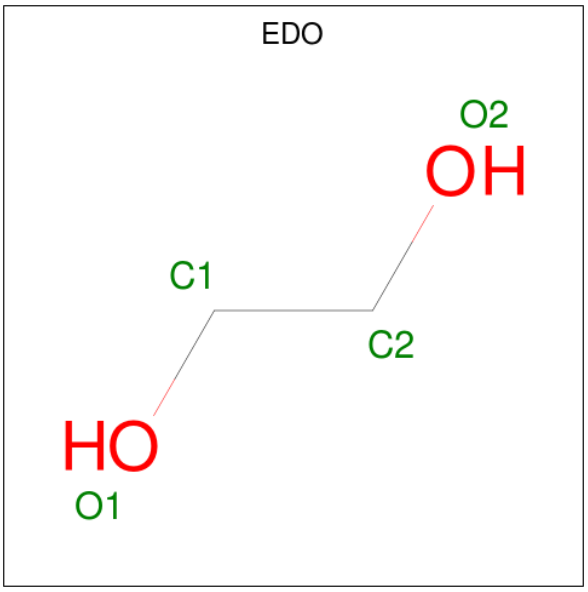
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 10 6 4	0	0
2	C	1	Total C O 10 6 4	0	0
2	D	1	Total C O 10 6 4	0	0
2	F	1	Total C O 10 6 4	0	0

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

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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$) (labeled as "Ligand of Interest" by depositor).



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

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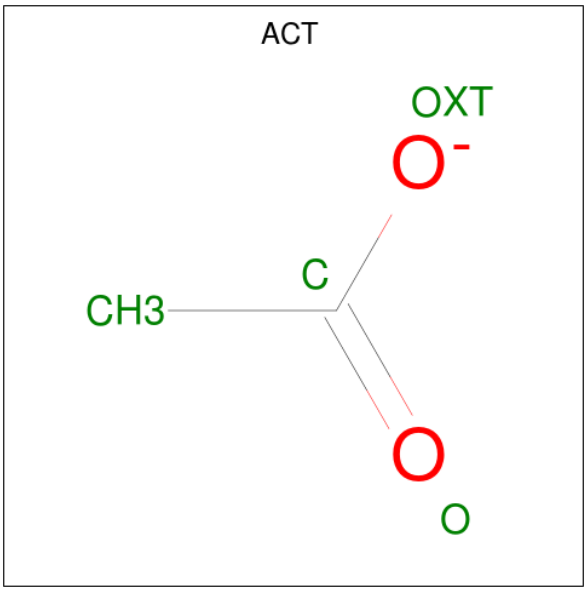
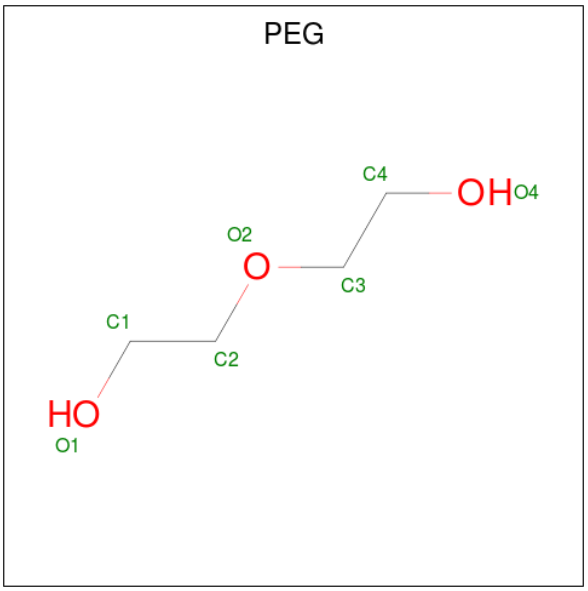
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 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	C	1	Total C O 7 4 3	0	0
6	D	1	Total C O 7 4 3	0	0

- Molecule 7 is water.

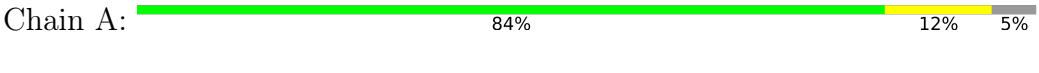
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	198	Total O 198 198	0	0
7	B	229	Total O 229 229	0	0
7	C	202	Total O 202 202	0	0
7	D	218	Total O 218 218	0	0
7	E	180	Total O 180 180	0	0
7	F	173	Total O 173 173	0	0

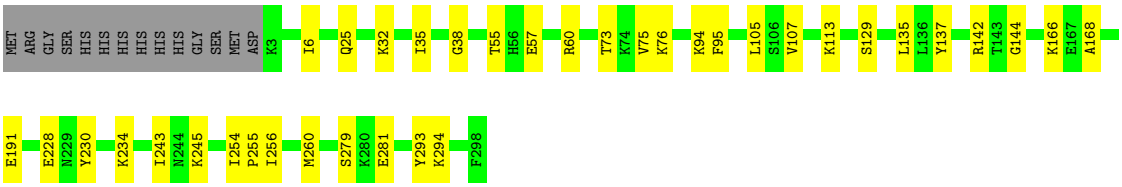
3 Residue-property plots (i)

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

• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

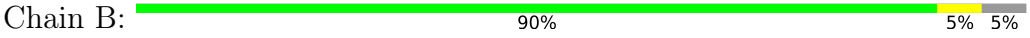
Chain A:





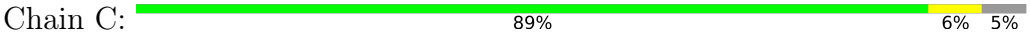
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain B:



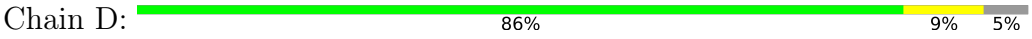
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

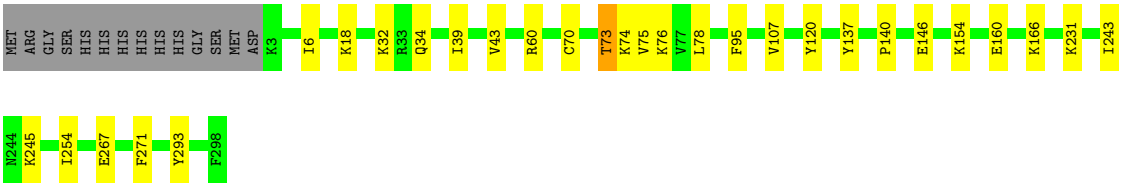
Chain C:



• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

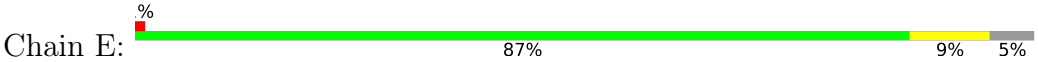
Chain D:

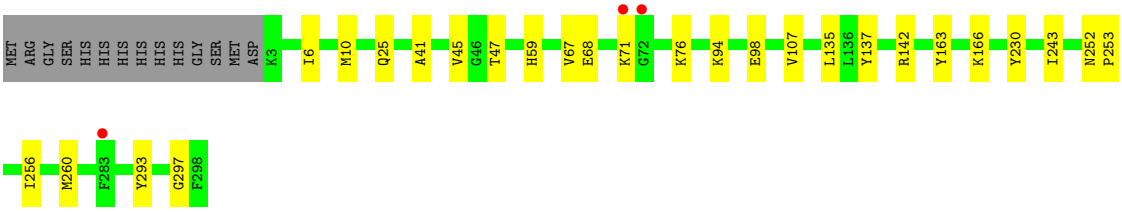




• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

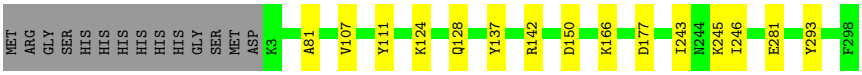
Chain E:





• 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	85.25Å 233.32Å 202.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.41 – 2.06 46.41 – 2.06	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.41-2.06) 95.6 (46.41-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.11 (at 2.07Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.163 , 0.191 0.164 , 0.190	Depositor DCC
R_{free} test set	6221 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 49.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14920	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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: MG, PEG, PGE, KPI, EDO, ACT

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	0.49	0/2303	0.57	0/3116
1	B	0.53	0/2288	0.54	0/3096
1	C	0.48	0/2298	0.56	0/3111
1	D	0.44	0/2292	0.58	0/3102
1	E	0.46	1/2285 (0.0%)	0.57	0/3095
1	F	0.43	0/2292	0.56	0/3101
All	All	0.47	1/13758 (0.0%)	0.56	0/18621

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	230	TYR	CE1-CZ	-5.45	1.31	1.38

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2278	0	2294	29	0
1	B	2264	0	2281	19	0
1	C	2273	0	2290	16	0
1	D	2268	0	2291	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2261	0	2269	17	0
1	F	2268	0	2285	14	0
2	A	10	0	14	0	0
2	B	10	0	14	5	0
2	C	10	0	14	1	0
2	D	10	0	14	2	0
2	F	10	0	14	1	0
3	A	2	0	0	0	0
3	D	2	0	0	0	0
4	A	4	0	6	5	0
4	C	8	0	12	0	0
4	D	8	0	12	3	0
4	E	4	0	6	0	0
5	A	4	0	3	3	0
5	B	4	0	3	1	0
5	E	4	0	3	1	0
5	F	4	0	3	2	0
6	C	7	0	10	6	0
6	D	7	0	10	1	0
7	A	198	0	0	4	0
7	B	229	0	0	0	0
7	C	202	0	0	3	0
7	D	218	0	0	0	0
7	E	180	0	0	2	0
7	F	173	0	0	4	0
All	All	14920	0	13848	111	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.

All (111) 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:C:60:ARG:HB2	1:C:95:PHE:HZ	1.33	0.92
1:F:142:ARG:HE	5:F:302:ACT:H1	1.40	0.87
1:A:73:THR:HB	4:A:304:EDO:C2	2.05	0.87
1:E:68:GLU:HA	1:E:71:LYS:HD2	1.61	0.81
1:A:142:ARG:HE	5:A:305:ACT:H1	1.45	0.80
1:A:142:ARG:HE	5:A:305:ACT:CH3	1.97	0.78
1:B:140:PRO:HG3	1:B:146:GLU:OE1	1.84	0.76
1:C:149:THR:H	6:C:304:PEG:H42	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:ARG:HB2	1:A:95:PHE:HZ	1.50	0.75
1:A:73:THR:HB	4:A:304:EDO:H22	1.67	0.75
1:B:154:LYS:NZ	2:B:301:PGE:H62	2.02	0.74
1:C:288:GLU:HA	1:C:291:LYS:HE2	1.69	0.74
6:C:304:PEG:H32	7:C:572:HOH:O	1.89	0.72
1:F:150:ASP:HB3	2:F:301:PGE:H62	1.70	0.71
1:A:73:THR:HB	4:A:304:EDO:H21	1.73	0.70
1:C:60:ARG:HB2	1:C:95:PHE:CZ	2.24	0.68
1:A:73:THR:CB	4:A:304:EDO:H22	2.23	0.67
1:E:107:VAL:HA	1:E:137:TYR:HB3	1.75	0.67
1:A:6:ILE:HG12	1:A:76:LYS:HD3	1.77	0.66
1:B:60:ARG:HB2	1:B:95:PHE:HZ	1.60	0.65
1:B:154:LYS:HZ3	2:B:301:PGE:H62	1.63	0.64
1:A:55:THR:OG1	1:A:57:GLU:HG2	1.99	0.63
1:D:107:VAL:HA	1:D:137:TYR:HB3	1.81	0.63
1:C:149:THR:H	6:C:304:PEG:C4	2.12	0.62
1:C:148:SER:HA	6:C:304:PEG:H31	1.82	0.62
1:B:5:ILE:HD12	1:B:186:MET:HE2	1.82	0.62
1:C:107:VAL:HA	1:C:137:TYR:HB3	1.80	0.61
1:B:107:VAL:HA	1:B:137:TYR:HB3	1.82	0.61
1:B:87:HIS:HB3	4:D:304:EDO:C2	2.30	0.61
1:D:154:LYS:HD3	2:D:301:PGE:H12	1.83	0.61
1:A:234:LYS:HD3	5:B:302:ACT:O	2.01	0.61
1:C:76:LYS:NZ	7:C:402:HOH:O	2.31	0.59
1:A:228:GLU:OE1	1:B:231:LYS:HD2	2.02	0.59
1:F:107:VAL:HA	1:F:137:TYR:HB3	1.83	0.59
1:A:107:VAL:HA	1:A:137:TYR:HB3	1.84	0.59
1:E:142:ARG:HH21	5:E:302:ACT:H2	1.68	0.58
1:A:32:LYS:HD3	7:A:523:HOH:O	2.04	0.58
1:E:94:LYS:O	1:E:98:GLU:HG3	2.04	0.58
1:C:149:THR:N	6:C:304:PEG:H42	2.18	0.57
1:E:6:ILE:HG12	1:E:76:LYS:HD3	1.84	0.57
1:B:87:HIS:HB3	4:D:304:EDO:H21	1.84	0.57
1:A:113:LYS:NZ	1:A:144:GLY:O	2.33	0.54
1:D:73:THR:O	1:D:74:LYS:HB2	2.09	0.53
1:F:124:LYS:HE2	1:F:128:GLN:HE22	1.74	0.52
1:F:142:ARG:NE	5:F:302:ACT:H1	2.20	0.51
1:B:154:LYS:NZ	2:B:301:PGE:H12	2.26	0.50
1:C:160:GLU:O	1:C:160:GLU:HG3	2.10	0.50
1:B:231:LYS:H	1:B:231:LYS:CE	2.25	0.49
1:E:10:MET:HG2	1:E:41:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:LYS:HE3	1:C:129:SER:HB2	1.93	0.49
1:F:124:LYS:HE2	1:F:128:GLN:NE2	2.28	0.49
1:E:252:ASN:ND2	1:E:253:PRO:HA	2.29	0.48
1:D:18:LYS:HD2	1:D:267:GLU:OE2	2.14	0.48
1:E:256:ILE:O	1:E:260:MET:HG2	2.14	0.47
1:B:154:LYS:HZ1	2:B:301:PGE:H12	1.79	0.47
1:E:67:VAL:HG12	1:E:71:LYS:NZ	2.30	0.47
1:C:292:LYS:HE3	1:C:293:TYR:CZ	2.49	0.47
1:A:94:LYS:HE2	1:A:129:SER:HB2	1.96	0.47
1:B:231:LYS:H	1:B:231:LYS:HE2	1.80	0.46
1:D:245:LYS:HA	1:D:245:LYS:HD2	1.74	0.46
1:A:142:ARG:NE	5:A:305:ACT:H1	2.23	0.46
1:B:7:ILE:HG21	1:B:186:MET:CE	2.46	0.46
1:C:154:LYS:NZ	2:C:301:PGE:H52	2.31	0.46
1:D:243:ILE:HB	1:D:293:TYR:CE2	2.51	0.46
1:A:38:GLY:O	7:A:401:HOH:O	2.21	0.45
1:A:243:ILE:HB	1:A:293:TYR:CE2	2.52	0.45
1:A:279:SER:OG	1:A:281:GLU:HG2	2.17	0.45
1:E:45:VAL:HG11	1:E:59:HIS:HA	1.98	0.45
1:A:245:LYS:HA	1:A:245:LYS:HD2	1.66	0.45
1:E:68:GLU:HA	1:E:71:LYS:CD	2.37	0.45
1:B:87:HIS:HB3	4:D:304:EDO:H22	1.99	0.45
1:E:243:ILE:HB	1:E:293:TYR:CE2	2.51	0.44
1:D:6:ILE:HG12	1:D:76:LYS:HD3	2.00	0.44
1:C:204:LYS:HD3	1:C:204:LYS:HA	1.79	0.44
1:E:47:THR:HG1	1:F:111:TYR:HH	1.64	0.44
1:F:245:LYS:HD2	1:F:245:LYS:HA	1.82	0.44
1:E:25:GLN:H	1:E:25:GLN:CD	2.21	0.43
1:A:256:ILE:O	1:A:260:MET:HG2	2.18	0.43
1:D:254:ILE:HA	1:D:271:PHE:CE2	2.53	0.43
1:D:73:THR:CG2	1:D:75:VAL:H	2.31	0.43
1:B:60:ARG:HB2	1:B:95:PHE:CZ	2.47	0.43
1:D:60:ARG:HG3	1:D:95:PHE:CZ	2.54	0.43
1:E:297:GLY:O	7:E:401:HOH:O	2.21	0.43
1:B:10:MET:HG2	1:B:41:ALA:HB3	2.01	0.43
1:D:120:TYR:CG	2:D:301:PGE:H3	2.54	0.43
1:E:25:GLN:NE2	7:E:405:HOH:O	2.47	0.43
1:A:254:ILE:HB	1:A:255:PRO:HD3	2.01	0.42
1:D:70:CYS:O	1:D:73:THR:HB	2.19	0.42
1:C:243:ILE:HB	1:C:293:TYR:CE2	2.54	0.42
1:D:34:GLN:HB3	1:D:39:ILE:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:VAL:HG22	1:D:78:LEU:HB3	2.01	0.42
1:F:243:ILE:HB	1:F:293:TYR:CE2	2.55	0.42
1:F:281:GLU:OE2	7:F:402:HOH:O	2.22	0.42
1:D:140:PRO:HG3	1:D:146:GLU:OE2	2.19	0.42
1:A:76:LYS:HA	7:A:406:HOH:O	2.19	0.42
1:A:73:THR:CG2	4:A:304:EDO:H22	2.50	0.42
1:A:168:ALA:HA	1:A:191:GLU:HG3	2.02	0.42
1:D:32:LYS:HE3	6:D:306:PEG:H31	2.02	0.42
1:A:57:GLU:CG	7:A:414:HOH:O	2.68	0.41
1:C:256:ILE:O	1:C:260:MET:HG2	2.20	0.41
1:F:293:TYR:HA	7:F:419:HOH:O	2.20	0.41
1:A:35:ILE:HG12	1:A:75:VAL:HG21	2.02	0.41
1:E:135:LEU:HD13	1:E:163:TYR:CZ	2.55	0.41
1:A:230:TYR:CD2	1:B:230:TYR:HD2	2.39	0.41
1:B:154:LYS:HD3	2:B:301:PGE:H52	2.01	0.41
6:C:304:PEG:H41	7:C:403:HOH:O	2.20	0.41
1:F:177:ASP:OD2	7:F:401:HOH:O	2.21	0.40
1:F:246:ILE:HD12	1:F:246:ILE:HA	1.98	0.40
1:A:105:LEU:HD13	1:A:135:LEU:HD23	2.04	0.40
1:D:73:THR:O	1:D:74:LYS:CB	2.70	0.40
1:F:81:ALA:O	7:F:404:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	294/310 (95%)	287 (98%)	7 (2%)	0	100	100
1	B	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
1	C	294/310 (95%)	288 (98%)	6 (2%)	0	100	100
1	D	293/310 (94%)	285 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	293/310 (94%)	285 (97%)	8 (3%)	0	100	100
1	F	293/310 (94%)	286 (98%)	7 (2%)	0	100	100
All	All	1760/1860 (95%)	1717 (98%)	43 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	246/260 (95%)	244 (99%)	2 (1%)	81	81
1	B	243/260 (94%)	240 (99%)	3 (1%)	71	69
1	C	245/260 (94%)	245 (100%)	0	100	100
1	D	245/260 (94%)	242 (99%)	3 (1%)	71	69
1	E	243/260 (94%)	243 (100%)	0	100	100
1	F	244/260 (94%)	244 (100%)	0	100	100
All	All	1466/1560 (94%)	1458 (100%)	8 (0%)	88	89

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	294	LYS
1	B	184	ARG
1	B	231	LYS
1	B	268	SER
1	D	73	THR
1	D	160	GLU
1	D	231	LYS

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

Mol	Chain	Res	Type
1	A	242	ASN
1	C	25	GLN
1	C	88	GLN
1	E	242	ASN
1	F	4	ASN
1	F	128	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	C	166	1	11,13,14	1.92	2 (18%)	10,15,17	3.79	6 (60%)
1	KPI	A	166	1	11,13,14	1.94	2 (18%)	10,15,17	3.50	6 (60%)
1	KPI	B	166	1	11,13,14	1.92	2 (18%)	10,15,17	4.10	6 (60%)
1	KPI	E	166	1	11,13,14	1.90	2 (18%)	10,15,17	3.82	6 (60%)
1	KPI	F	166	1	11,13,14	1.89	2 (18%)	10,15,17	3.64	6 (60%)
1	KPI	D	166	1	11,13,14	1.10	1 (9%)	10,15,17	3.52	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	C	166	1	-	1/13/14/16	-
1	KPI	A	166	1	-	2/13/14/16	-
1	KPI	B	166	1	-	0/13/14/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KPI	E	166	1	-	2/13/14/16	-
1	KPI	F	166	1	-	3/13/14/16	-
1	KPI	D	166	1	-	0/13/14/16	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	166	KPI	O2-CX2	5.48	1.37	1.22
1	A	166	KPI	O2-CX2	5.46	1.37	1.22
1	E	166	KPI	O2-CX2	5.45	1.37	1.22
1	F	166	KPI	O2-CX2	5.39	1.36	1.22
1	C	166	KPI	O2-CX2	5.32	1.36	1.22
1	E	166	KPI	O1-CX2	-2.27	1.24	1.30
1	C	166	KPI	O1-CX2	-2.26	1.24	1.30
1	A	166	KPI	O1-CX2	-2.25	1.24	1.30
1	F	166	KPI	O1-CX2	-2.23	1.24	1.30
1	D	166	KPI	O1-CX2	2.23	1.37	1.30
1	B	166	KPI	O1-CX2	-2.06	1.24	1.30

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	166	KPI	C1-CX1-CX2	-9.53	108.91	118.17
1	D	166	KPI	C1-CX1-CX2	-8.46	109.94	118.17
1	E	166	KPI	C1-CX1-CX2	-8.22	110.17	118.17
1	C	166	KPI	C1-CX1-CX2	-8.21	110.19	118.17
1	F	166	KPI	C1-CX1-CX2	-7.33	111.04	118.17
1	A	166	KPI	C1-CX1-CX2	-7.23	111.14	118.17
1	F	166	KPI	O2-CX2-CX1	-5.31	114.60	121.38
1	E	166	KPI	O2-CX2-CX1	-5.18	114.76	121.38
1	B	166	KPI	O2-CX2-CX1	-5.18	114.76	121.38
1	C	166	KPI	O1-CX2-CX1	5.18	127.60	116.35
1	F	166	KPI	O1-CX2-CX1	5.07	127.36	116.35
1	D	166	KPI	O2-CX2-CX1	4.99	127.75	121.38
1	E	166	KPI	O1-CX2-CX1	4.84	126.86	116.35
1	A	166	KPI	O1-CX2-CX1	4.83	126.85	116.35
1	B	166	KPI	O1-CX2-CX1	4.82	126.82	116.35
1	C	166	KPI	O2-CX2-CX1	-4.63	115.47	121.38
1	A	166	KPI	O2-CX2-CX1	-4.54	115.58	121.38
1	E	166	KPI	C1-CX1-NZ	3.57	132.45	123.11
1	B	166	KPI	C1-CX1-NZ	3.27	131.67	123.11
1	F	166	KPI	C1-CX1-NZ	3.24	131.58	123.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	166	KPI	C1-CX1-NZ	3.12	131.28	123.11
1	D	166	KPI	C1-CX1-NZ	3.12	131.28	123.11
1	C	166	KPI	O1-CX2-O2	-2.92	116.94	123.61
1	C	166	KPI	C1-CX1-NZ	2.91	130.72	123.11
1	D	166	KPI	O1-CX2-O2	-2.68	117.48	123.61
1	A	166	KPI	O1-CX2-O2	-2.64	117.57	123.61
1	F	166	KPI	O1-CX2-O2	-2.43	118.04	123.61
1	E	166	KPI	CE-NZ-CX1	2.35	128.11	121.70
1	A	166	KPI	CE-NZ-CX1	2.33	128.05	121.70
1	E	166	KPI	O1-CX2-O2	-2.29	118.37	123.61
1	D	166	KPI	CE-NZ-CX1	2.28	127.91	121.70
1	B	166	KPI	O1-CX2-O2	-2.27	118.42	123.61
1	B	166	KPI	CE-NZ-CX1	2.14	127.52	121.70
1	C	166	KPI	CD-CE-NZ	2.01	114.33	110.66
1	F	166	KPI	CE-NZ-CX1	2.00	127.15	121.70

There are no chirality outliers.

All (8) torsion outliers are listed below:

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

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 21 ligands modelled in this entry, 4 are monoatomic - leaving 17 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	$\#\|Z\| > 2$
4	EDO	A	304	-	3,3,3	0.32	0	2,2,2	0.32	0
2	PGE	F	301	-	9,9,9	0.30	0	8,8,8	0.33	0
2	PGE	B	301	-	9,9,9	0.30	0	8,8,8	0.38	0
2	PGE	D	301	-	9,9,9	0.33	0	8,8,8	0.29	0
5	ACT	F	302	-	3,3,3	1.21	0	3,3,3	1.47	0
5	ACT	B	302	-	3,3,3	1.25	1 (33%)	3,3,3	1.34	1 (33%)
2	PGE	C	301	-	9,9,9	0.29	0	8,8,8	0.37	0
4	EDO	C	302	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	E	301	-	3,3,3	0.41	0	2,2,2	0.50	0
6	PEG	C	304	-	6,6,6	0.45	0	5,5,5	1.03	0
6	PEG	D	306	-	6,6,6	0.48	0	5,5,5	0.28	0
4	EDO	C	303	-	3,3,3	0.20	0	2,2,2	0.53	0
4	EDO	D	305	-	3,3,3	0.48	0	2,2,2	0.36	0
5	ACT	A	305	-	3,3,3	1.37	1 (33%)	3,3,3	2.47	1 (33%)
2	PGE	A	301	-	9,9,9	0.30	0	8,8,8	0.38	0
5	ACT	E	302	-	3,3,3	1.02	0	3,3,3	1.59	0
4	EDO	D	304	-	3,3,3	0.42	0	2,2,2	0.32	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
4	EDO	A	304	-	-	1/1/1/1	-
2	PGE	F	301	-	-	3/7/7/7	-
2	PGE	B	301	-	-	3/7/7/7	-
2	PGE	D	301	-	-	3/7/7/7	-
2	PGE	C	301	-	-	5/7/7/7	-
4	EDO	C	302	-	-	1/1/1/1	-
4	EDO	E	301	-	-	1/1/1/1	-
6	PEG	D	306	-	-	2/4/4/4	-
4	EDO	C	303	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	D	305	-	-	0/1/1/1	-
6	PEG	C	304	-	-	4/4/4/4	-
2	PGE	A	301	-	-	1/7/7/7	-
4	EDO	D	304	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	305	ACT	OXT-C	-2.15	1.20	1.30
5	B	302	ACT	OXT-C	-2.12	1.20	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	305	ACT	OXT-C-O	-3.48	109.23	122.05
5	B	302	ACT	OXT-C-O	-2.05	114.49	122.05

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	PGE	O2-C3-C4-O3
2	C	301	PGE	O2-C3-C4-O3
2	F	301	PGE	O2-C3-C4-O3
2	D	301	PGE	O3-C5-C6-O4
6	C	304	PEG	O2-C3-C4-O4
2	C	301	PGE	O1-C1-C2-O2
2	A	301	PGE	O3-C5-C6-O4
2	B	301	PGE	O1-C1-C2-O2
6	C	304	PEG	O1-C1-C2-O2
4	A	304	EDO	O1-C1-C2-O2
4	C	302	EDO	O1-C1-C2-O2
2	B	301	PGE	O2-C3-C4-O3
6	D	306	PEG	O2-C3-C4-O4
2	F	301	PGE	O3-C5-C6-O4
2	D	301	PGE	C3-C4-O3-C5
6	C	304	PEG	C1-C2-O2-C3
2	C	301	PGE	O3-C5-C6-O4
2	F	301	PGE	C6-C5-O3-C4
2	C	301	PGE	C3-C4-O3-C5
6	C	304	PEG	C4-C3-O2-C2

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Mol	Chain	Res	Type	Atoms
4	E	301	EDO	O1-C1-C2-O2
6	D	306	PEG	O1-C1-C2-O2
2	B	301	PGE	C3-C4-O3-C5
2	C	301	PGE	C1-C2-O2-C3

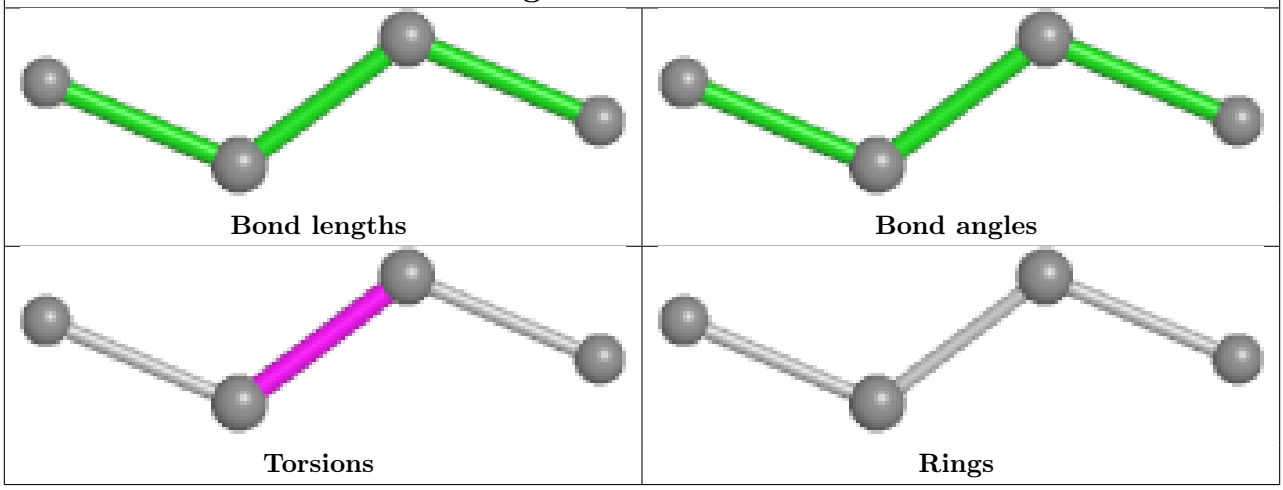
There are no ring outliers.

12 monomers are involved in 31 short contacts:

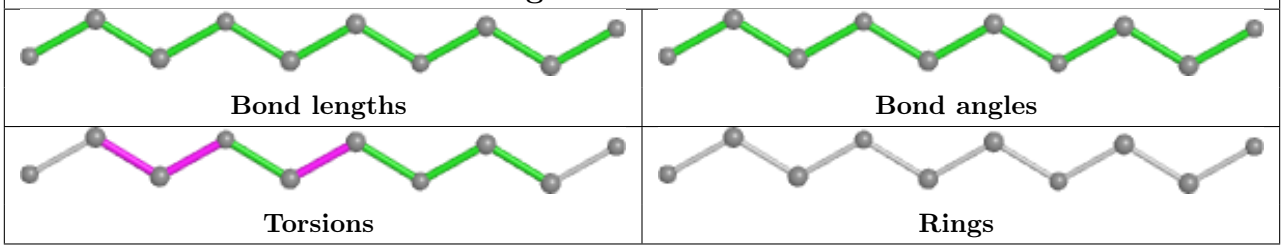
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	304	EDO	5	0
2	F	301	PGE	1	0
2	B	301	PGE	5	0
2	D	301	PGE	2	0
5	F	302	ACT	2	0
5	B	302	ACT	1	0
2	C	301	PGE	1	0
6	C	304	PEG	6	0
6	D	306	PEG	1	0
5	A	305	ACT	3	0
5	E	302	ACT	1	0
4	D	304	EDO	3	0

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.

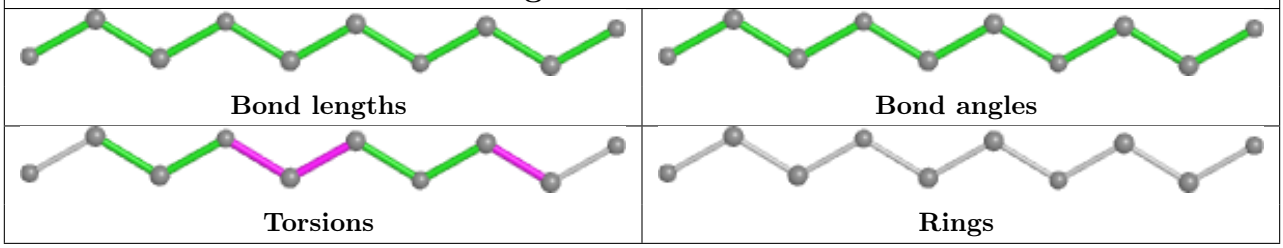
Ligand EDO A 304



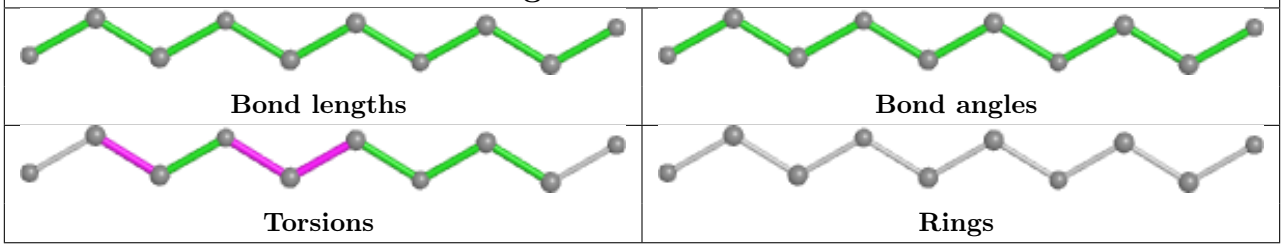
Ligand PGE F 301



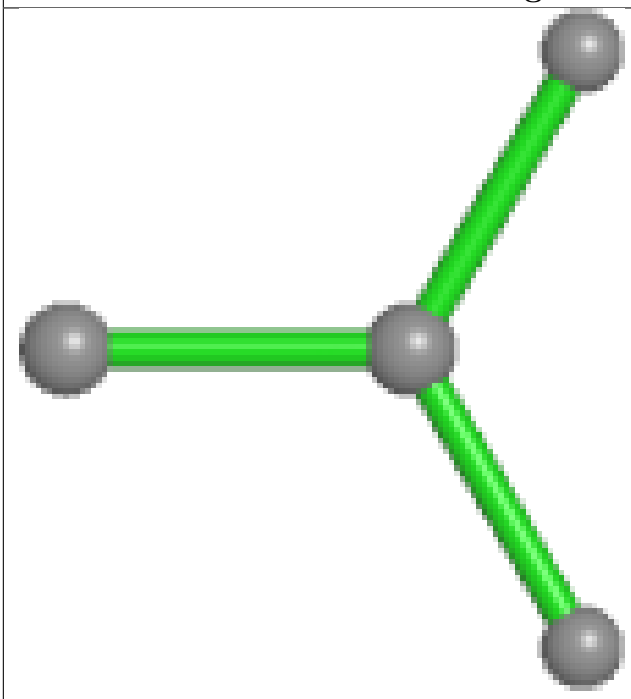
Ligand PGE B 301



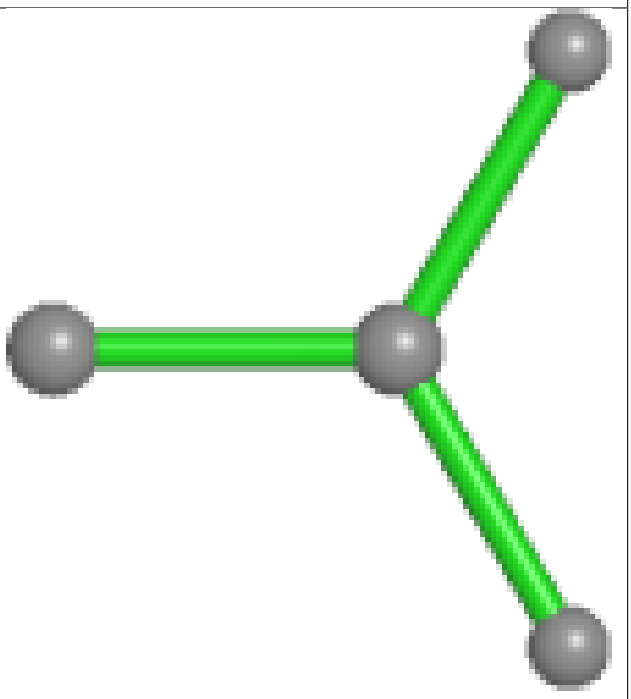
Ligand PGE D 301



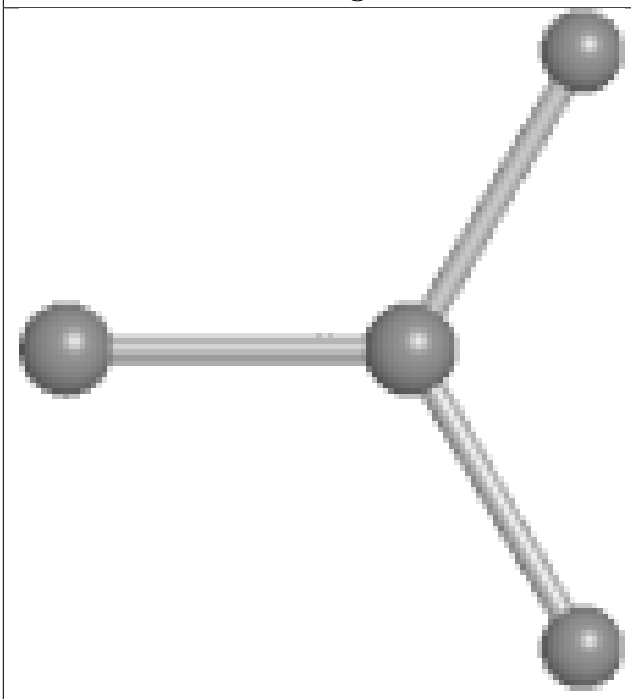
Ligand ACT F 302



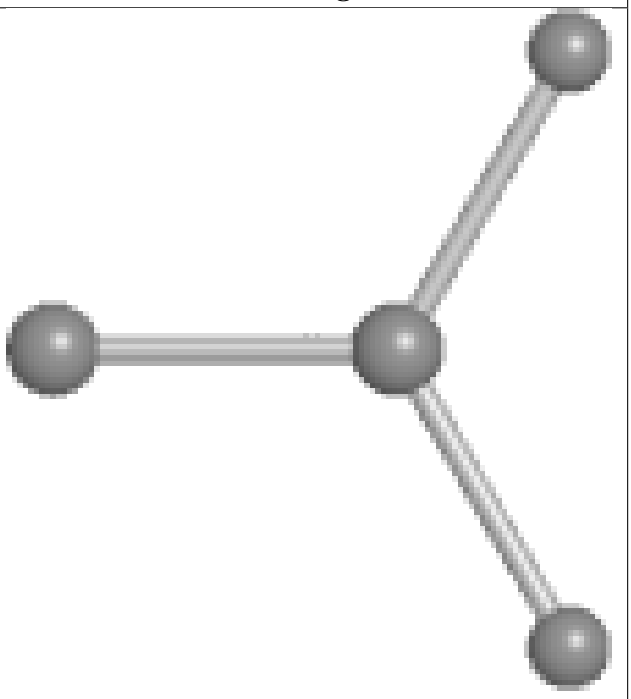
Bond lengths



Bond angles

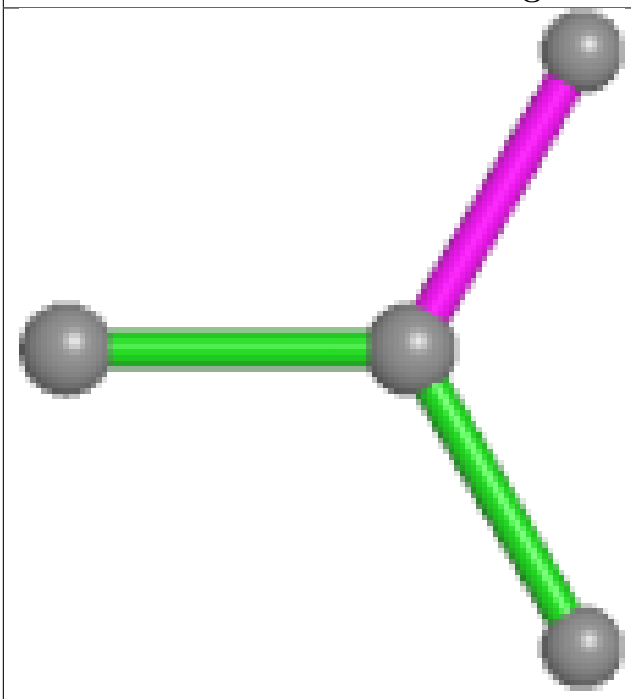


Torsions

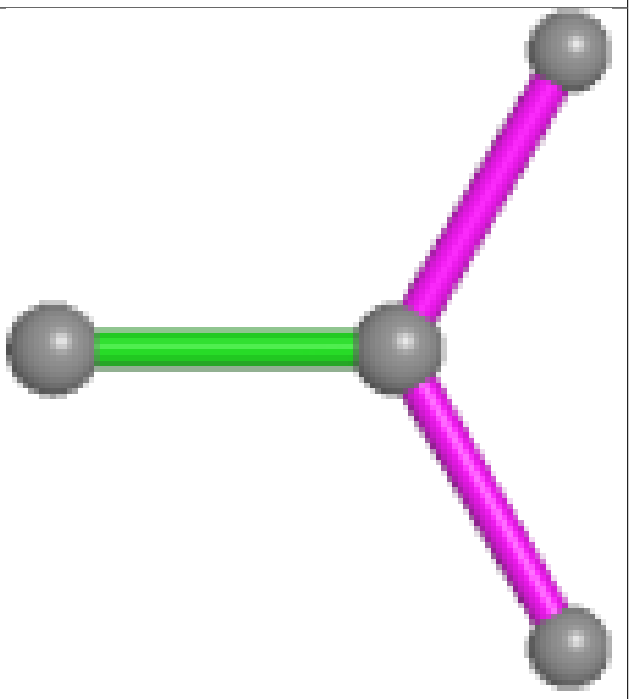


Rings

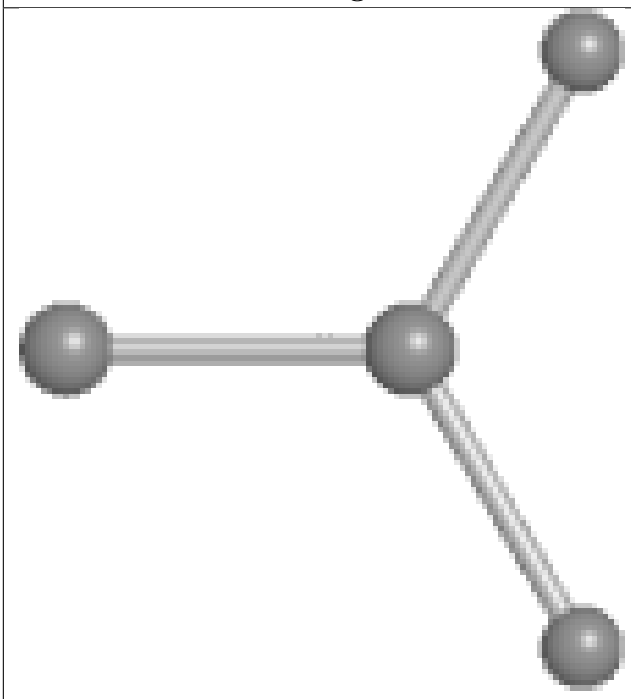
Ligand ACT B 302



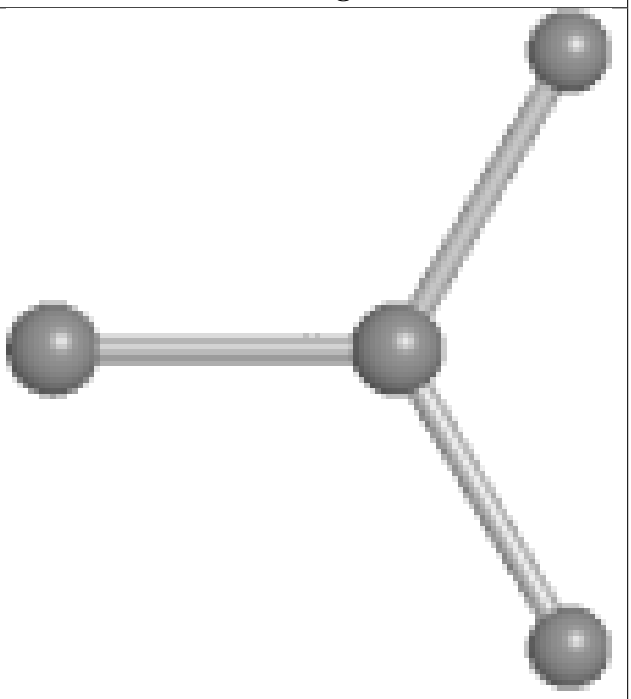
Bond lengths



Bond angles



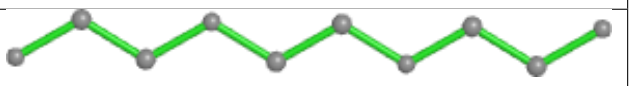
Torsions



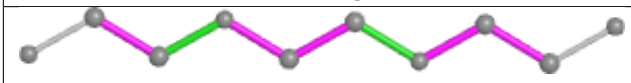
Rings

Ligand PGE C 301

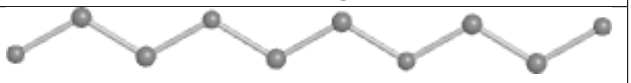
Bond lengths



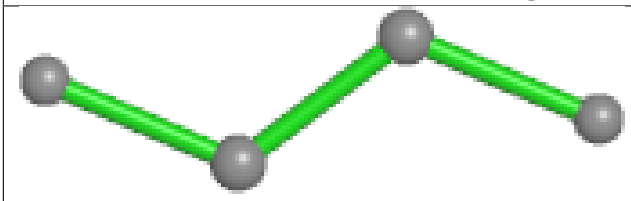
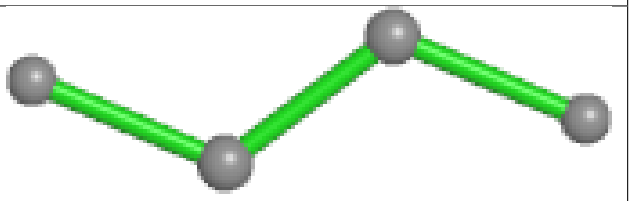
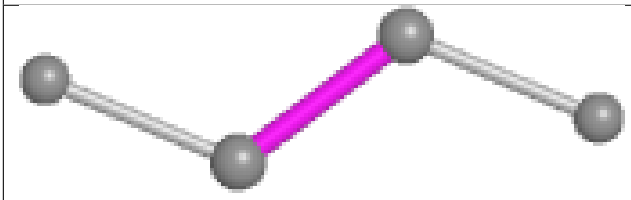
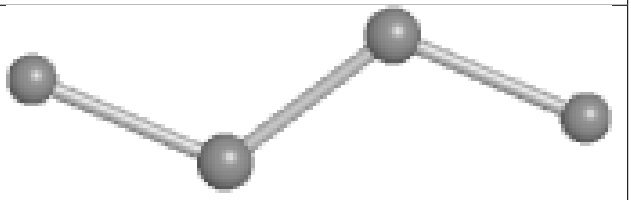
Bond angles

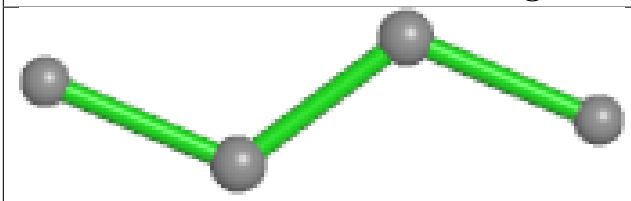
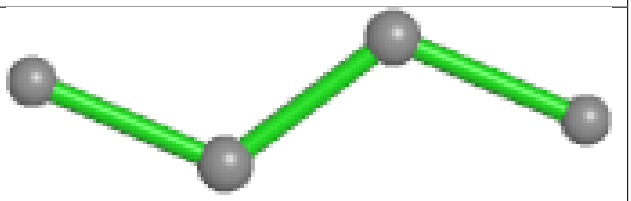
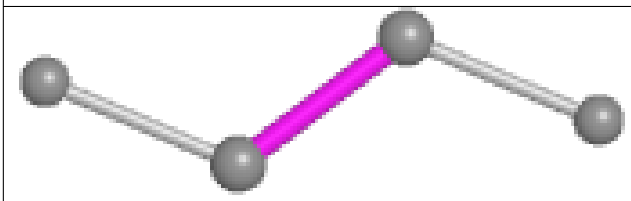
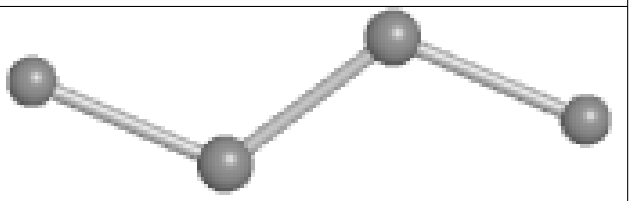


Torsions

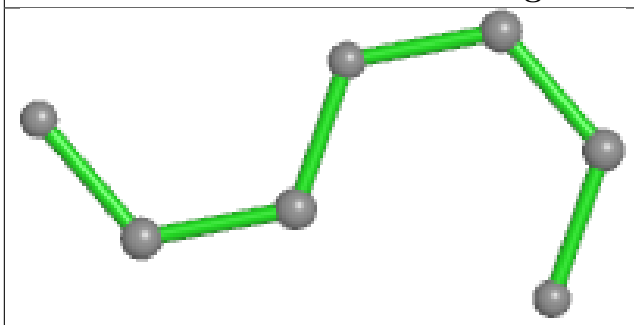


Rings

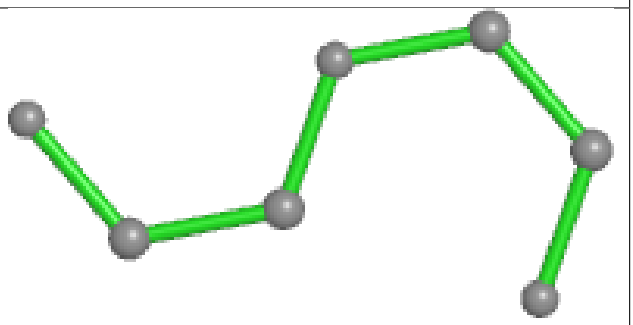
Ligand EDO C 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand EDO E 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

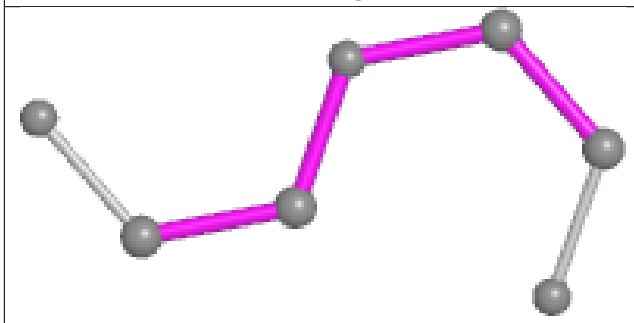
Ligand PEG C 304



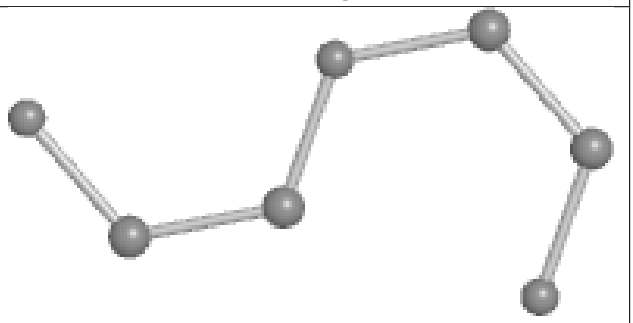
Bond lengths



Bond angles

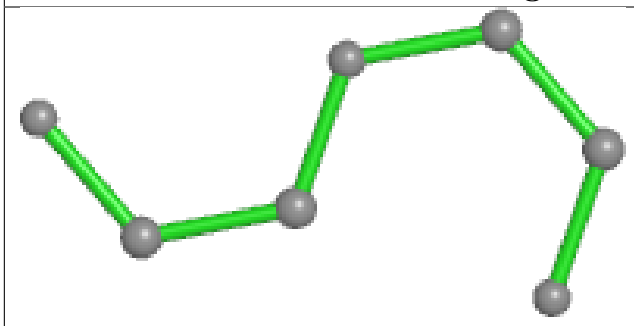


Torsions

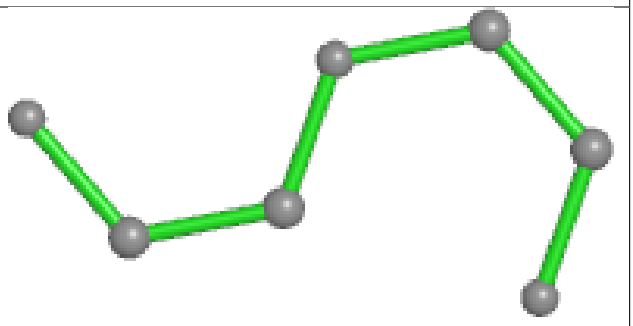


Rings

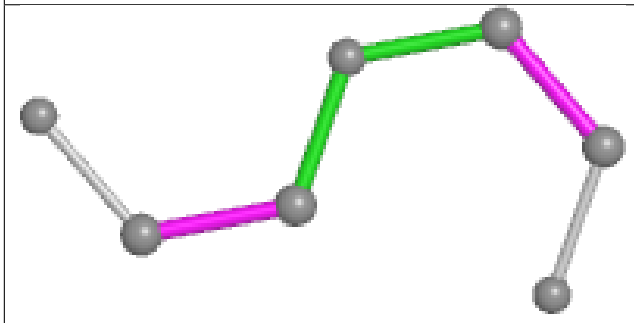
Ligand PEG D 306



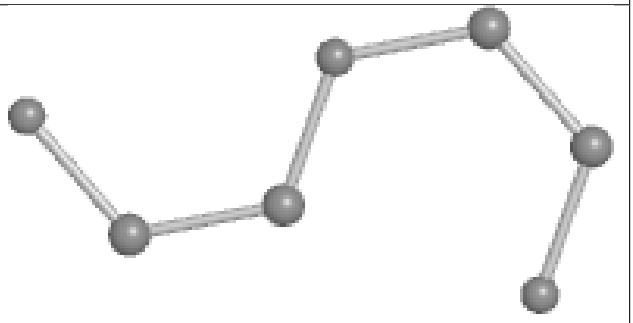
Bond lengths



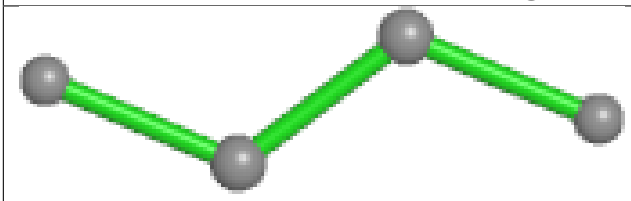
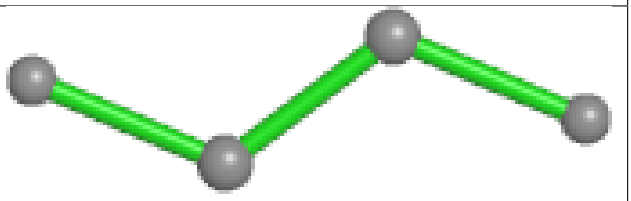
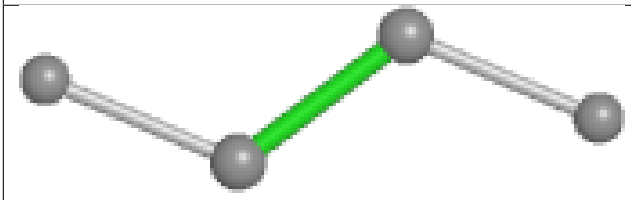
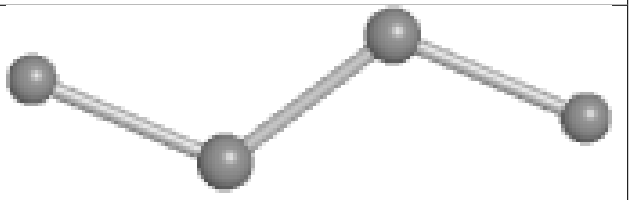
Bond angles

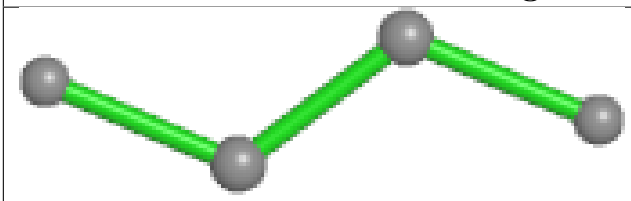
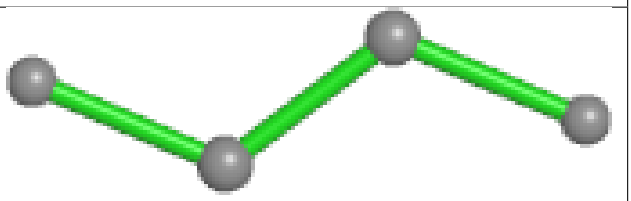
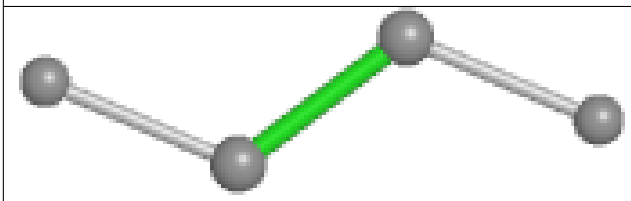
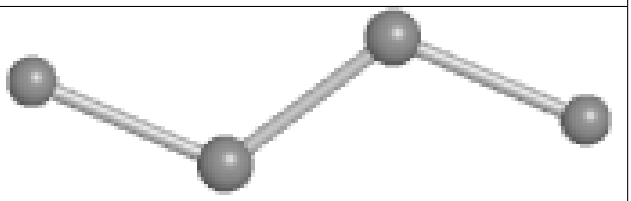


Torsions

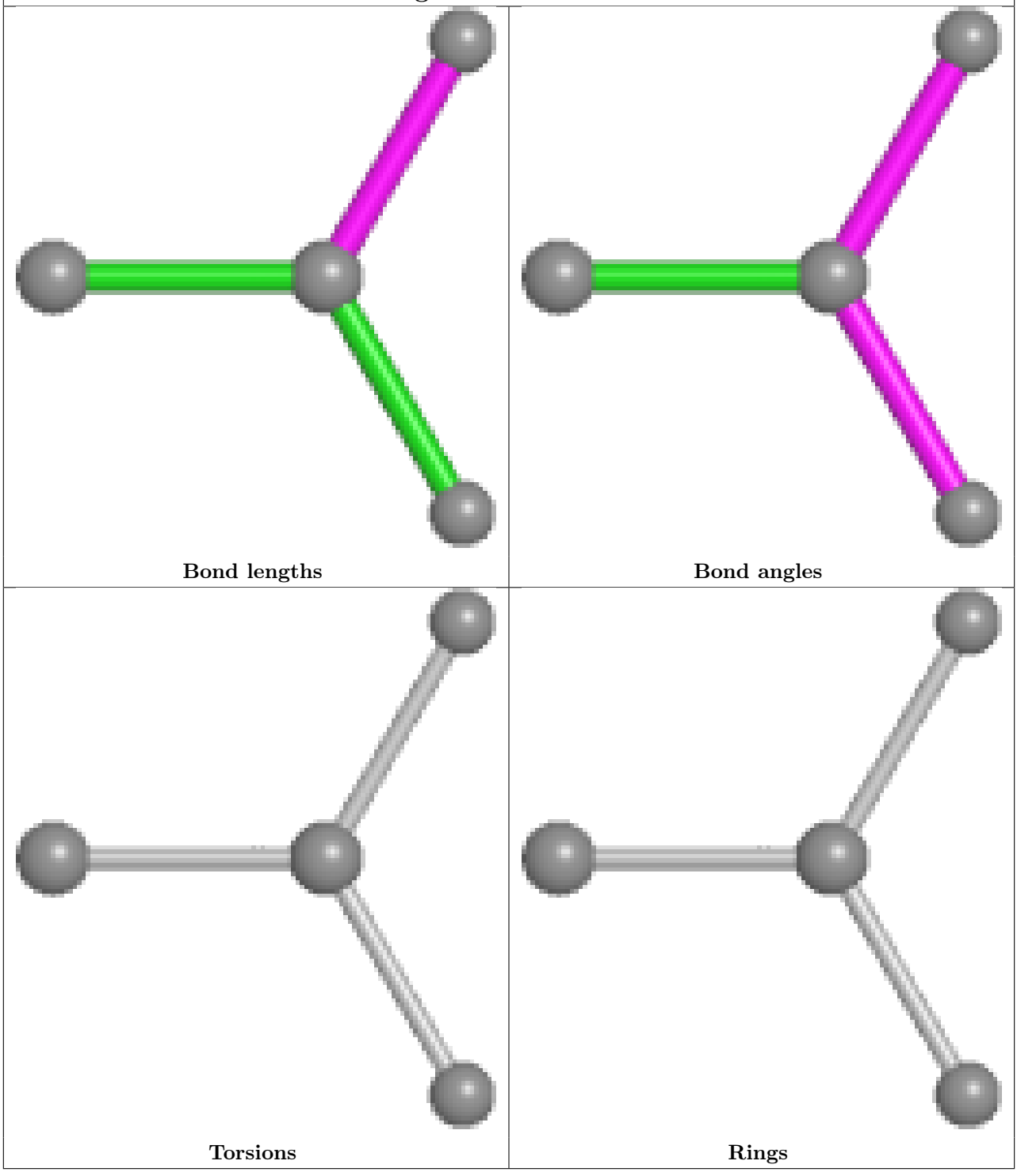


Rings

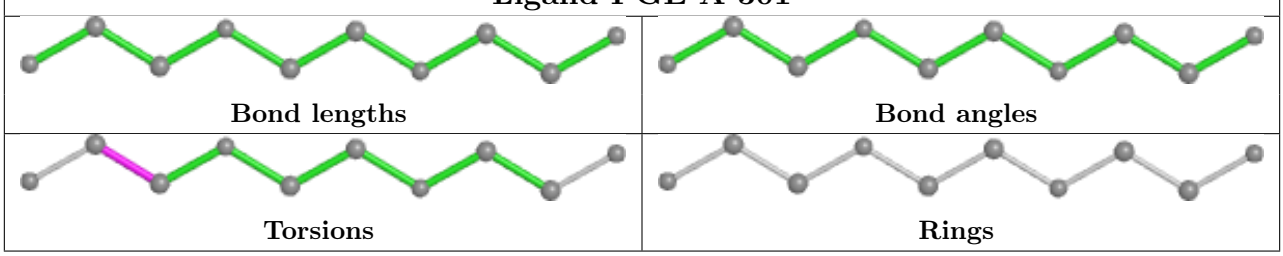
Ligand EDO C 303	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand EDO D 305	
	
Bond lengths	Bond angles
	
Torsions	Rings

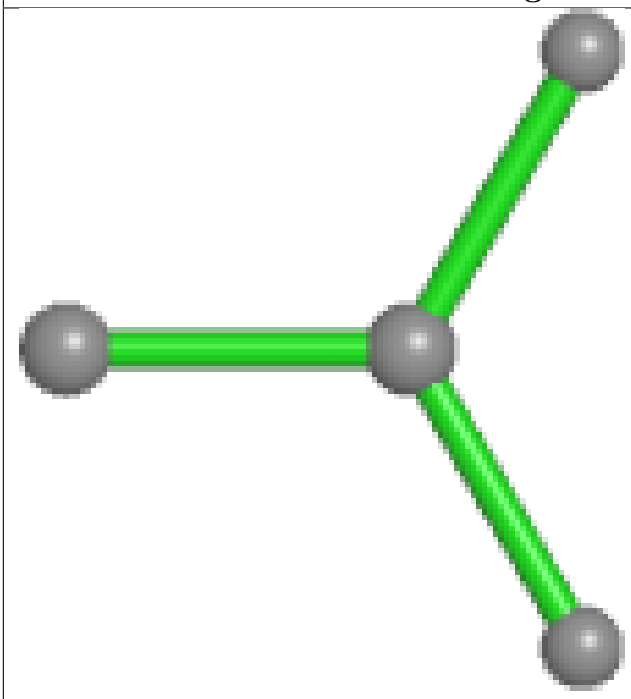
Ligand ACT A 305



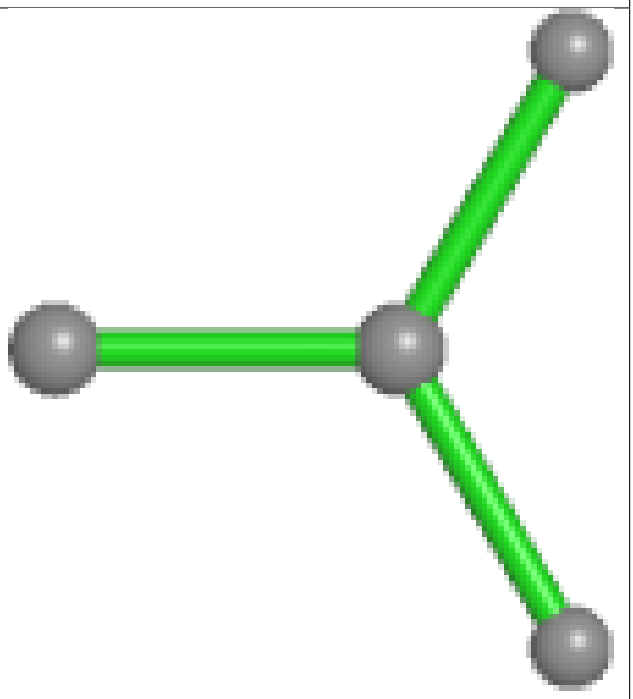
Ligand PGE A 301



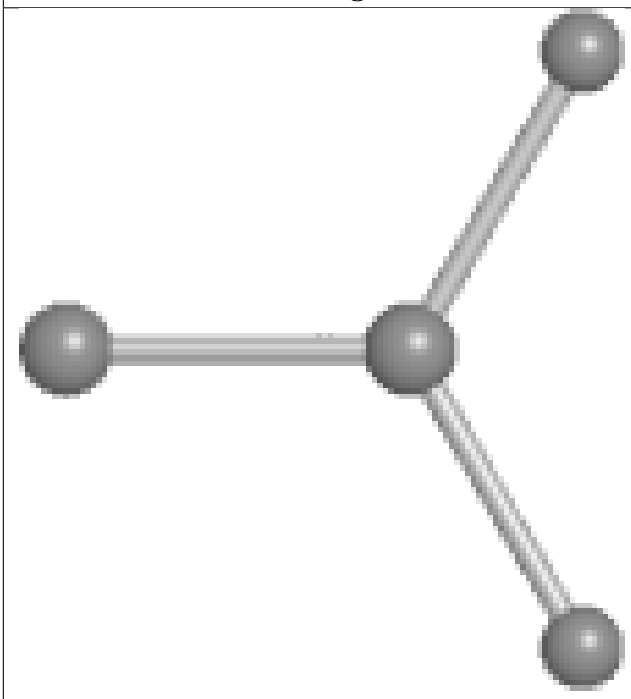
Ligand ACT E 302



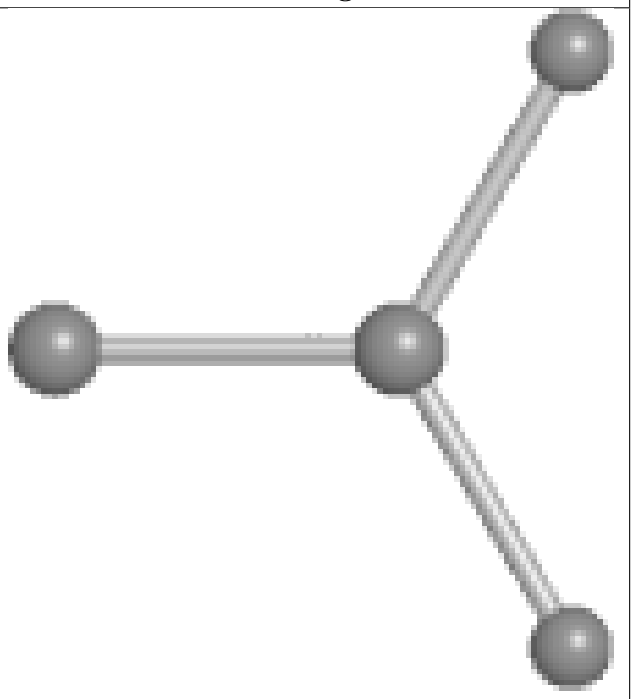
Bond lengths



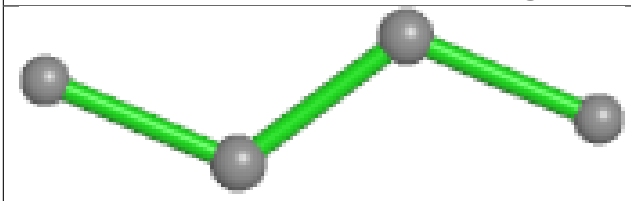
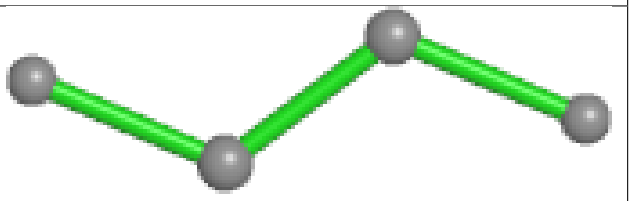
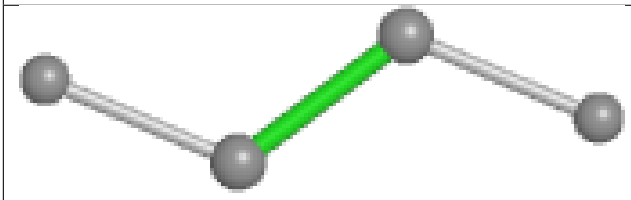
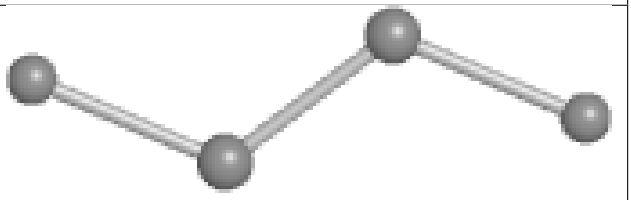
Bond angles



Torsions



Rings

Ligand EDO D 304	
 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	295/310 (95%)	-0.46	0 100 100	24, 31, 50, 64	0
1	B	295/310 (95%)	-0.43	0 100 100	23, 30, 46, 62	0
1	C	295/310 (95%)	-0.42	0 100 100	25, 33, 50, 67	0
1	D	295/310 (95%)	-0.41	0 100 100	24, 31, 51, 65	0
1	E	295/310 (95%)	-0.27	3 (1%) 82 83	24, 37, 60, 73	0
1	F	295/310 (95%)	-0.42	0 100 100	25, 36, 55, 71	0
All	All	1770/1860 (95%)	-0.40	3 (0%) 95 95	23, 33, 53, 73	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	283	PHE	2.8
1	E	72	GLY	2.5
1	E	71	LYS	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, 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
1	KPI	F	166	14/15	0.86	0.15	26,35,48,48	0
1	KPI	C	166	14/15	0.87	0.16	25,32,42,45	0
1	KPI	D	166	14/15	0.87	0.14	22,26,42,45	0
1	KPI	A	166	14/15	0.87	0.14	25,30,45,46	0
1	KPI	E	166	14/15	0.88	0.16	27,30,51,51	0
1	KPI	B	166	14/15	0.90	0.14	21,25,42,44	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

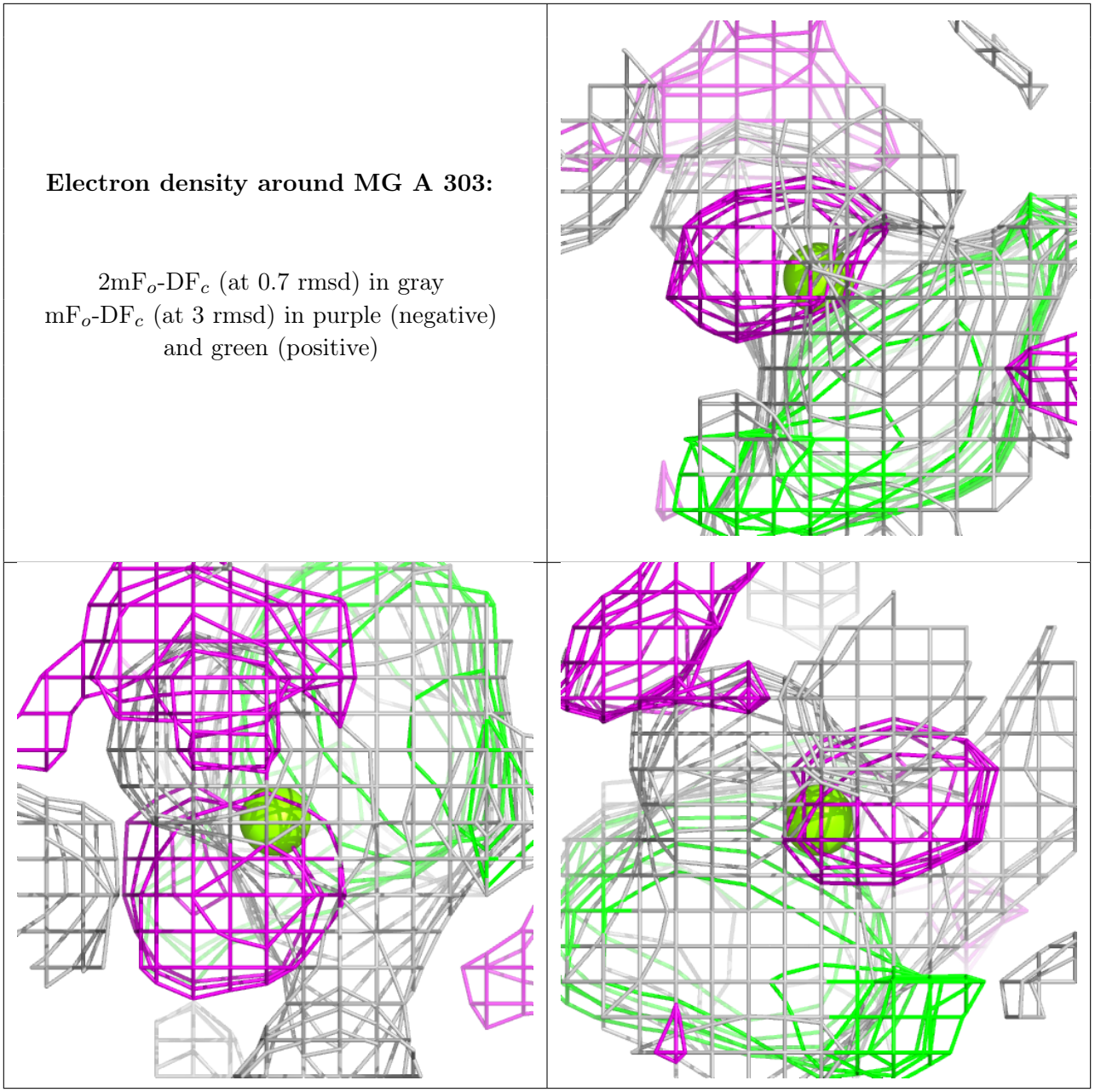
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	MG	A	303	1/1	0.30	0.29	49,49,49,49	0
3	MG	A	302	1/1	0.49	0.10	34,34,34,34	0
3	MG	D	302	1/1	0.79	0.08	44,44,44,44	0
5	ACT	B	302	4/4	0.82	0.45	20,20,20,20	0
5	ACT	E	302	4/4	0.82	0.15	40,46,48,52	0
2	PGE	B	301	10/10	0.83	0.19	45,53,64,66	0
6	PEG	C	304	7/7	0.85	0.55	20,20,20,20	0
2	PGE	D	301	10/10	0.86	0.14	47,50,55,59	0
2	PGE	C	301	10/10	0.87	0.17	45,53,59,59	0
5	ACT	A	305	4/4	0.89	0.37	20,20,20,20	0
6	PEG	D	306	7/7	0.89	0.15	55,57,59,60	0
4	EDO	D	304	4/4	0.91	0.16	51,51,52,52	0
4	EDO	A	304	4/4	0.91	0.44	20,20,20,20	0
4	EDO	C	303	4/4	0.91	0.38	20,20,20,20	0
2	PGE	A	301	10/10	0.92	0.14	44,46,54,54	0
4	EDO	E	301	4/4	0.93	0.16	47,51,52,55	0
3	MG	D	303	1/1	0.93	0.35	53,53,53,53	0
2	PGE	F	301	10/10	0.93	0.10	50,55,60,61	0
5	ACT	F	302	4/4	0.94	0.12	38,39,43,44	0
4	EDO	C	302	4/4	0.95	0.34	20,20,20,20	0
4	EDO	D	305	4/4	0.97	0.12	32,33,35,36	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.

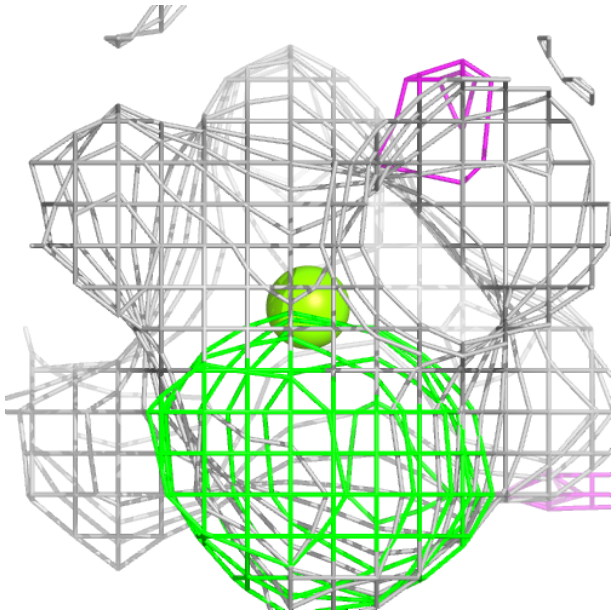
Electron density around MG A 303:

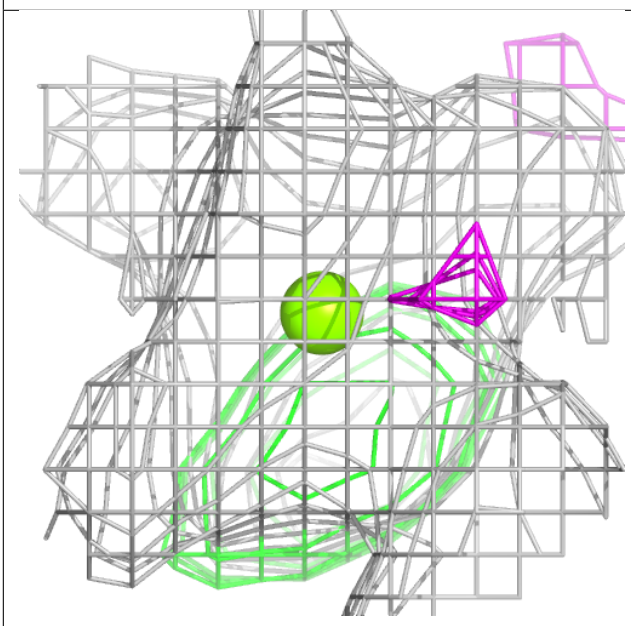
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

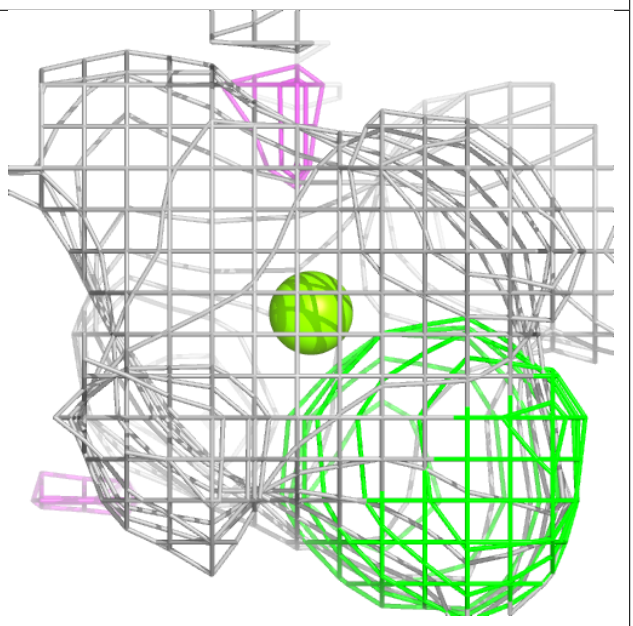


Electron density around MG A 302:

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

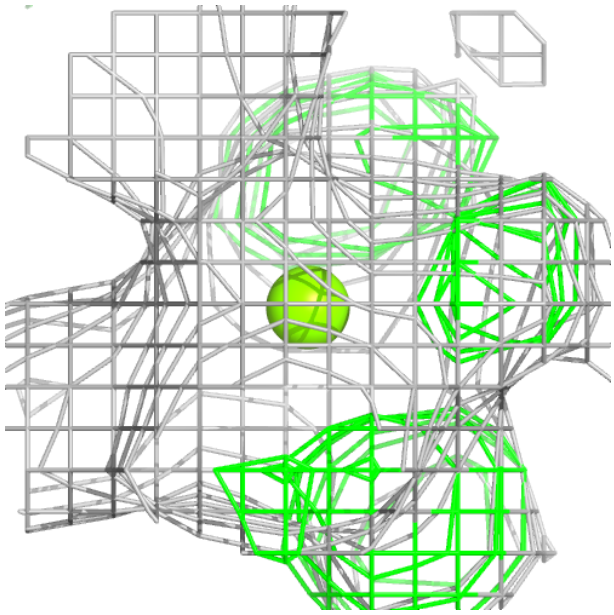


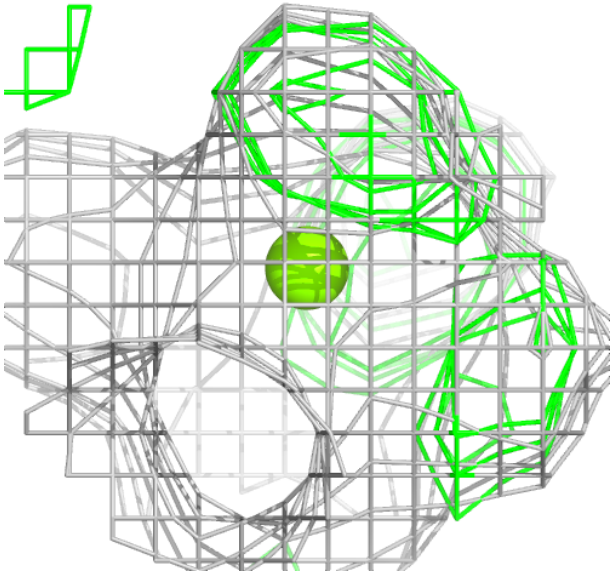


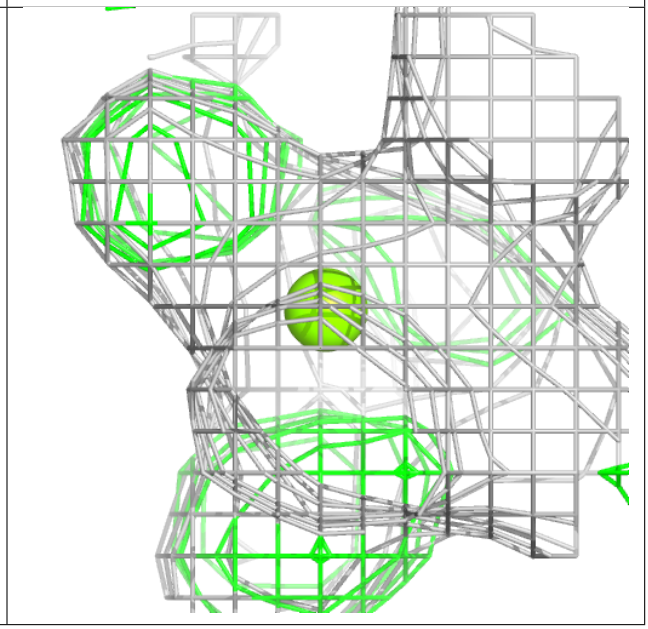


Electron density around MG D 302:

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

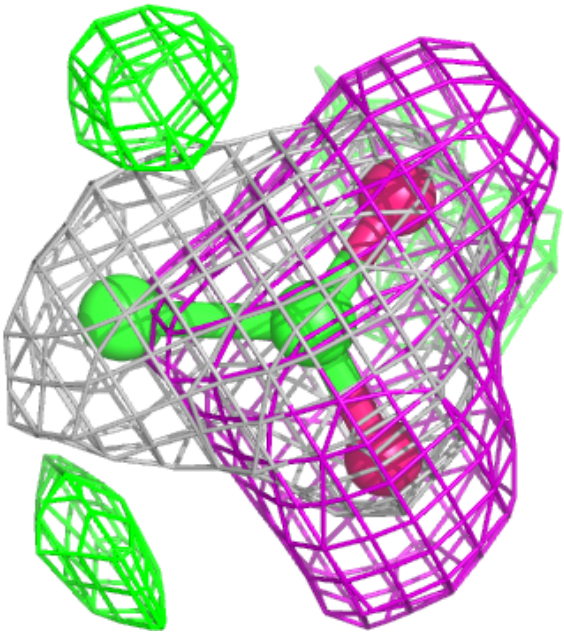


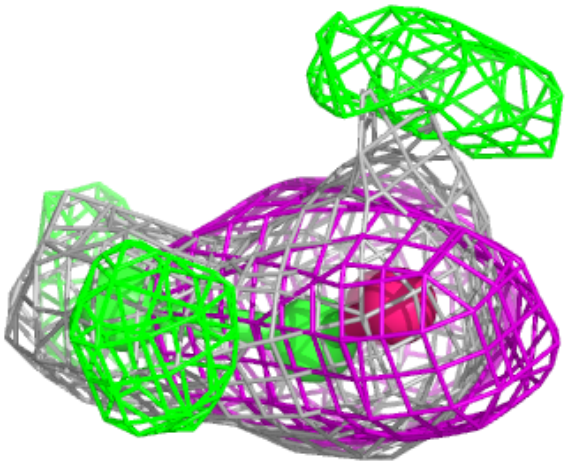


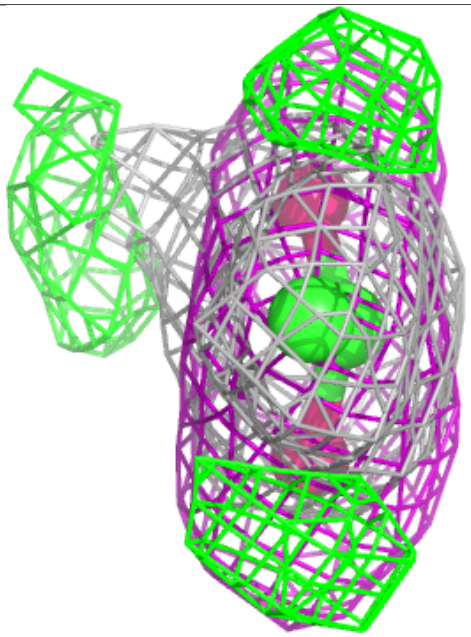


Electron density around ACT B 302:

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

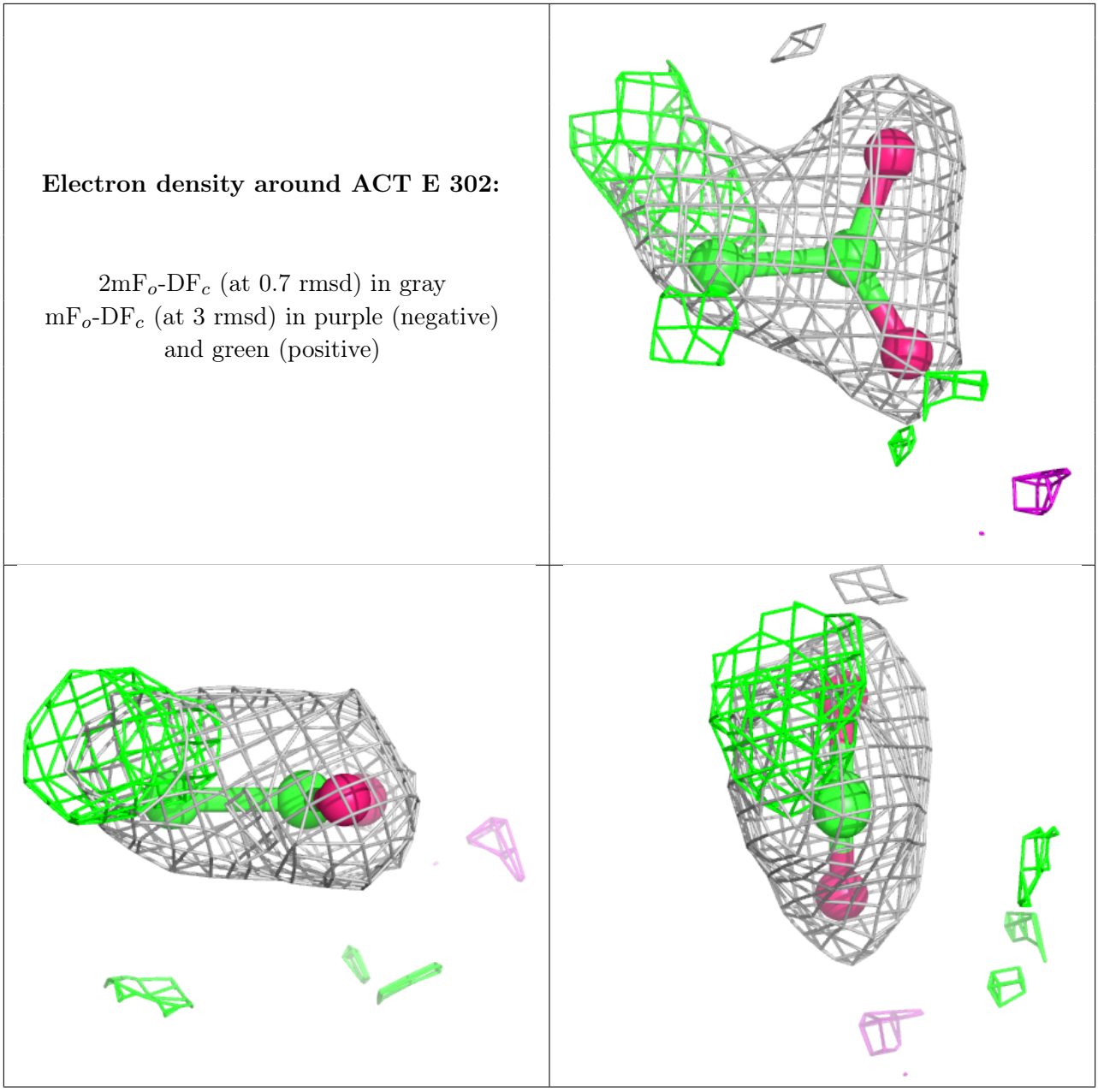






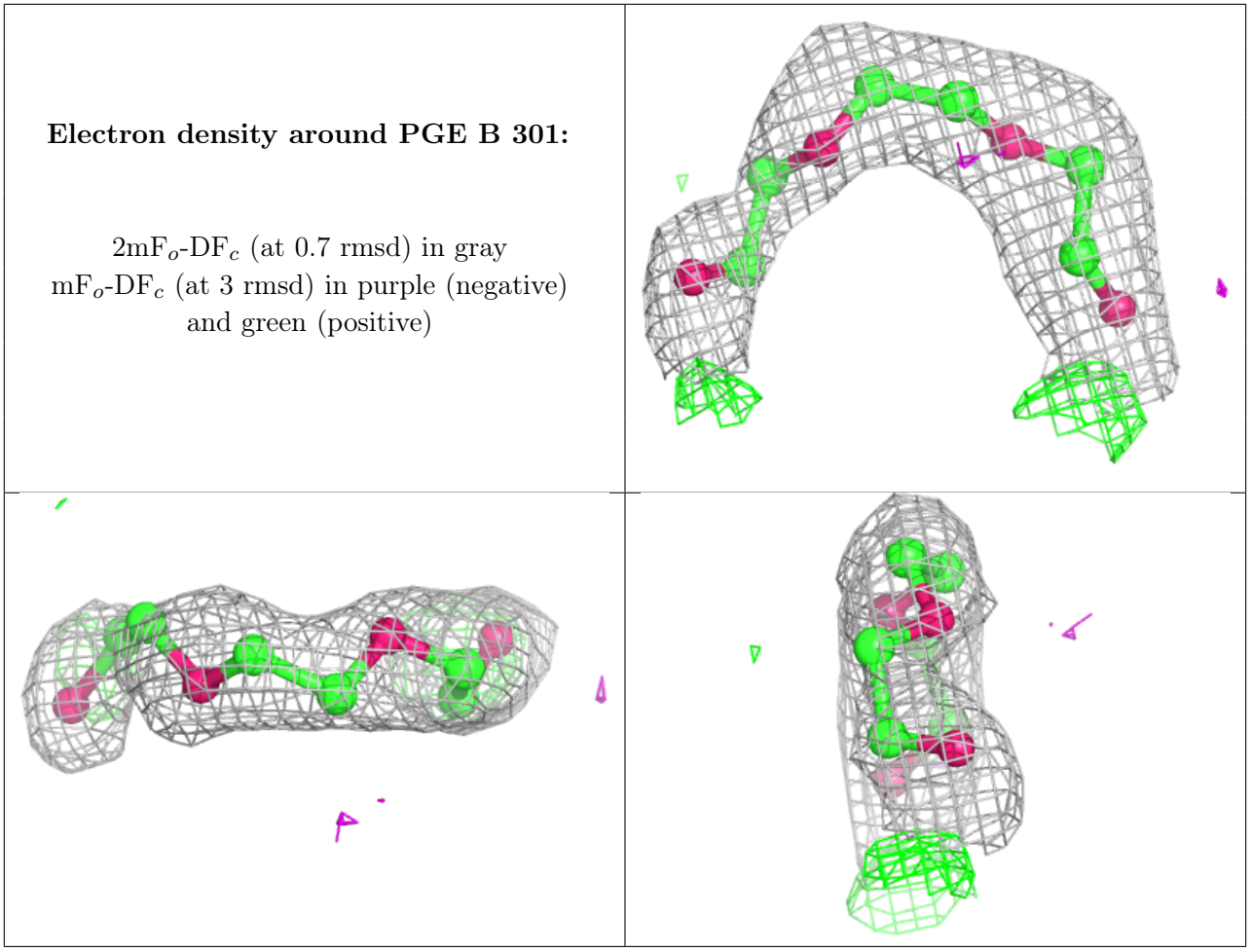
Electron density around ACT E 302:

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



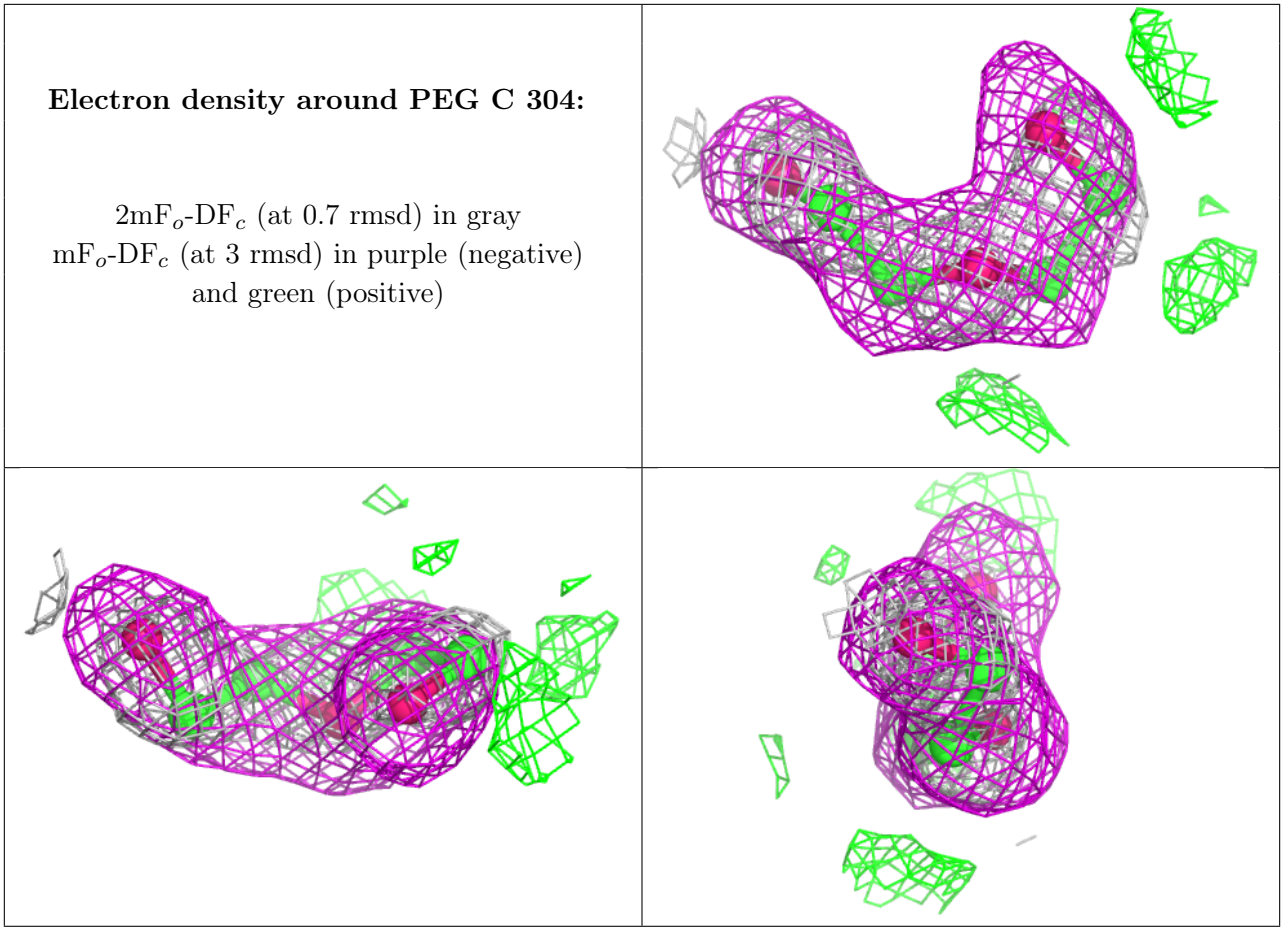
Electron density around PGE B 301:

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



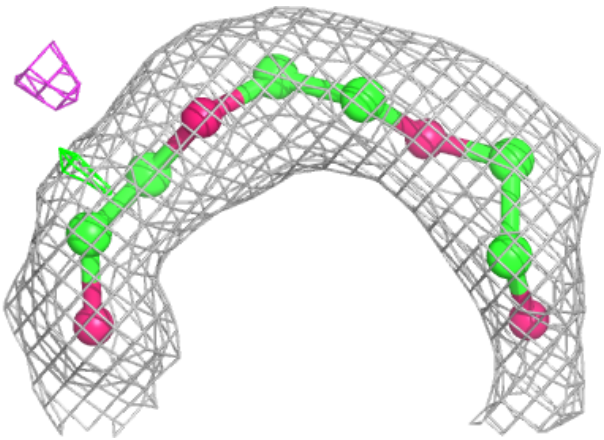
Electron density around PEG C 304:

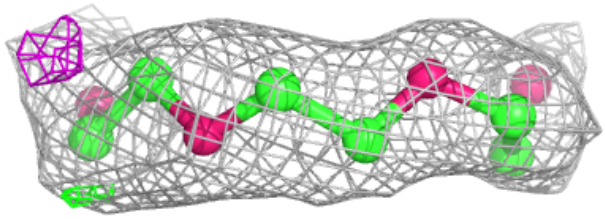
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

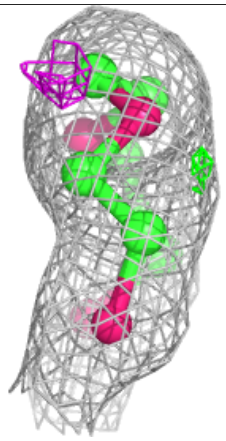


Electron density around PGE D 301:

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

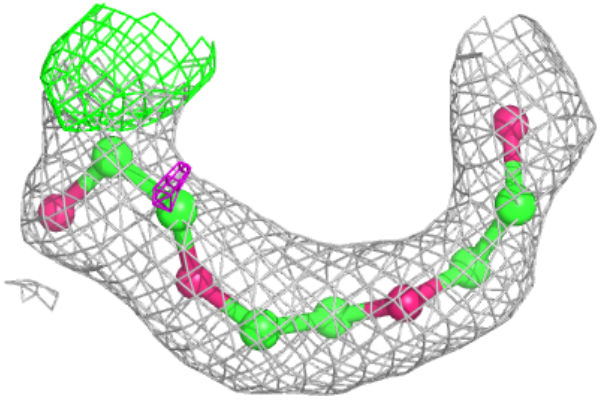


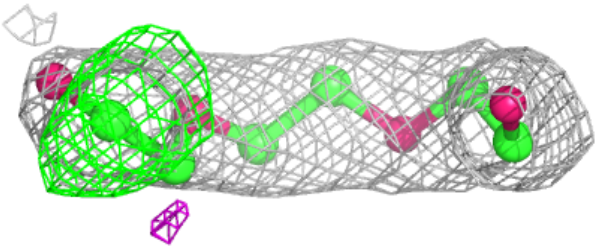


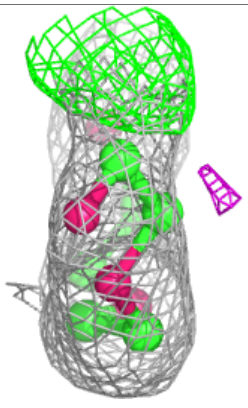


Electron density around PGE C 301:

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

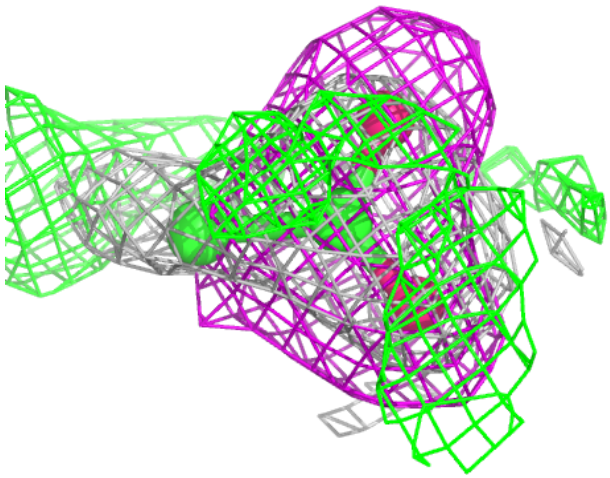


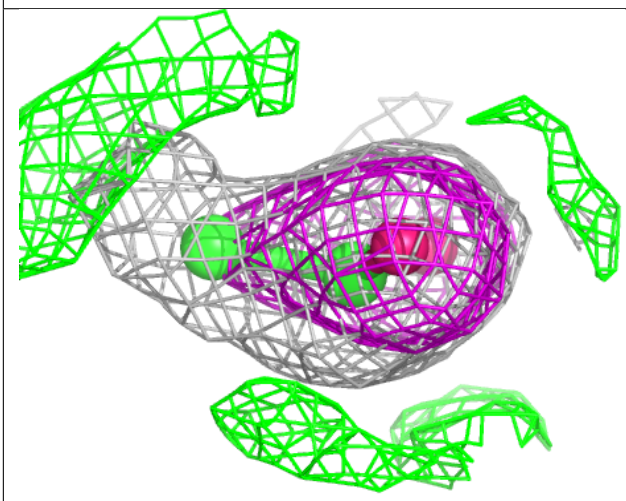


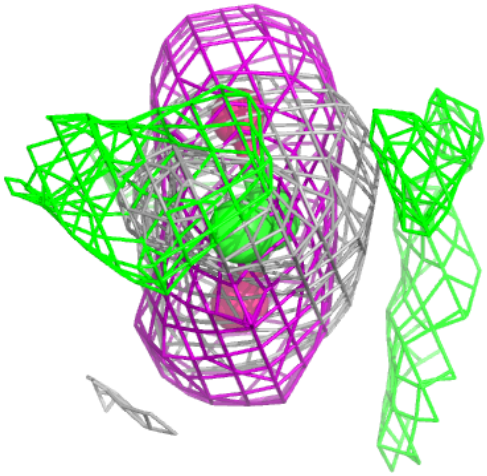


Electron density around ACT A 305:

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

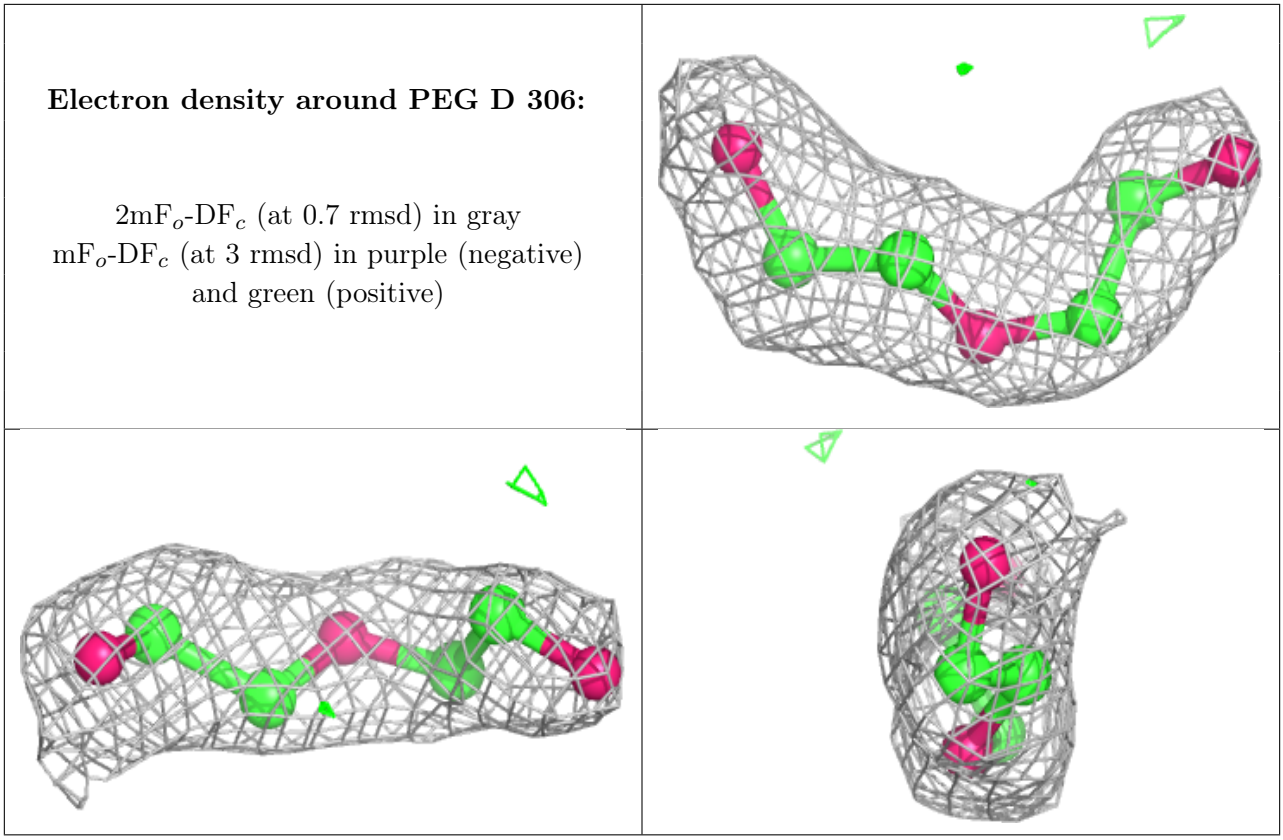






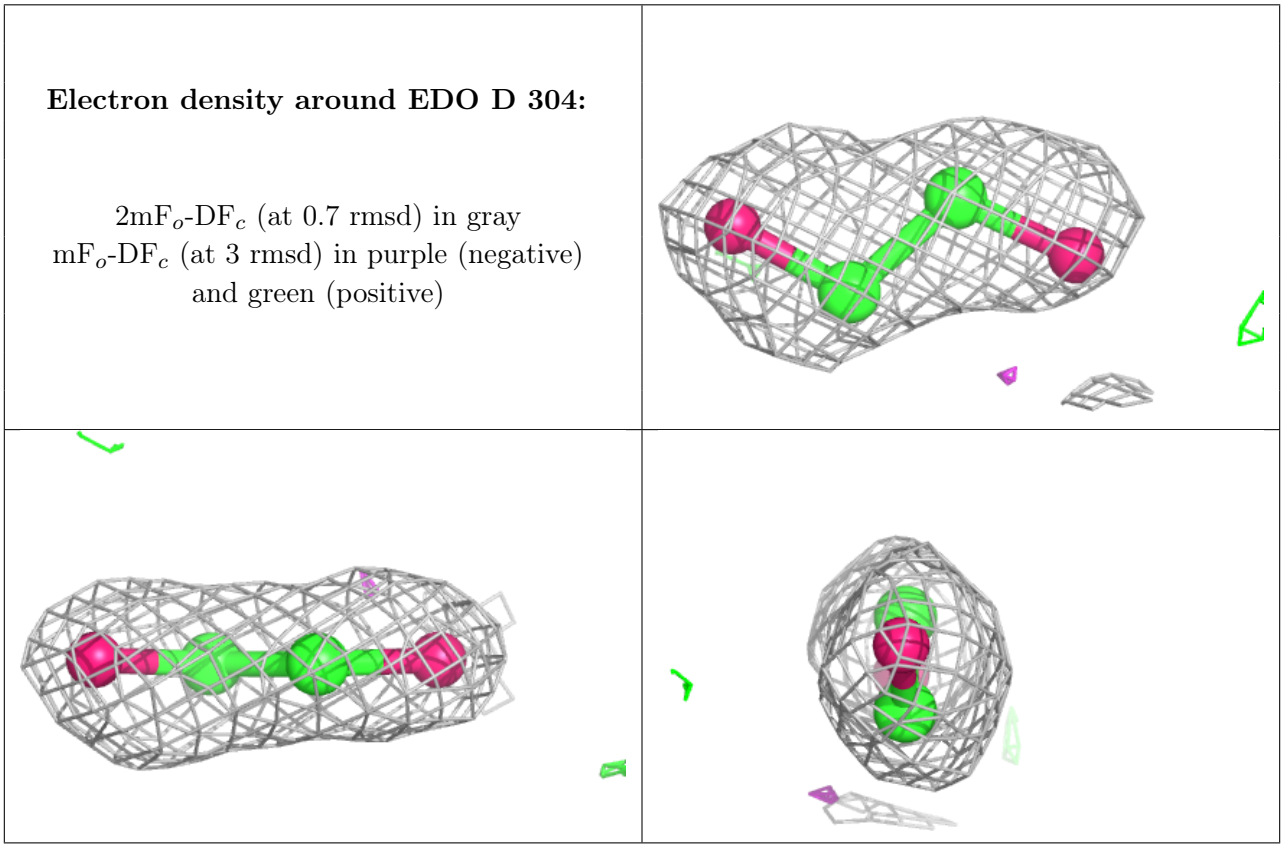
Electron density around PEG D 306:

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



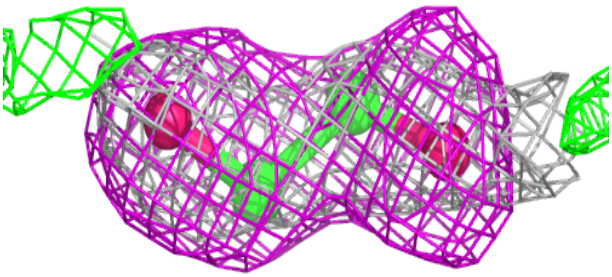
Electron density around EDO D 304:

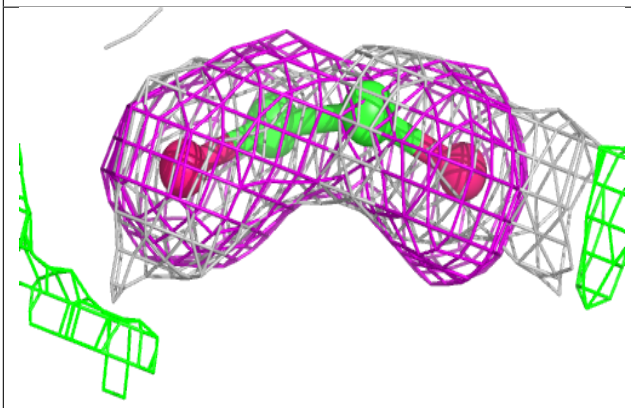
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

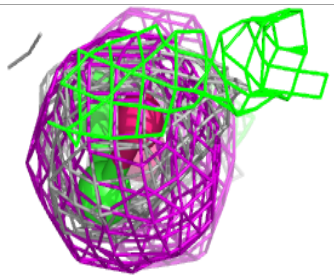


Electron density around EDO A 304:

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

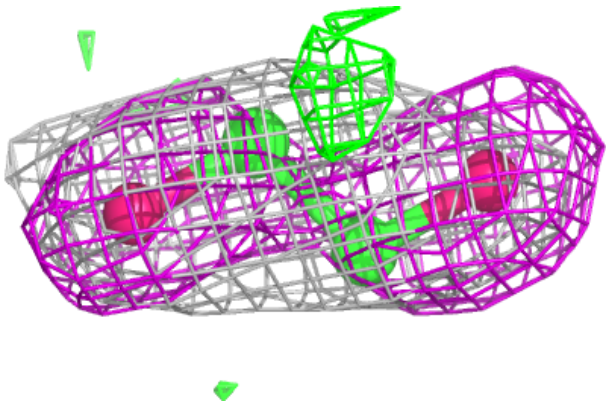


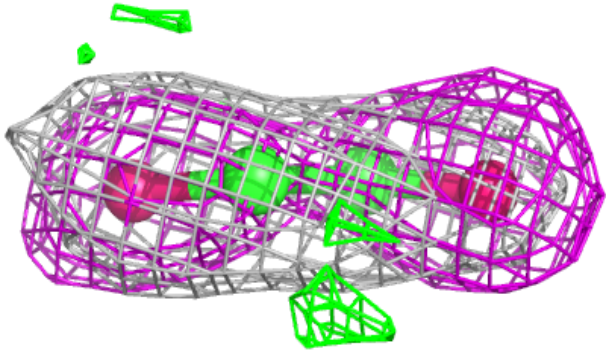


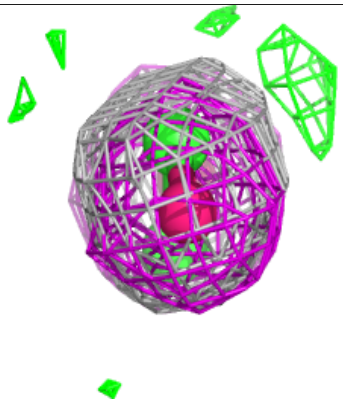


Electron density around EDO C 303:

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

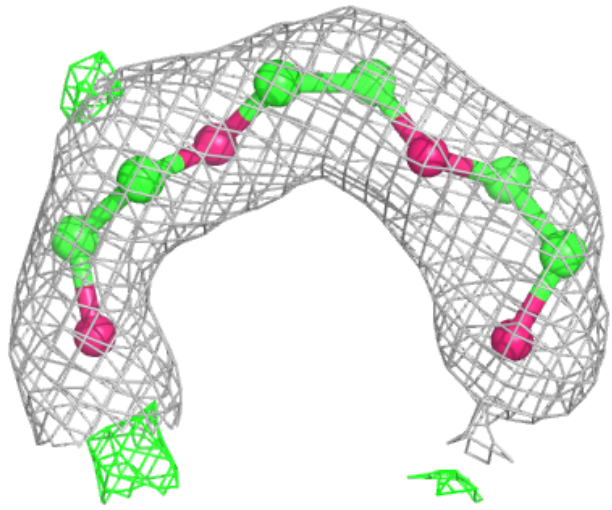


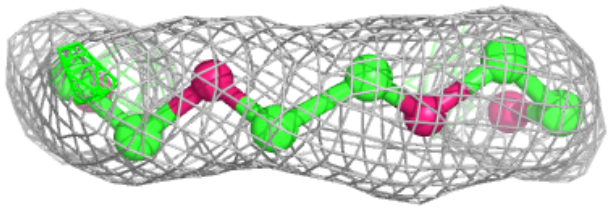


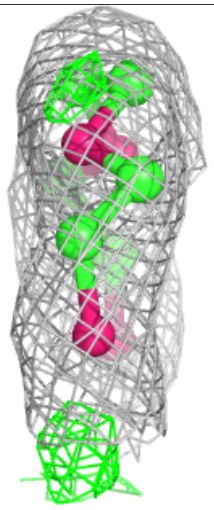


Electron density around PGE A 301:

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

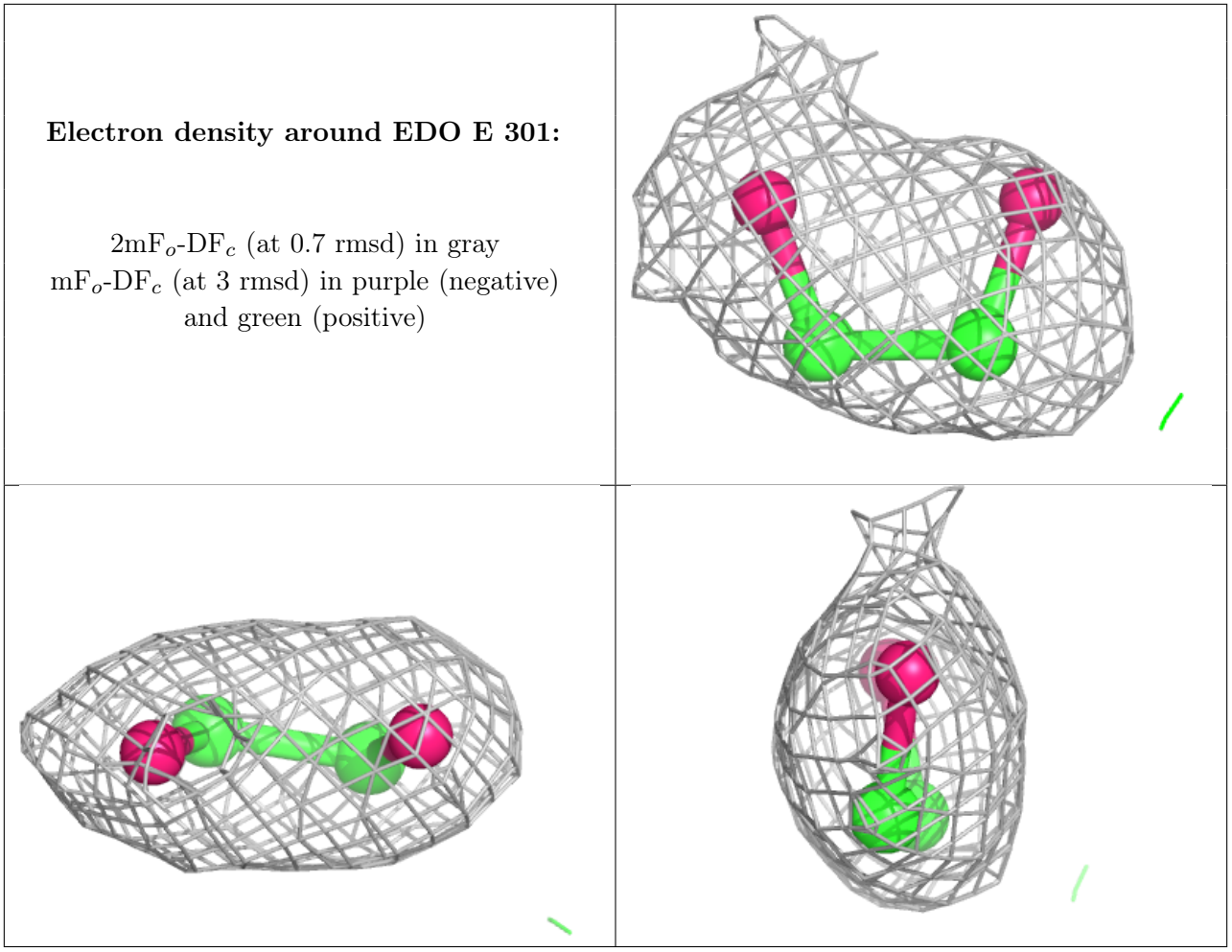






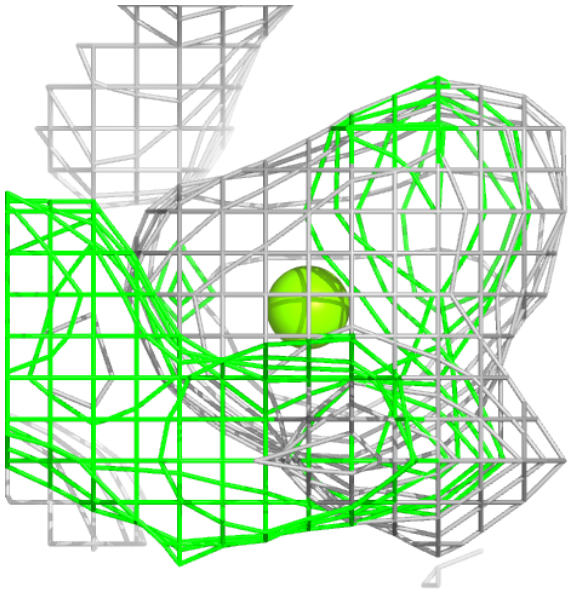
Electron density around EDO E 301:

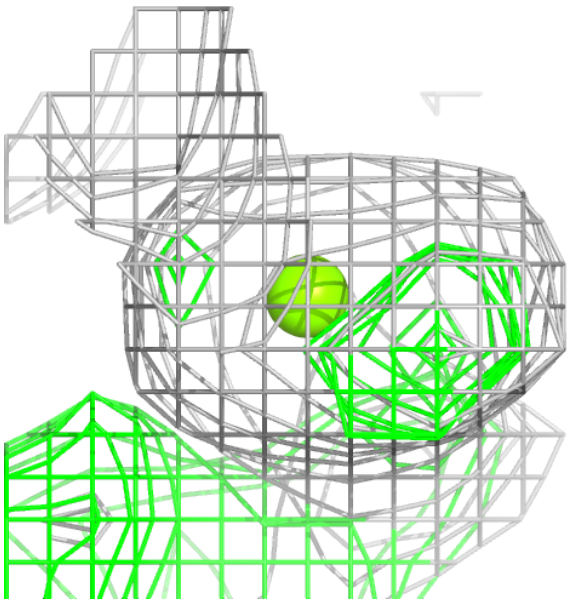
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

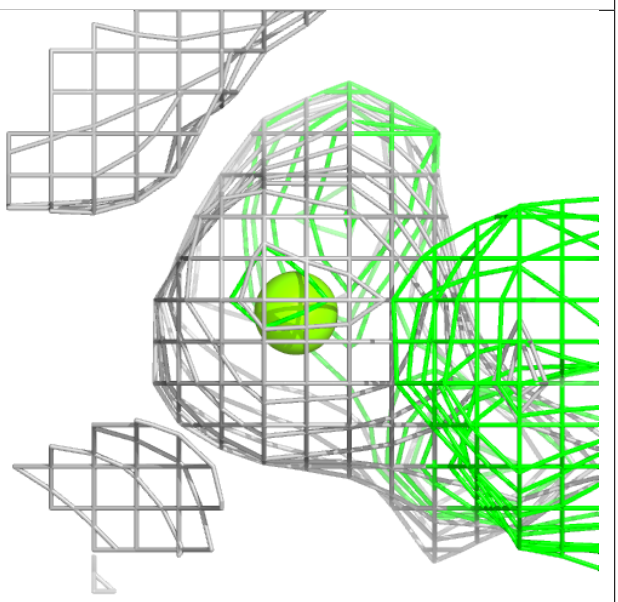


Electron density around MG D 303:

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

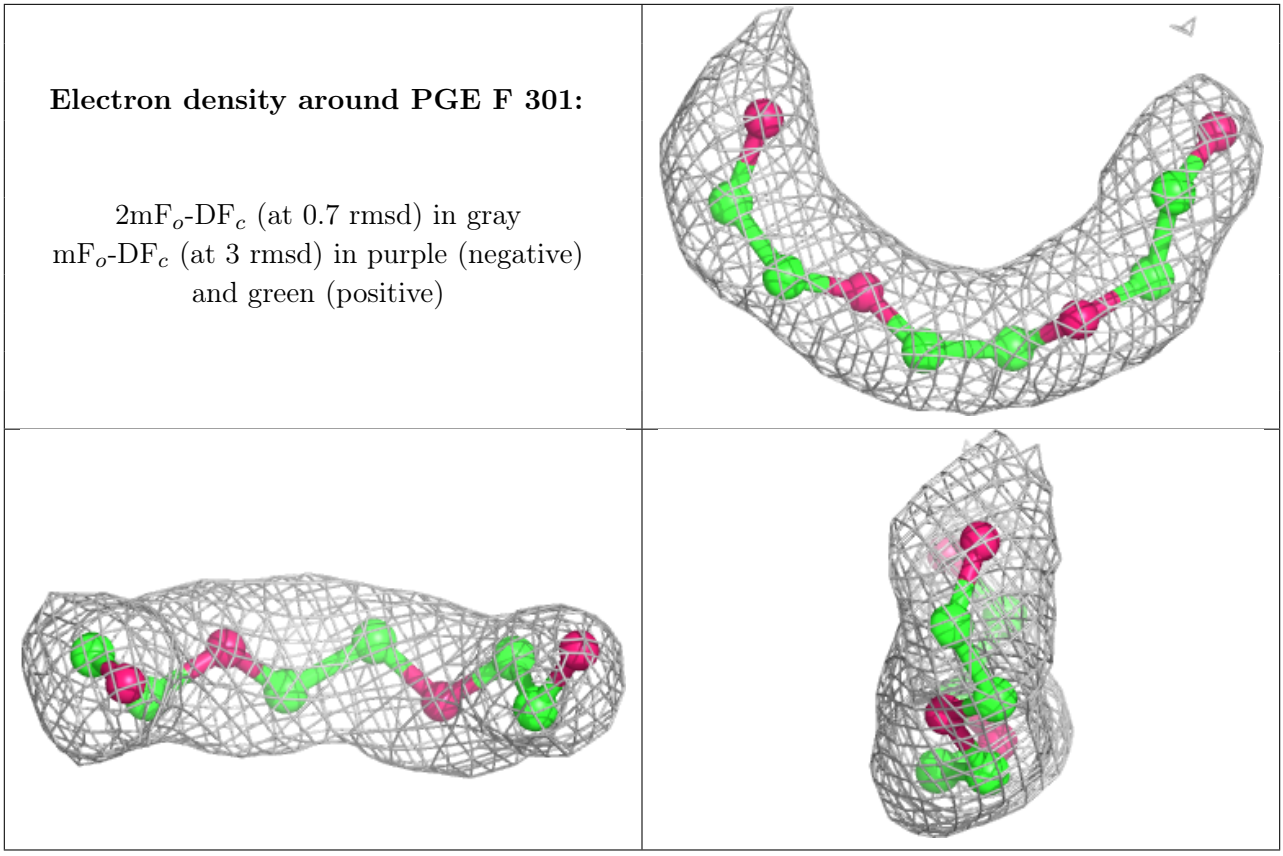






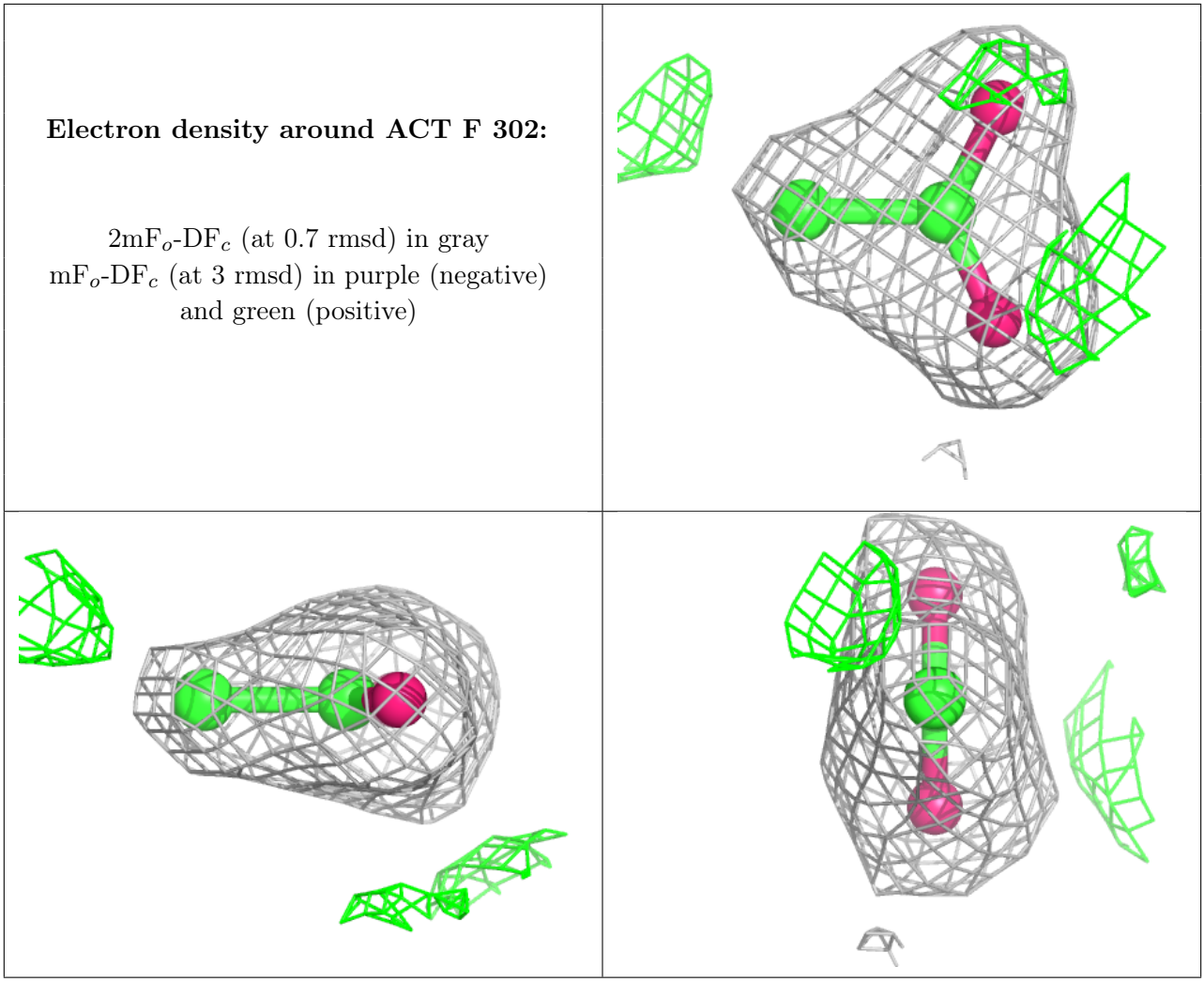
Electron density around PGE F 301:

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



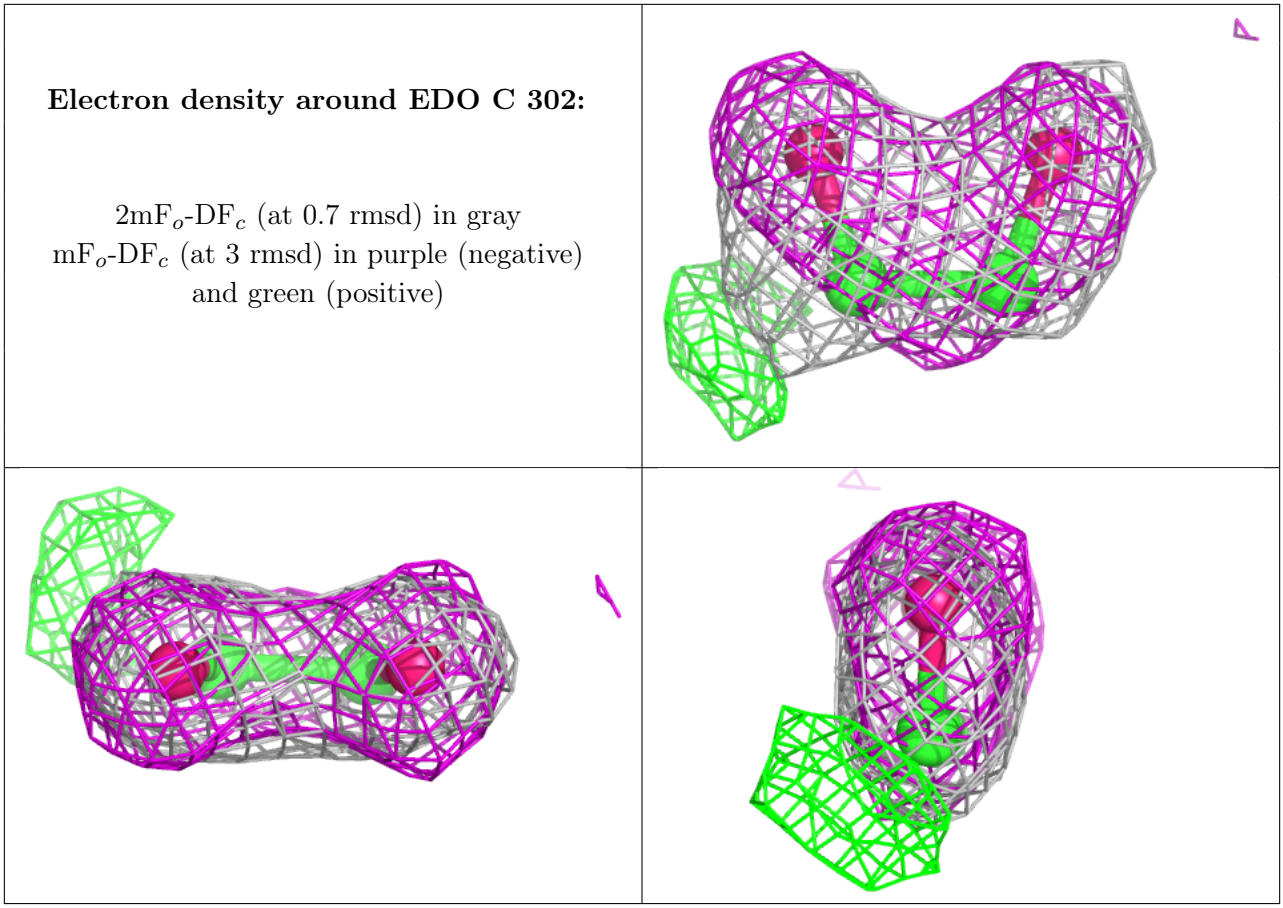
Electron density around ACT F 302:

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



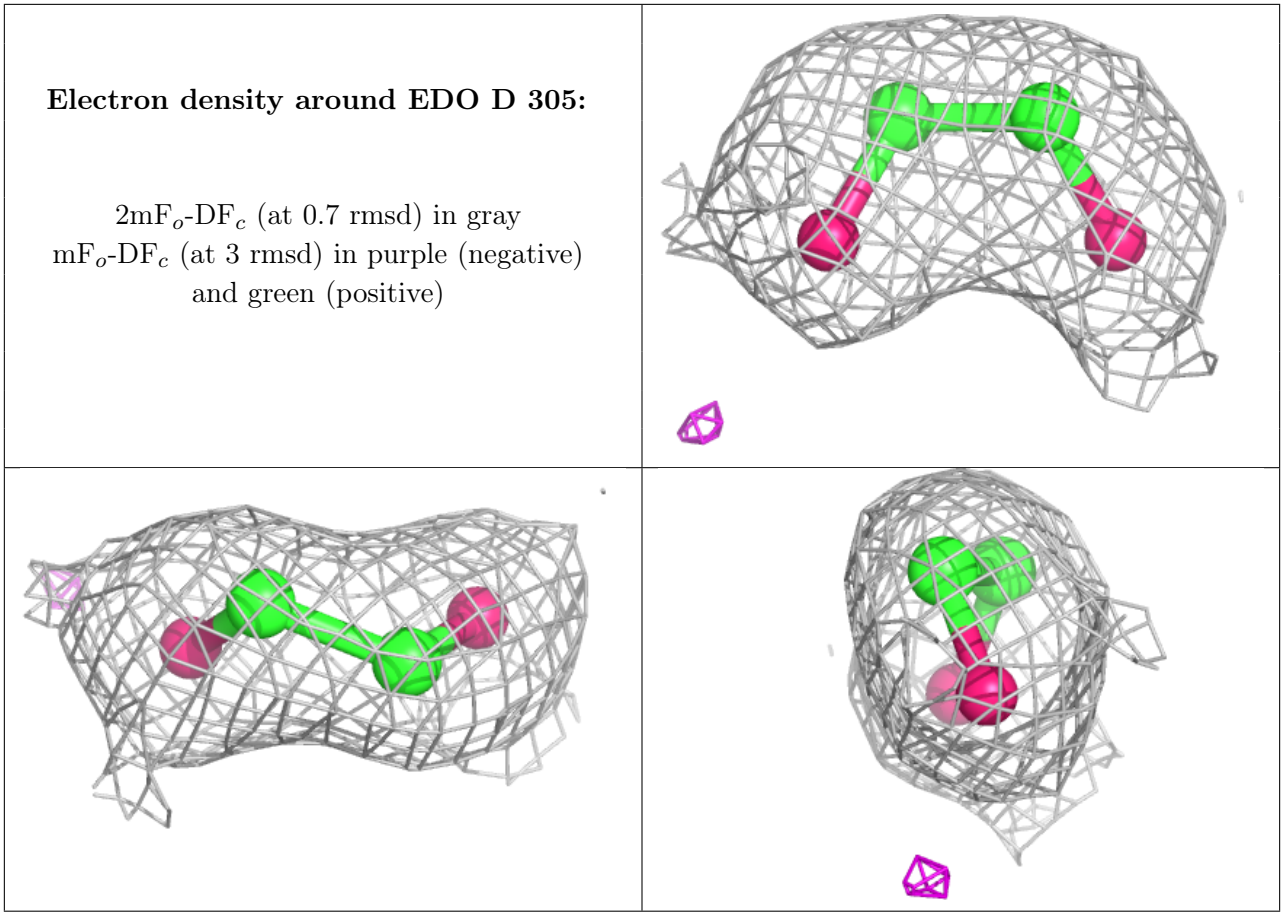
Electron density around EDO C 302:

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



Electron density around 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)



6.5 Other polymers

There are no such residues in this entry.