



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:41 PM UTC

PDB ID : 9E4V / pdb_00009e4v
Title : The structure of human vacuolar protein sorting 34 catalytic domain bound to MES
Authors : Abiodun, W.O.; Fullmer, A.; Tsubaki, E.; Doukov, T.; Moody, J.D.
Deposited on : 2024-10-25
Resolution : 2.36 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

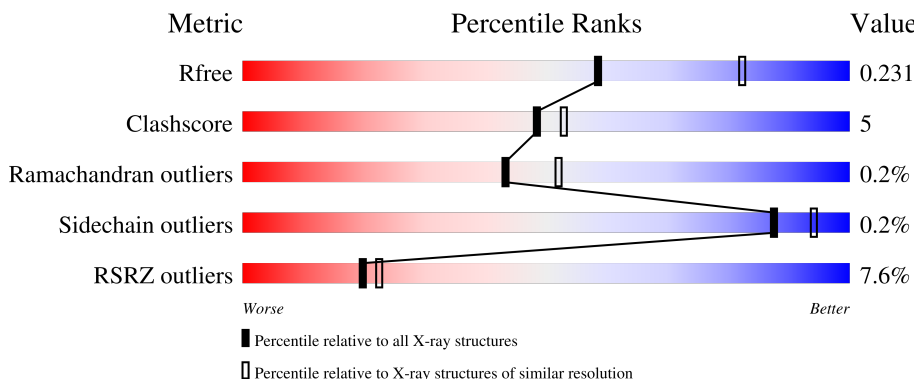
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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

Mol	Chain	Length	Quality of chain
1	B	594	

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
5	PEG	B	905	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PEG	B	911	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 4378 atoms, of which 70 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.

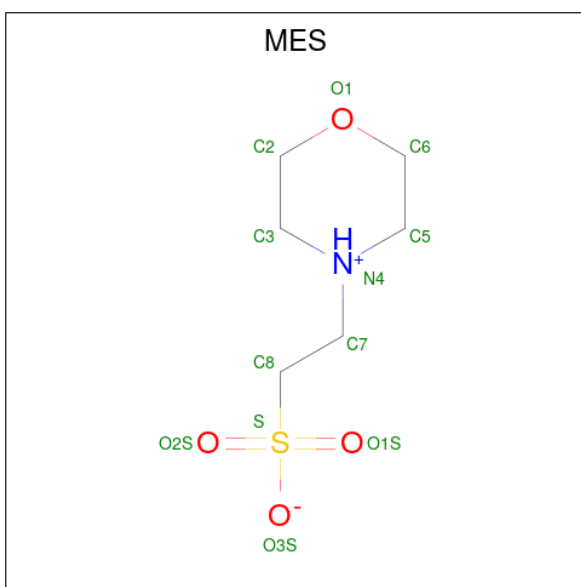
- Molecule 1 is a protein called Phosphatidylinositol 3-kinase catalytic subunit type 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	528	Total	C	N	O	S	0	4	0
			4152	2673	697	759	23			

There are 12 discrepancies between the modelled and reference sequences:

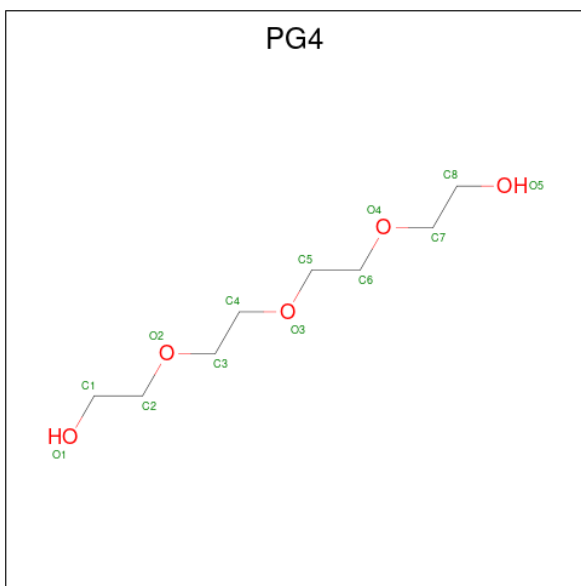
Chain	Residue	Modelled	Actual	Comment	Reference
B	278	MET	-	expression tag	UNP Q8NEB9
B	279	GLY	-	expression tag	UNP Q8NEB9
B	280	HIS	-	expression tag	UNP Q8NEB9
B	281	HIS	-	expression tag	UNP Q8NEB9
B	282	HIS	-	expression tag	UNP Q8NEB9
B	283	HIS	-	expression tag	UNP Q8NEB9
B	284	HIS	-	expression tag	UNP Q8NEB9
B	285	HIS	-	expression tag	UNP Q8NEB9
B	286	HIS	-	expression tag	UNP Q8NEB9
B	287	HIS	-	expression tag	UNP Q8NEB9
B	288	HIS	-	expression tag	UNP Q8NEB9
B	289	HIS	-	expression tag	UNP Q8NEB9

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S) (labeled as "Ligand of Interest" by depositor).



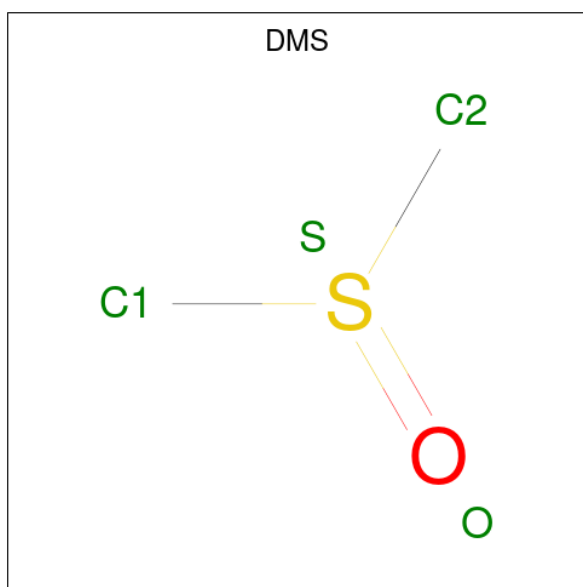
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	S	
			25	6	13	1	4	1	

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$) (labeled as "Ligand of Interest" by depositor).



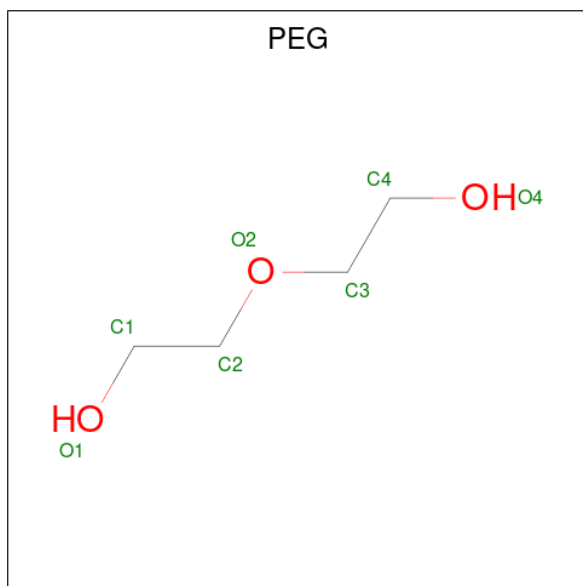
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O		
			31	8	18	5	0	0

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



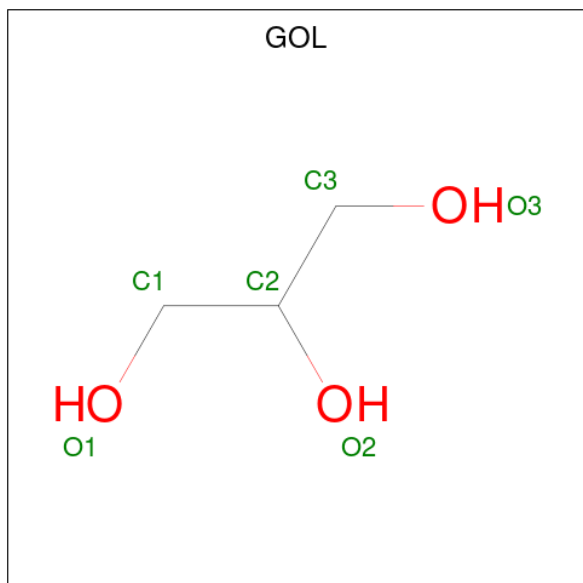
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			12	4	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			9	4	4	1		
5	B	1	Total	C	H	O	0	0
			10	4	5	1		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	4	Total	Cl	0	0
			4	4		

- Molecule 8 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	3	Total	K	0	0
			3	3		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	91	Total 91	O 91	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.09Å 114.09Å 145.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.31 – 2.36 61.31 – 2.36	Depositor EDS
% Data completeness (in resolution range)	100.0 (61.31-2.36) 92.5 (61.31-2.36)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.199 , 0.231 0.198 , 0.231	Depositor DCC
R_{free} test set	2065 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	47.4	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 61.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4378	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MES, GOL, K, PEG, DMS, PG4, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.42	0/4237	0.57	0/5736

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	B	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	536	ARG	Sidechain
1	B	602	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4152	0	4080	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	12	13	12	1	0
3	B	13	18	18	0	0
4	B	4	6	6	0	0
5	B	23	25	25	5	0
6	B	6	8	8	0	0
7	B	4	0	0	1	0
8	B	3	0	0	0	0
9	B	91	0	0	0	0
All	All	4308	70	4149	46	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 5.

All (46) 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:694:LEU:HD11	1:B:782:GLU:HG2	1.52	0.90
1:B:753:LYS:H	5:B:905:PEG:H31	1.34	0.89
1:B:777:MET:HB2	1:B:866:SER:OG	1.93	0.68
1:B:580:ASN:OD1	1:B:584:ASN:HA	1.98	0.64
1:B:574:GLN:HG2	1:B:606:PRO:O	2.00	0.62
1:B:753:LYS:HG3	5:B:905:PEG:H21	1.82	0.61
1:B:580:ASN:ND2	1:B:587:ASP:HB3	2.14	0.61
1:B:360:VAL:HG13	1:B:384:LEU:HD23	1.84	0.59
1:B:397[B]:LEU:C	1:B:397[B]:LEU:HD23	2.29	0.58
1:B:366:LEU:HB2	1:B:380:ALA:HB2	1.87	0.56
1:B:495:TRP:O	1:B:498:ILE:HG22	2.06	0.56
1:B:408:PHE:HB2	5:B:912:PEG:H21	1.88	0.56
1:B:411:ILE:O	1:B:523:ARG:HD2	2.07	0.54
1:B:753:LYS:N	5:B:905:PEG:H31	2.14	0.52
1:B:534:SER:O	1:B:537:VAL:HG12	2.11	0.49
1:B:397[B]:LEU:HD23	1:B:397[B]:LEU:O	2.13	0.49
1:B:641:LEU:HD22	1:B:680:GLY:HA3	1.94	0.49
1:B:663:LEU:HD22	1:B:804:THR:HG22	1.95	0.48
1:B:532:ASP:OD1	1:B:535:VAL:HG23	2.14	0.47
1:B:726:VAL:HG13	1:B:798:PHE:HB2	1.97	0.47
1:B:753:LYS:HE3	5:B:905:PEG:H21	1.96	0.47
1:B:311:GLU:HG3	7:B:907:CL:CL	2.52	0.46
1:B:384:LEU:HD23	1:B:384:LEU:HA	1.77	0.46
1:B:504:GLN:O	1:B:508:GLN:HG3	2.16	0.46
1:B:658:LEU:HD22	1:B:663:LEU:HD23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:725:TYR:OH	1:B:783:MET:HA	2.16	0.45
1:B:737:TYR:CE1	1:B:862:LEU:HD21	2.52	0.45
1:B:605:ILE:CG1	1:B:624:LYS:HG3	2.47	0.44
1:B:589:GLU:O	1:B:590:LEU:C	2.60	0.44
1:B:330:LEU:HD13	1:B:355:TRP:CD2	2.52	0.44
1:B:551:ARG:HD2	1:B:583:MET:O	2.17	0.43
1:B:672:VAL:HG22	1:B:682:MET:HG2	2.01	0.43
1:B:360:VAL:HG11	1:B:387:ALA:HB2	2.01	0.42
1:B:685:ILE:HG12	2:B:901:MES:H22	2.01	0.42
1:B:568:LYS:HB2	1:B:568:LYS:HE2	1.74	0.42
1:B:670:TYR:CE2	1:B:760:ILE:HG22	2.55	0.42
1:B:393:LEU:HD11	1:B:492:TYR:CD2	2.55	0.41
1:B:806:PHE:HB2	1:B:859:MET:HE3	2.02	0.41
1:B:706:LYS:HE2	1:B:707:TYR:CZ	2.55	0.41
1:B:836:ASP:OD2	1:B:837:LYS:HE2	2.20	0.41
1:B:502:GLU:CD	1:B:677:THR:H	2.29	0.41
1:B:330:LEU:HD23	1:B:358:MET:HE2	2.02	0.41
1:B:555:LEU:HD21	1:B:573:LEU:HD12	2.01	0.41
1:B:647:ILE:HD13	1:B:647:ILE:HA	1.94	0.40
1:B:714:PRO:HD2	1:B:717:ILE: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	B	528/594 (89%)	518 (98%)	9 (2%)	1 (0%)	43 52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	590	LEU

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	B	431/538 (80%)	430 (100%)	1 (0%)	87	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	828	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	338	ASN
1	B	473	GLN
1	B	545	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 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	MES	B	901	-	12,12,12	2.05	1 (8%)	15,16,16	2.60	5 (33%)
5	PEG	B	912	-	4,4,6	0.25	0	3,3,5	0.24	0
6	GOL	B	906	-	5,5,5	0.10	0	5,5,5	0.25	0
5	PEG	B	911	-	4,4,6	0.22	0	3,3,5	0.26	0
5	PEG	B	904	-	6,6,6	0.18	0	5,5,5	0.18	0
3	PG4	B	902	-	12,12,12	0.13	0	11,11,11	0.71	0
4	DMS	B	903	-	3,3,3	0.72	0	3,3,3	1.13	0
5	PEG	B	905	-	5,5,6	0.24	0	4,4,5	0.18	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	MES	B	901	-	-	2/6/14/14	0/1/1/1
5	PEG	B	912	-	-	1/2/2/4	-
6	GOL	B	906	-	-	0/4/4/4	-
5	PEG	B	911	-	-	2/2/2/4	-
5	PEG	B	904	-	-	2/4/4/4	-
3	PG4	B	902	-	-	3/10/10/10	-
5	PEG	B	905	-	-	1/3/3/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	MES	C8-S	-6.79	1.68	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	MES	O1S-S-C8	6.58	116.67	106.73
2	B	901	MES	C5-N4-C3	5.30	120.25	108.84
2	B	901	MES	O2S-S-O1S	-2.62	105.31	113.82
2	B	901	MES	C2-C3-N4	-2.45	106.40	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	MES	O2S-S-C8	2.29	110.19	106.73

There are no chirality outliers.

All (11) torsion outliers are listed below:

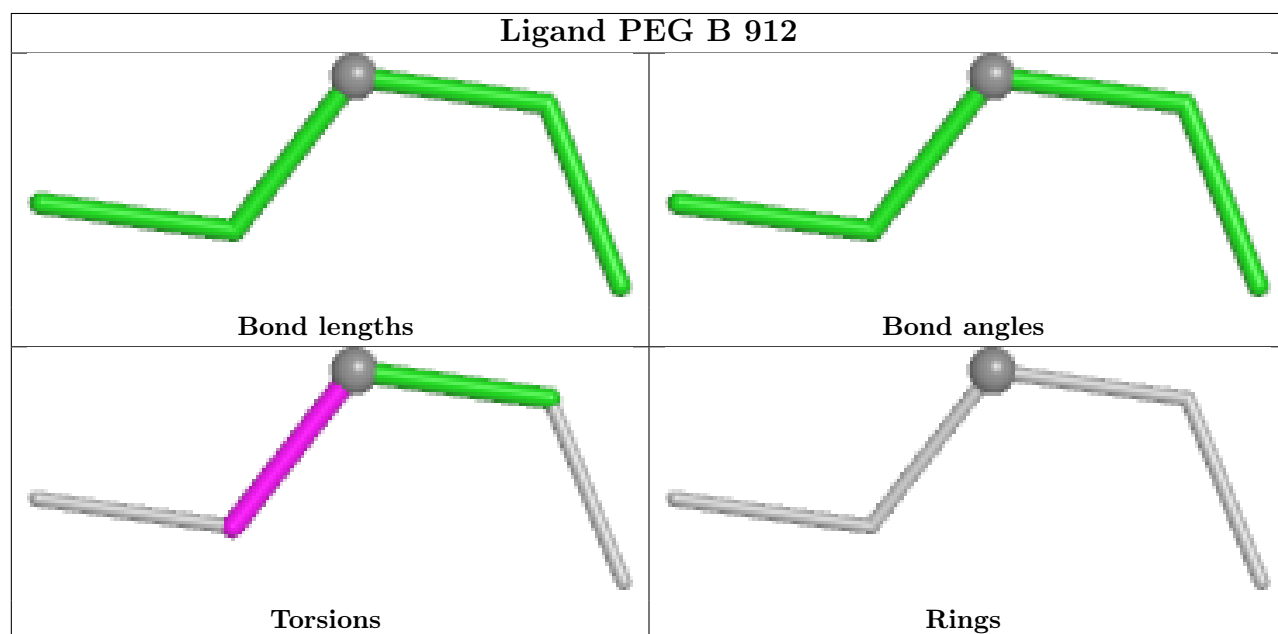
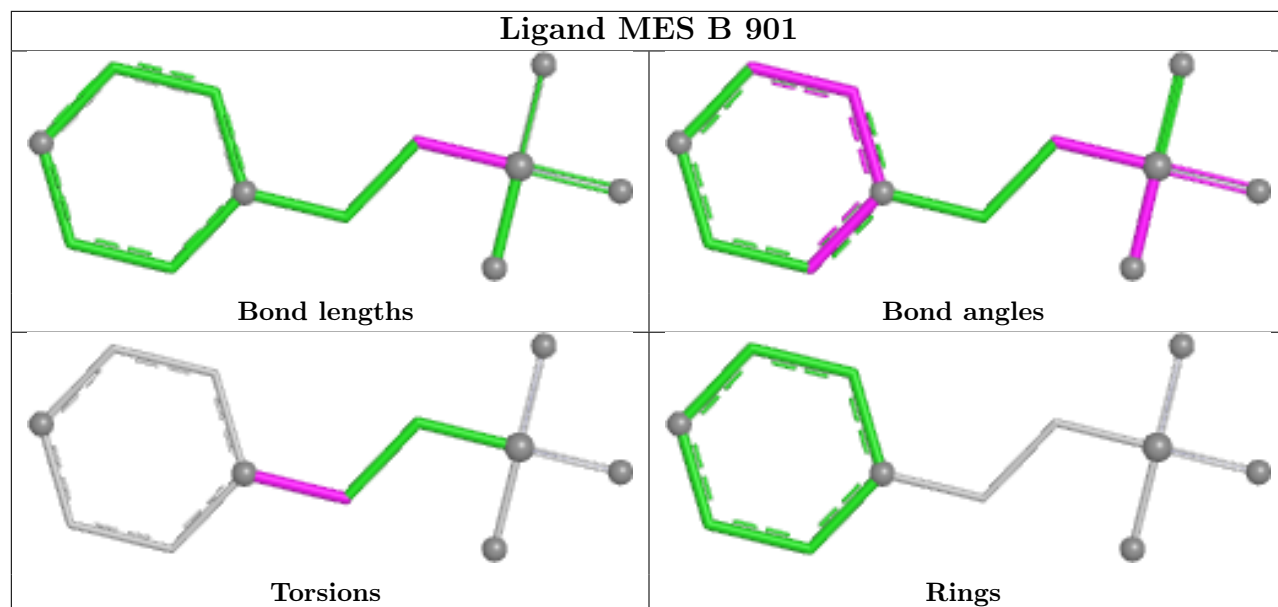
Mol	Chain	Res	Type	Atoms
3	B	902	PG4	O2-C3-C4-O3
5	B	904	PEG	O1-C1-C2-O2
2	B	901	MES	C8-C7-N4-C3
5	B	904	PEG	C4-C3-O2-C2
5	B	905	PEG	C1-C2-O2-C3
5	B	911	PEG	C1-C2-O2-C3
5	B	911	PEG	C4-C3-O2-C2
2	B	901	MES	C8-C7-N4-C5
3	B	902	PG4	C5-C6-O4-C7
5	B	912	PEG	C1-C2-O2-C3
3	B	902	PG4	O3-C5-C6-O4

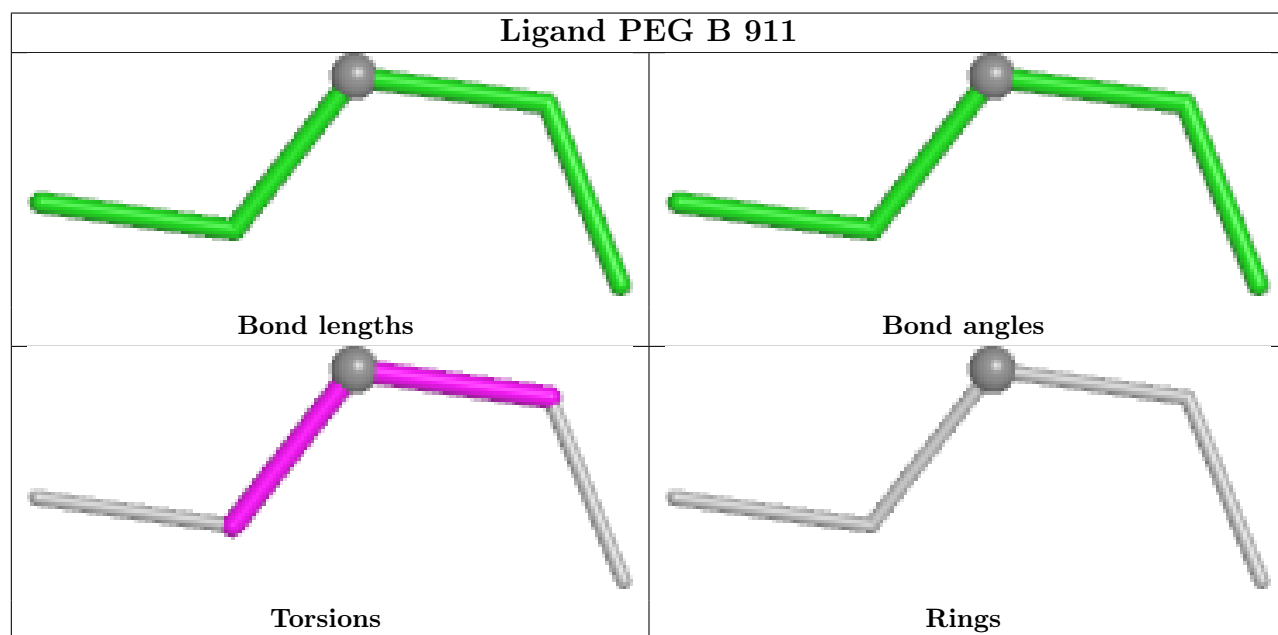
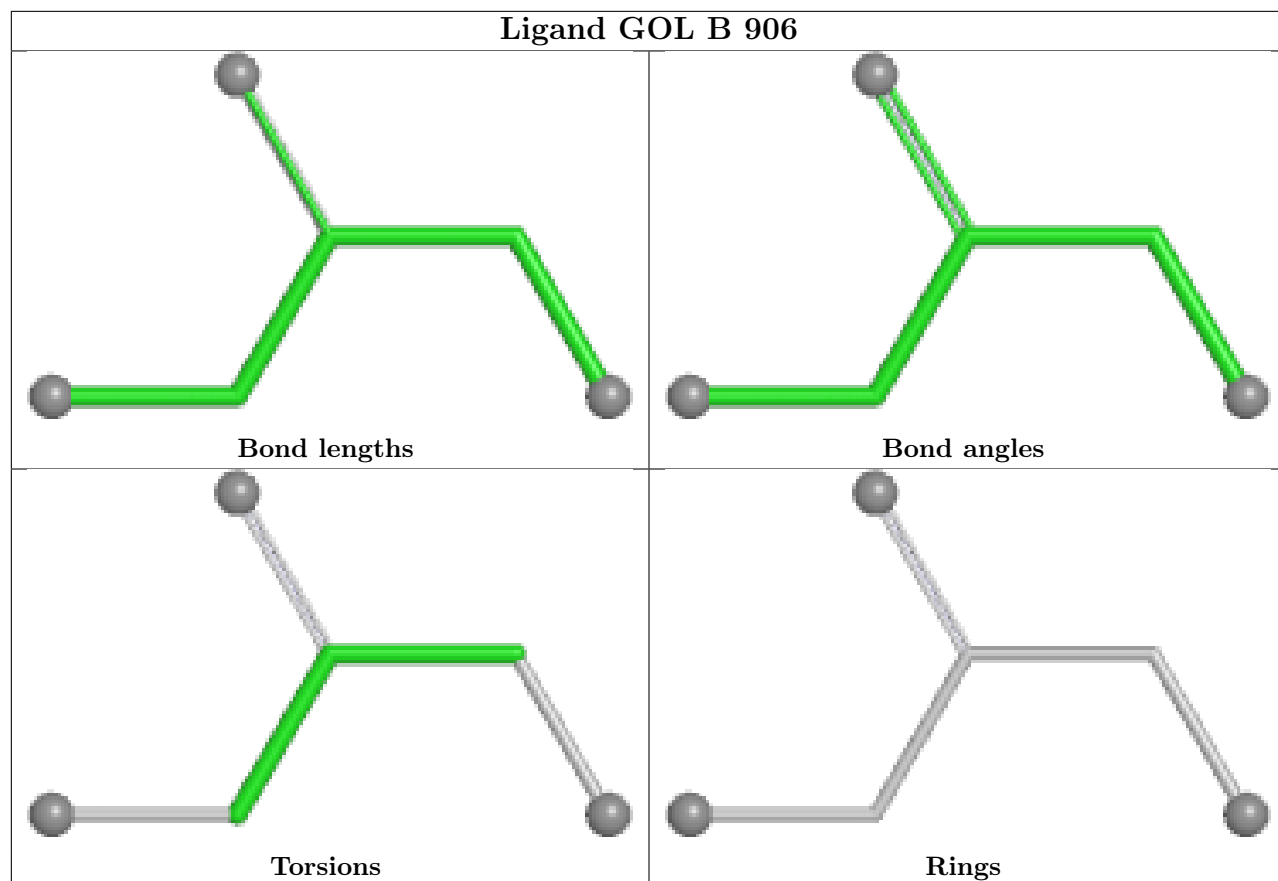
There are no ring outliers.

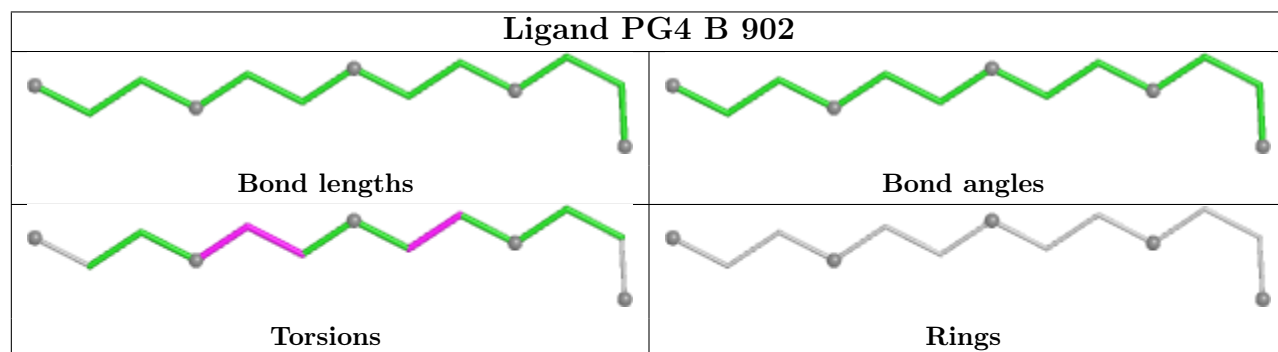
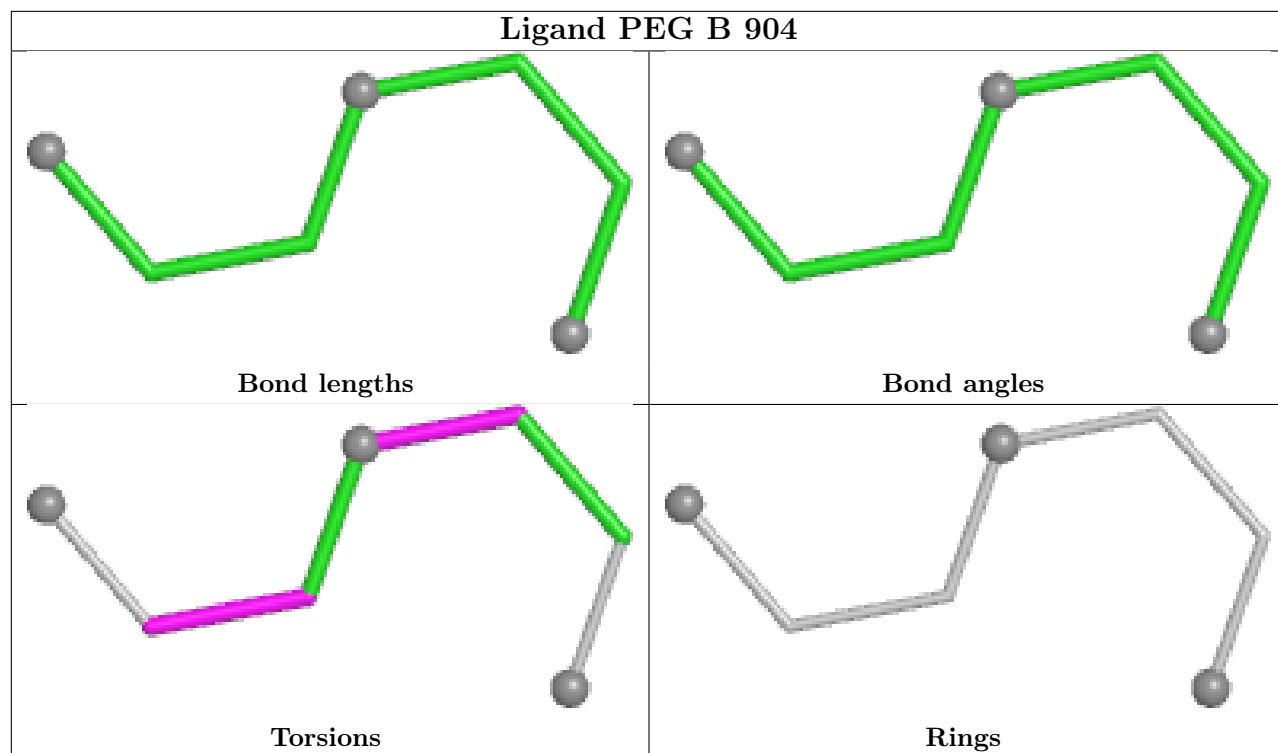
3 monomers are involved in 6 short contacts:

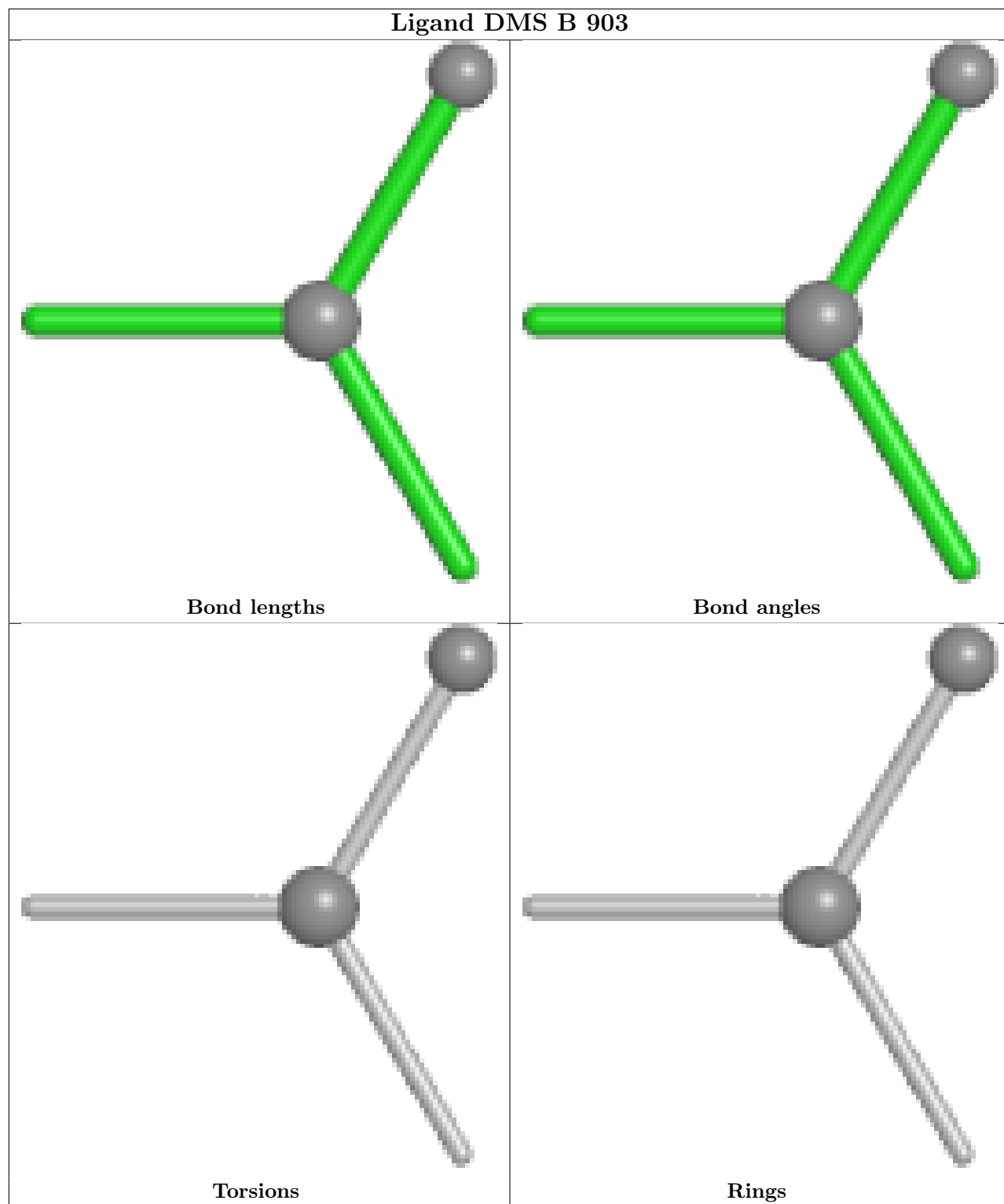
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	MES	1	0
5	B	912	PEG	1	0
5	B	905	PEG	4	0

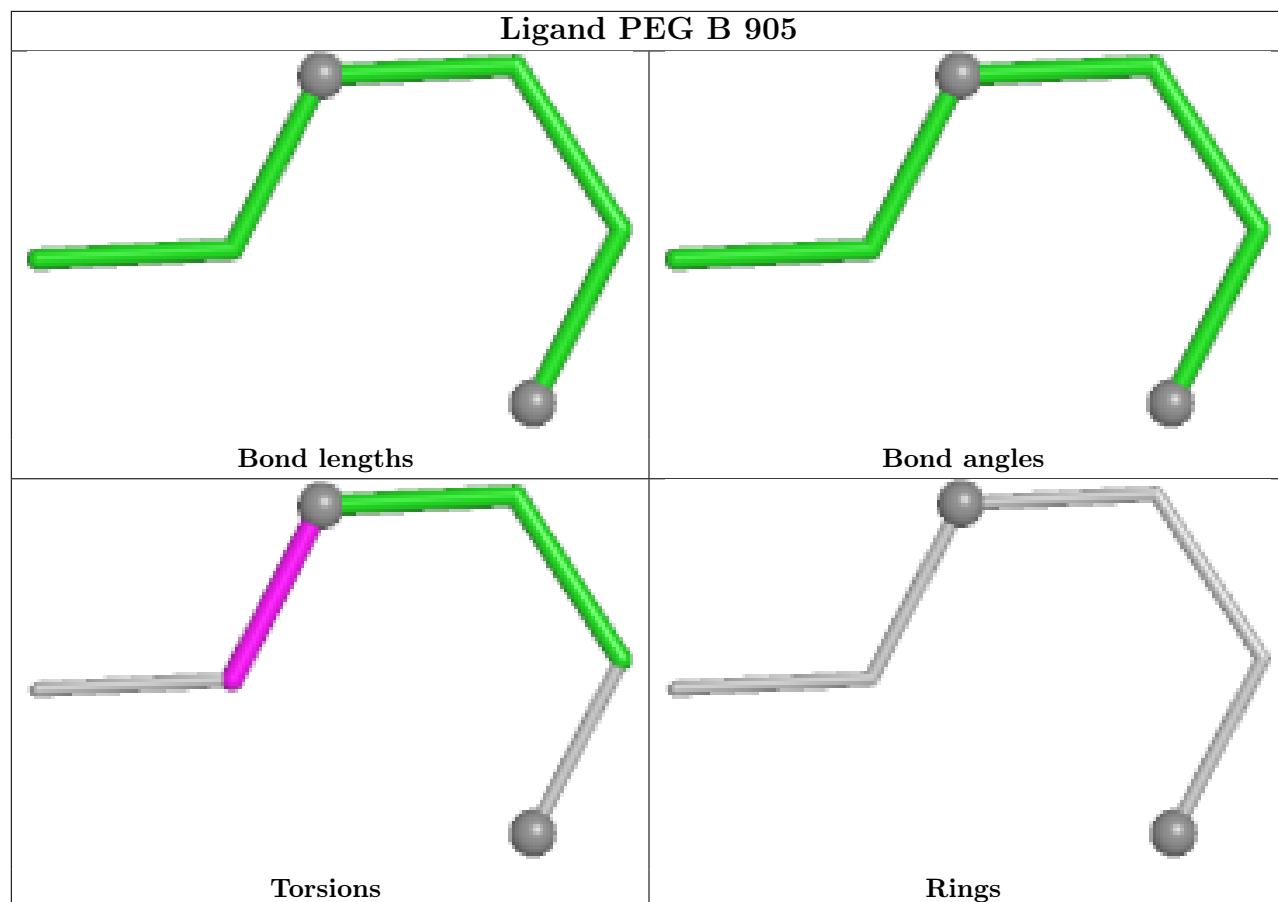
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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.











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, 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	B	528/594 (88%)	0.48	40 (7%) 20 22	22, 61, 94, 118	4 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	ASP	5.8
1	B	336	CYS	5.4
1	B	292	THR	4.6
1	B	712	ASN	4.5
1	B	868	HIS	4.0
1	B	579	ASP	4.0
1	B	294	ASP	3.6
1	B	582	LYS	3.5
1	B	305	THR	3.5
1	B	417	PRO	3.5
1	B	291	ALA	3.4
1	B	583	MET	3.2
1	B	535	VAL	3.1
1	B	322	TYR	3.1
1	B	711	GLU	3.1
1	B	309	THR	3.1
1	B	791	GLN	3.0
1	B	532	ASP	2.8
1	B	867	VAL	2.8
1	B	864	ASP	2.7
1	B	562	GLU	2.6
1	B	853	GLU	2.6
1	B	470	ASN	2.5
1	B	870	LEU	2.5
1	B	591	ILE	2.5
1	B	472	GLU	2.4
1	B	857	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	803	TYR	2.4
1	B	590	LEU	2.4
1	B	416	GLU	2.4
1	B	293	ARG	2.3
1	B	307	GLN	2.3
1	B	326	GLN	2.2
1	B	761	ASP	2.2
1	B	773	LEU	2.1
1	B	394[A]	MET	2.1
1	B	327	GLU	2.1
1	B	584	ASN	2.0
1	B	624	LYS	2.0
1	B	720	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.

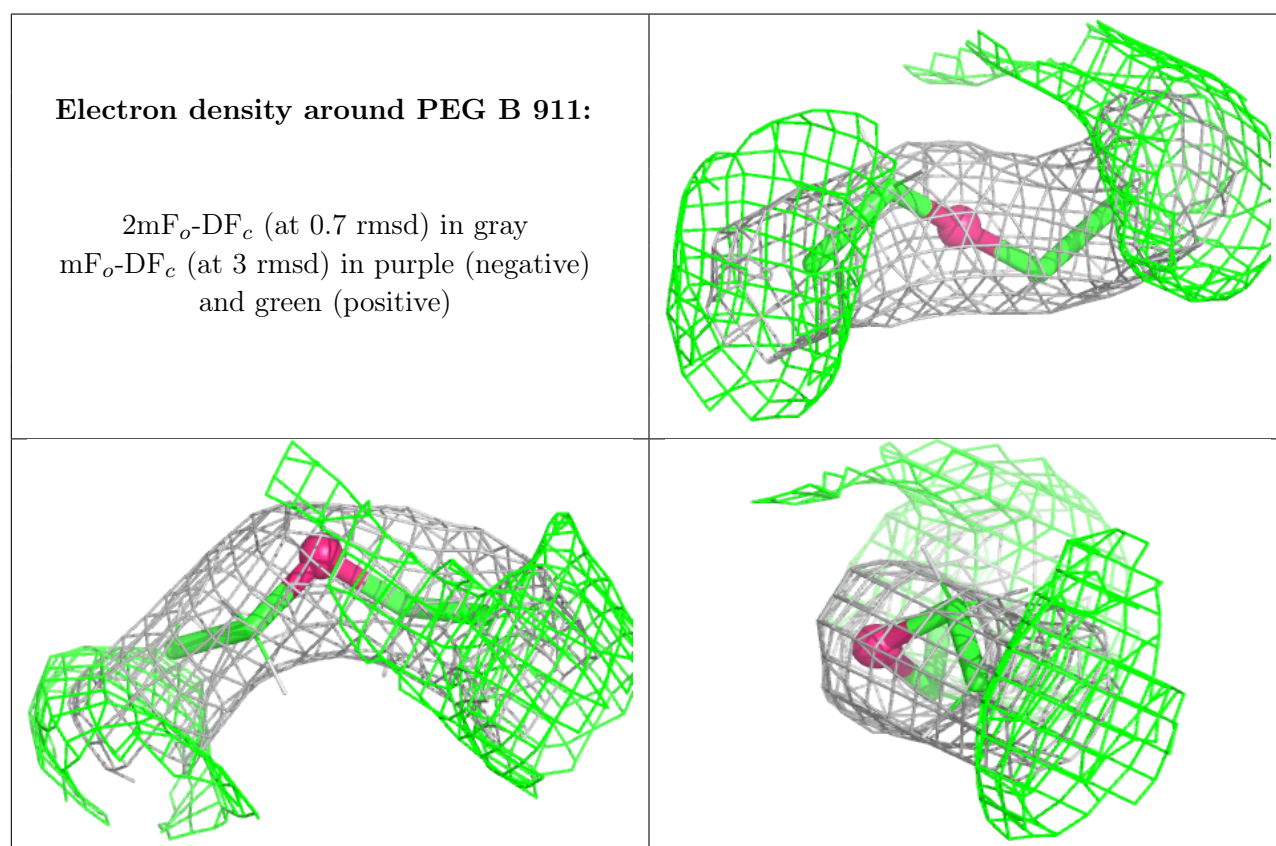
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PEG	B	911	5/7	0.60	0.41	74,78,104,104	0
5	PEG	B	905	6/7	0.75	0.20	64,76,88,91	0
3	PG4	B	902	13/13	0.77	0.22	65,82,98,117	0
5	PEG	B	912	5/7	0.78	0.31	81,99,107,107	0
6	GOL	B	906	6/6	0.78	0.21	91,109,116,116	0
7	CL	B	909	1/1	0.85	0.39	99,99,99,99	0
5	PEG	B	904	7/7	0.86	0.15	68,82,89,89	0
4	DMS	B	903	4/4	0.88	0.21	67,80,90,94	0
8	K	B	915	1/1	0.88	0.19	93,93,93,93	0
8	K	B	914	1/1	0.90	0.18	88,88,88,88	0

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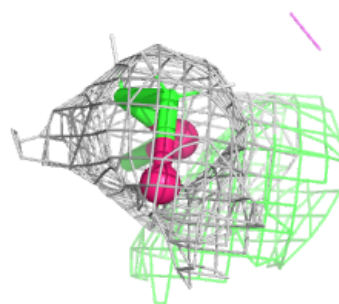
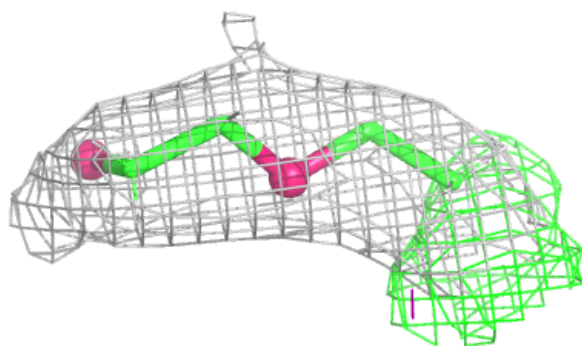
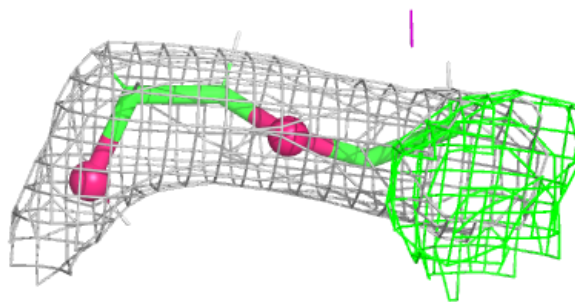
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	CL	B	910	1/1	0.91	0.16	85,85,85,85	0
7	CL	B	908	1/1	0.92	0.19	91,91,91,91	0
7	CL	B	907	1/1	0.95	0.18	93,93,93,93	0
2	MES	B	901	12/12	0.95	0.09	39,53,64,77	0
8	K	B	913	1/1	0.97	0.13	83,83,83,83	0

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.

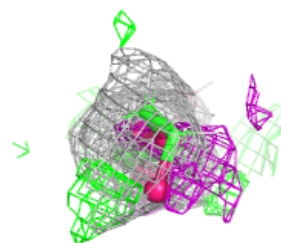
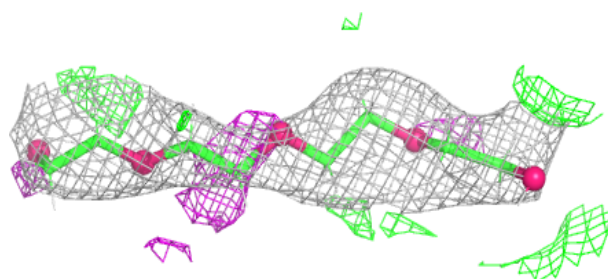
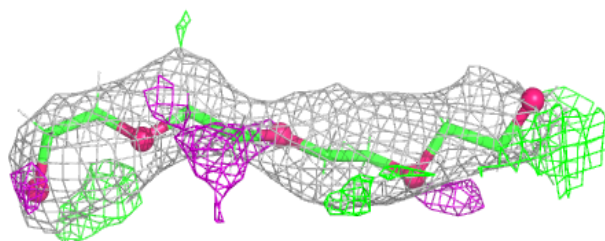


Electron density around PEG B 905:

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

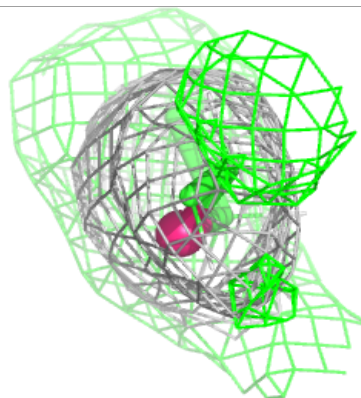
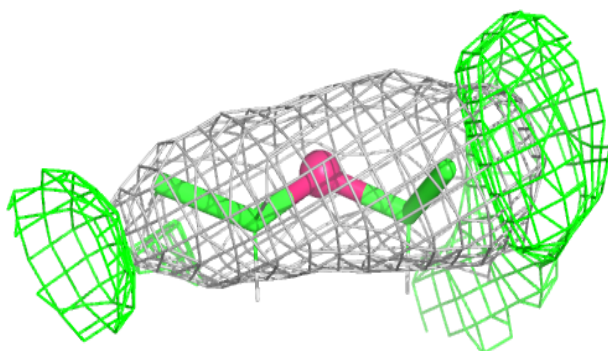
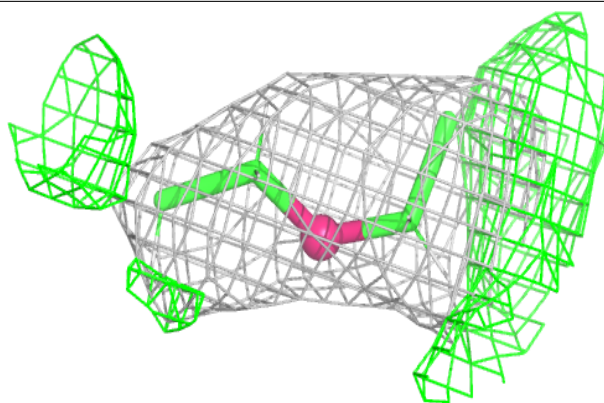
**Electron density around PG4 B 902:**

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

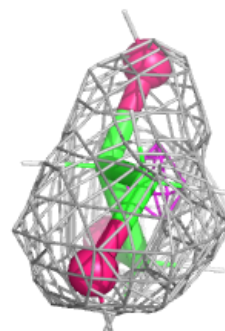
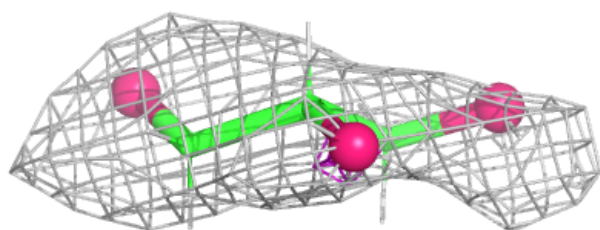
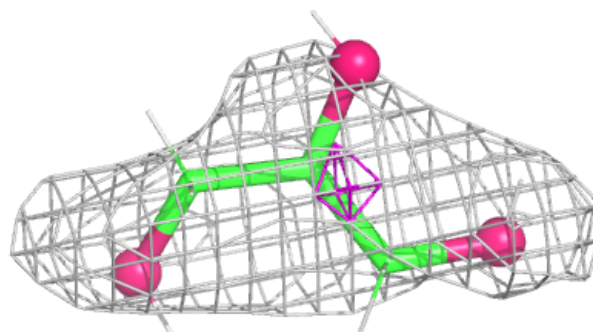


Electron density around PEG B 912:

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

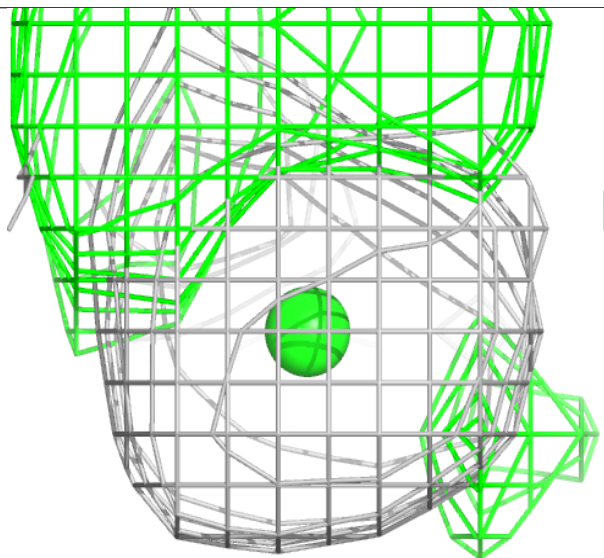
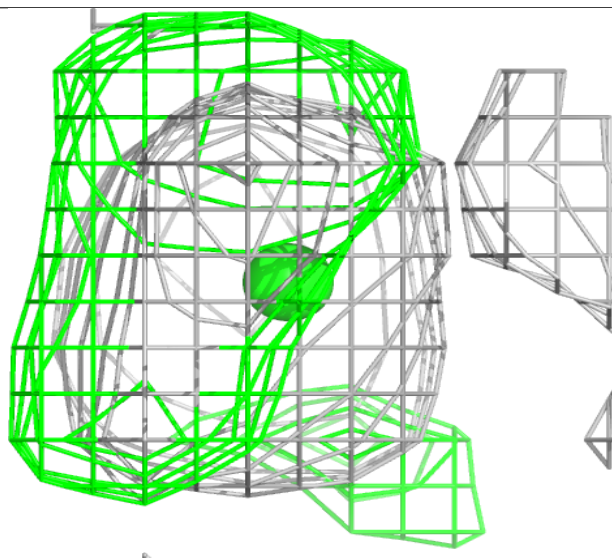
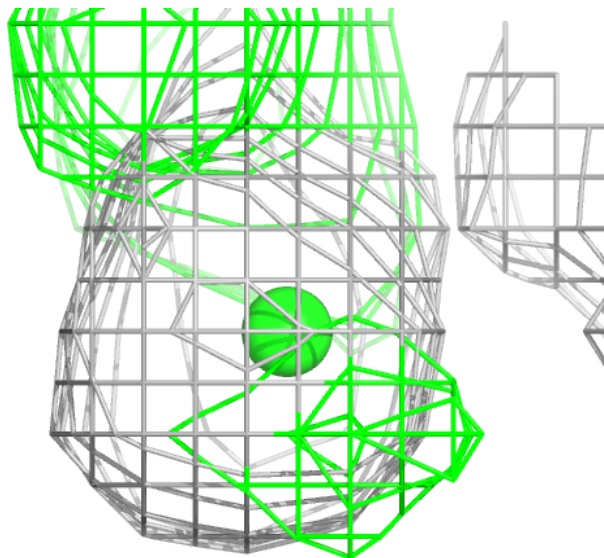
**Electron density around GOL B 906:**

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



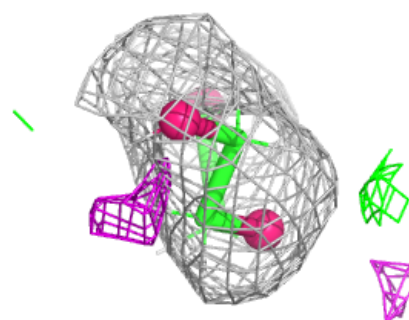
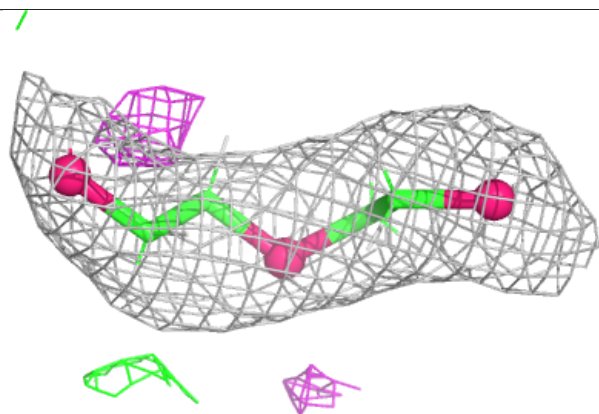
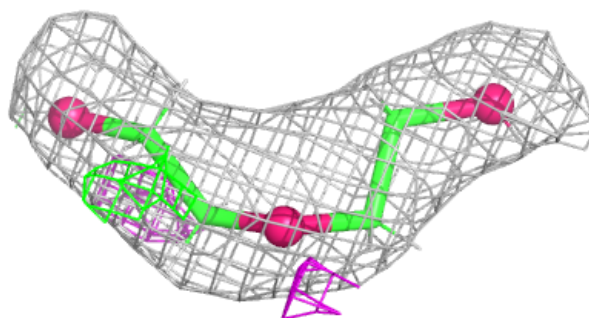
Electron density around CL B 909:

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



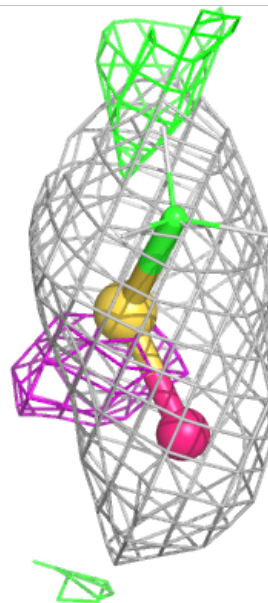
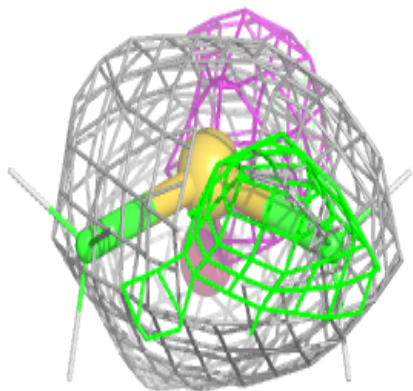
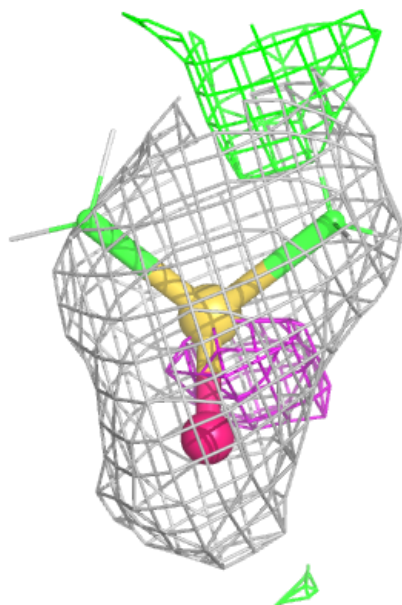
Electron density around PEG B 904:

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



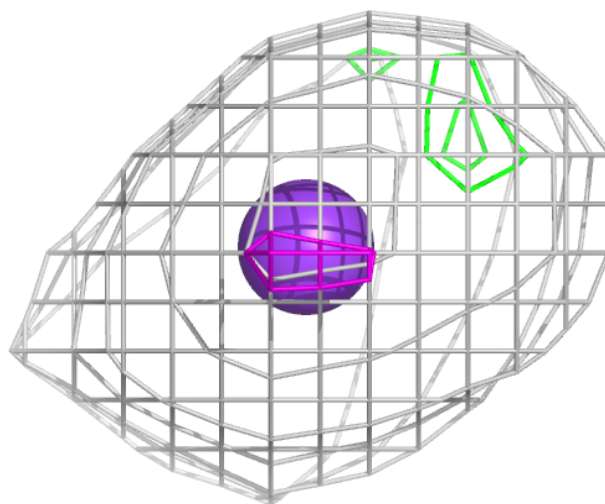
Electron density around DMS B 903:

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

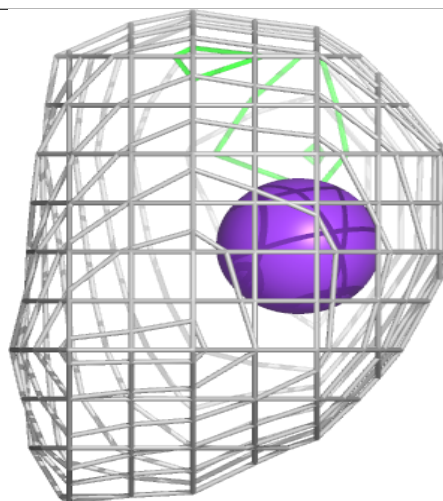
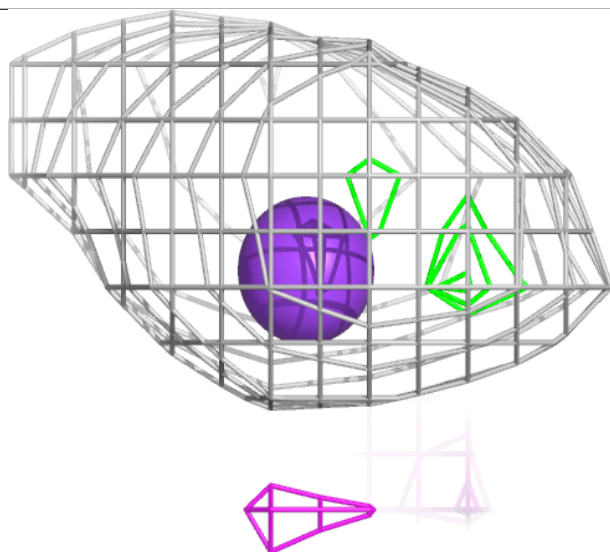


Electron density around K B 915:

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



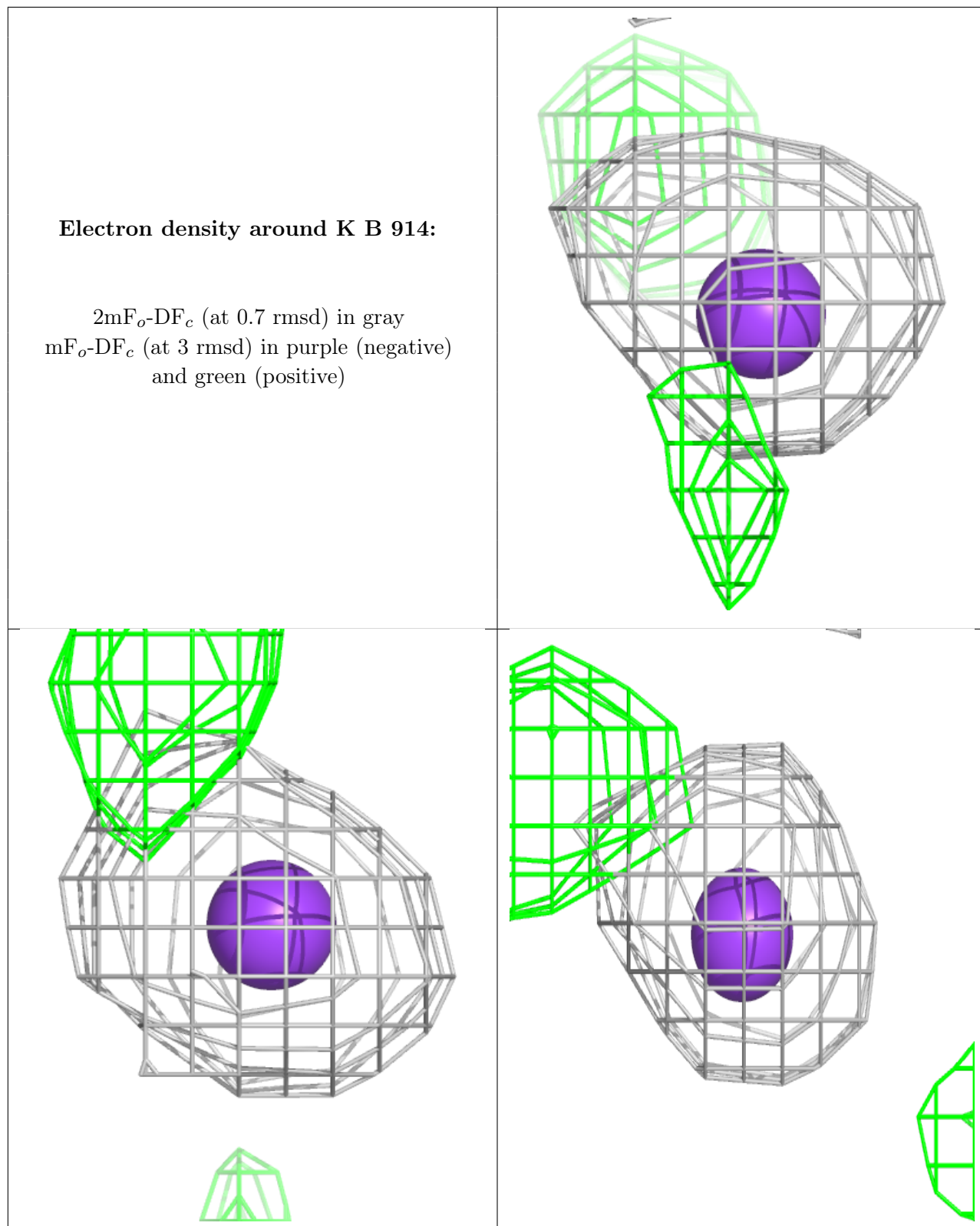
A



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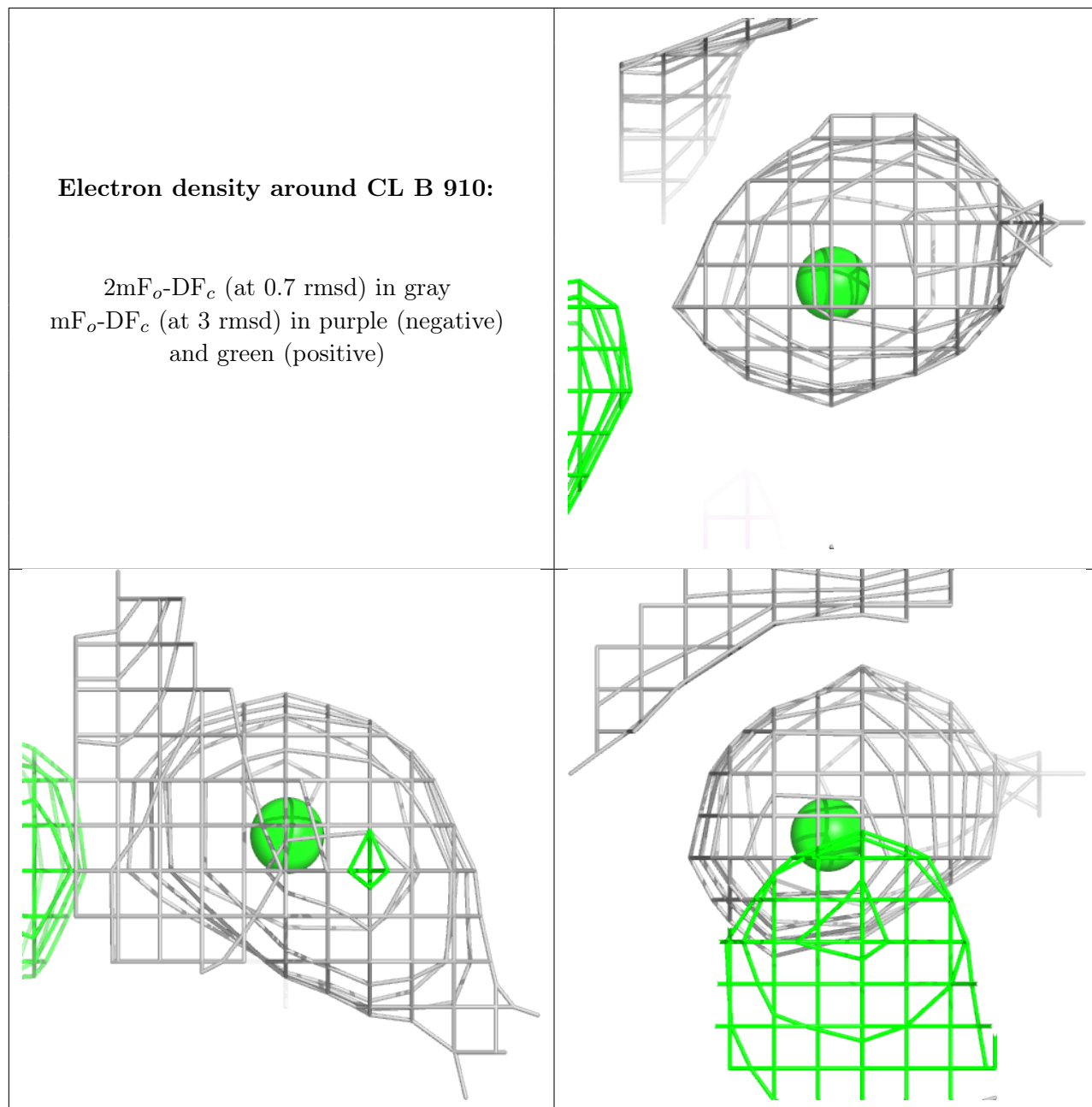
Electron density around K B 914:

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



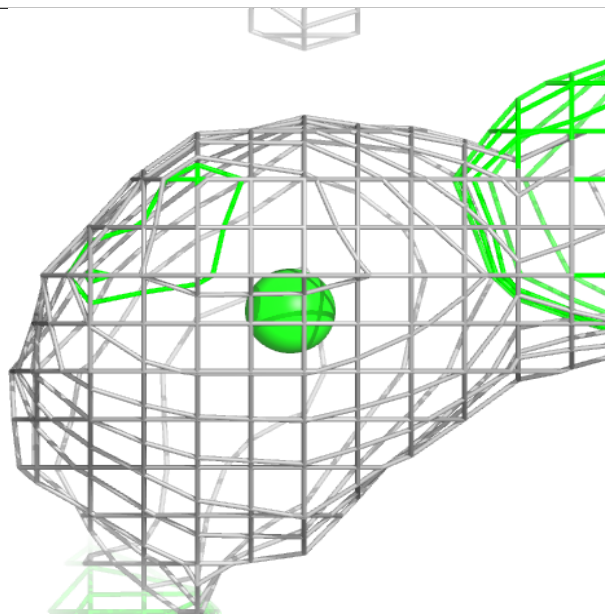
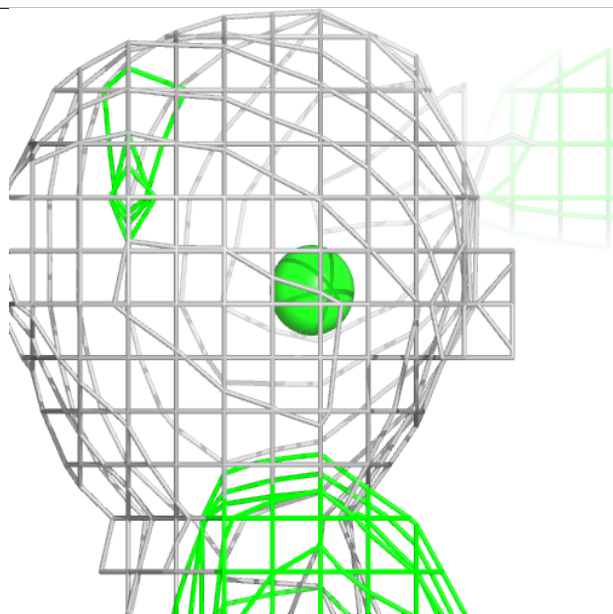
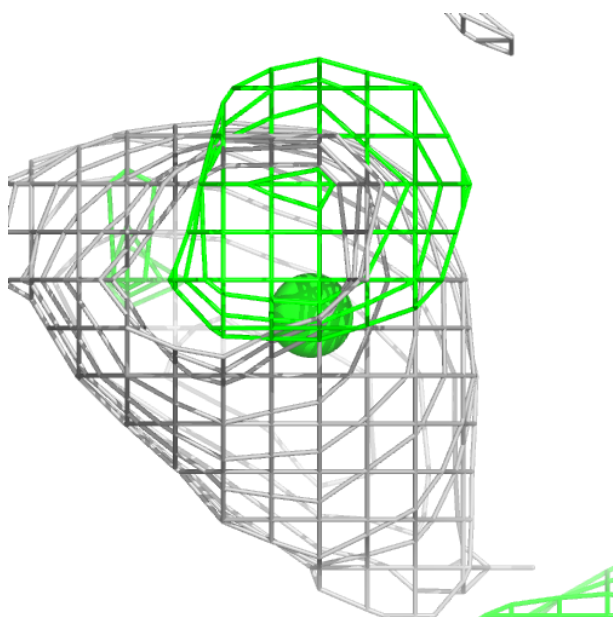
Electron density around CL B 910:

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



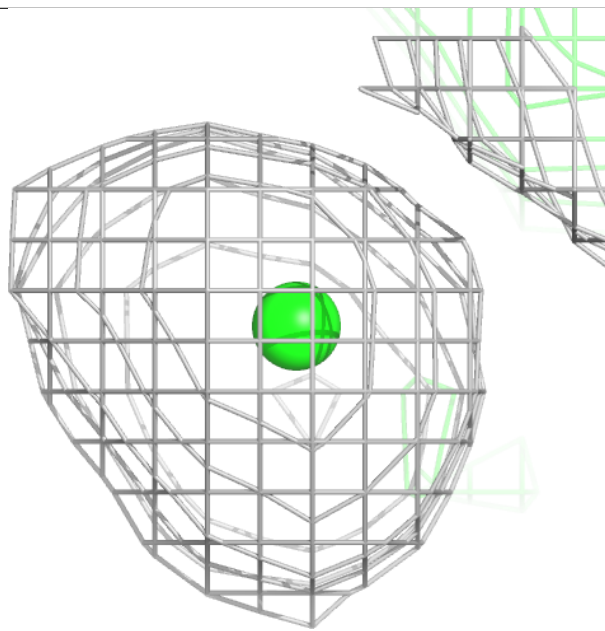
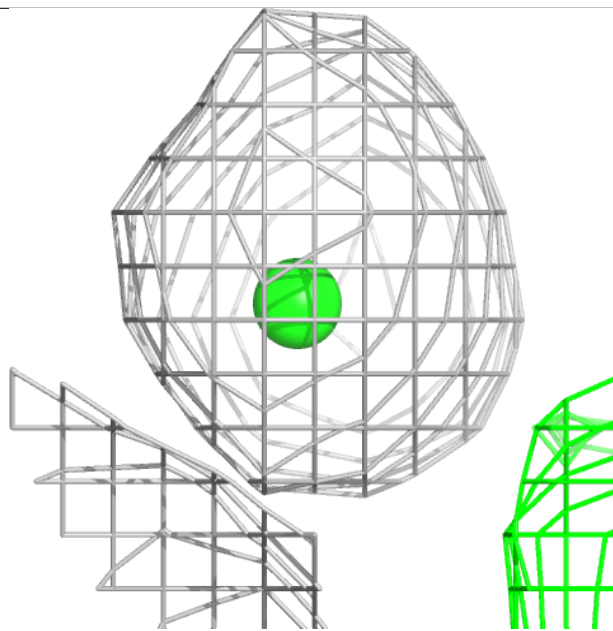
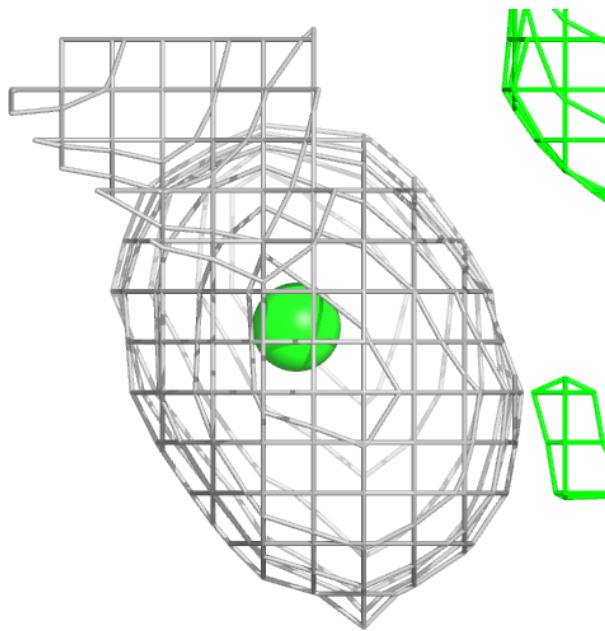
Electron density around CL B 908:

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



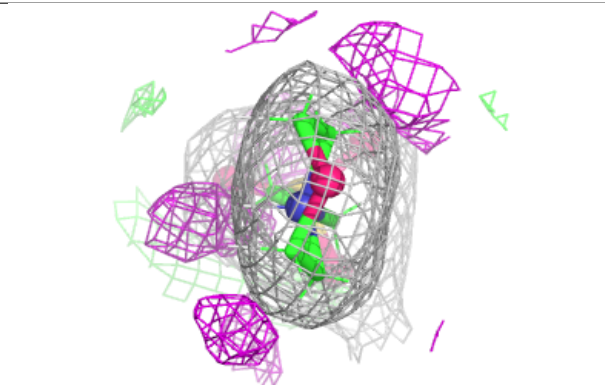
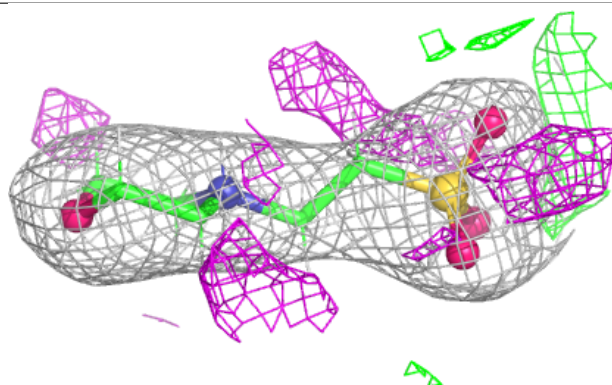
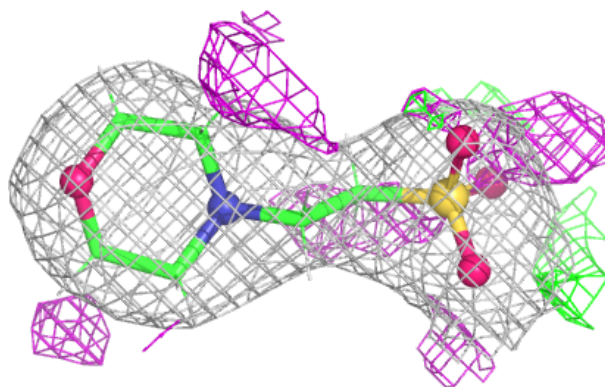
Electron density around CL B 907:

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

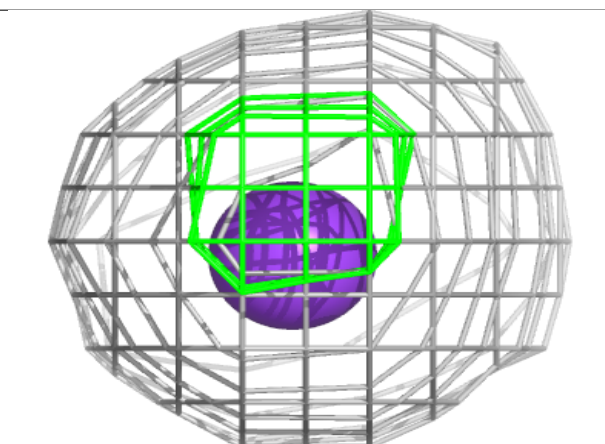
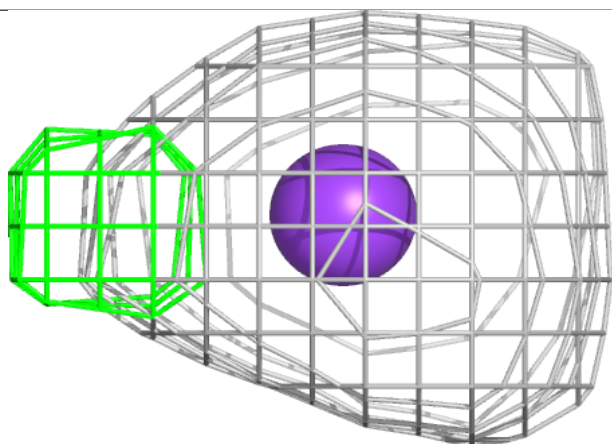
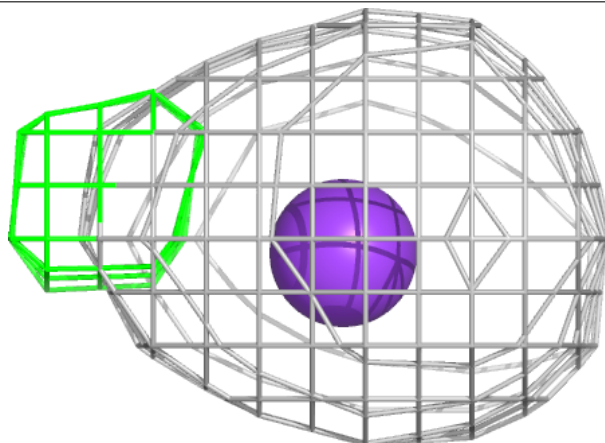


Electron density around MES B 901:

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

**Electron density around K B 913:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.