



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:38 AM UTC

PDB ID : 8HQL / pdb_00008hql
Title : Crystal structure of mouse SNX25 PX domain
Authors : Yu, Z.; Xu, J.; Liu, J.
Deposited on : 2022-12-13
Resolution : 2.40 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

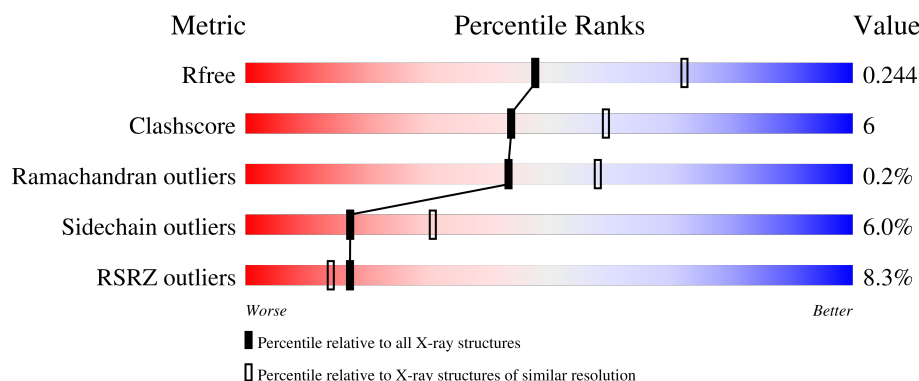
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	128	5% 80% 14% • 5%
1	B	128	9% 75% 16% • 8%
1	C	128	6% 78% 17% 5%
1	D	128	5% 79% 12% • 8%
1	E	128	14% 78% 16% • 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
3	GOL	C	702	-	-	X	-
3	GOL	E	703	-	-	X	-
4	CL	E	706	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5209 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 Sorting nexin-25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	S	0	0	0
			985	627	172	182	4			
1	B	118	Total	C	N	O	S	0	0	0
			953	607	167	175	4			
1	C	122	Total	C	N	O	S	0	0	0
			985	627	172	182	4			
1	D	118	Total	C	N	O	S	0	0	0
			952	605	167	176	4			
1	E	121	Total	C	N	O	S	0	0	0
			976	622	171	179	4			

There are 45 discrepancies between the modelled and reference sequences:

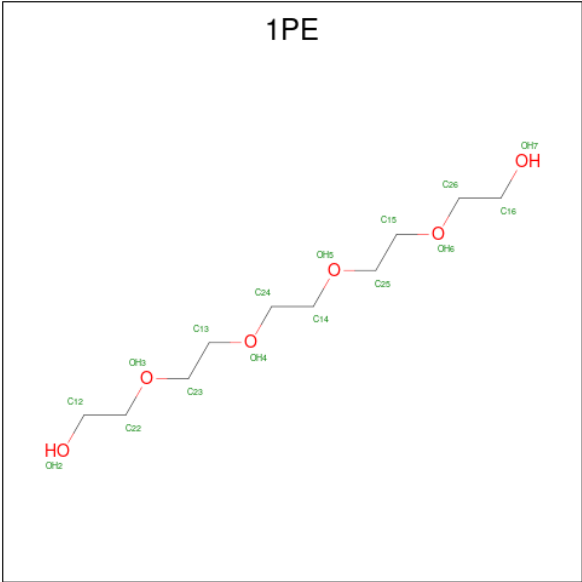
Chain	Residue	Modelled	Actual	Comment	Reference
A	505	MET	-	initiating methionine	UNP Q3ZT31
A	625	LEU	-	expression tag	UNP Q3ZT31
A	626	GLU	-	expression tag	UNP Q3ZT31
A	627	HIS	-	expression tag	UNP Q3ZT31
A	628	HIS	-	expression tag	UNP Q3ZT31
A	629	HIS	-	expression tag	UNP Q3ZT31
A	630	HIS	-	expression tag	UNP Q3ZT31
A	631	HIS	-	expression tag	UNP Q3ZT31
A	632	HIS	-	expression tag	UNP Q3ZT31
B	505	MET	-	initiating methionine	UNP Q3ZT31
B	625	LEU	-	expression tag	UNP Q3ZT31
B	626	GLU	-	expression tag	UNP Q3ZT31
B	627	HIS	-	expression tag	UNP Q3ZT31
B	628	HIS	-	expression tag	UNP Q3ZT31
B	629	HIS	-	expression tag	UNP Q3ZT31
B	630	HIS	-	expression tag	UNP Q3ZT31
B	631	HIS	-	expression tag	UNP Q3ZT31
B	632	HIS	-	expression tag	UNP Q3ZT31
C	505	MET	-	initiating methionine	UNP Q3ZT31

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Chain	Residue	Modelled	Actual	Comment	Reference
C	625	LEU	-	expression tag	UNP Q3ZT31
C	626	GLU	-	expression tag	UNP Q3ZT31
C	627	HIS	-	expression tag	UNP Q3ZT31
C	628	HIS	-	expression tag	UNP Q3ZT31
C	629	HIS	-	expression tag	UNP Q3ZT31
C	630	HIS	-	expression tag	UNP Q3ZT31
C	631	HIS	-	expression tag	UNP Q3ZT31
C	632	HIS	-	expression tag	UNP Q3ZT31
D	505	MET	-	initiating methionine	UNP Q3ZT31
D	625	LEU	-	expression tag	UNP Q3ZT31
D	626	GLU	-	expression tag	UNP Q3ZT31
D	627	HIS	-	expression tag	UNP Q3ZT31
D	628	HIS	-	expression tag	UNP Q3ZT31
D	629	HIS	-	expression tag	UNP Q3ZT31
D	630	HIS	-	expression tag	UNP Q3ZT31
D	631	HIS	-	expression tag	UNP Q3ZT31
D	632	HIS	-	expression tag	UNP Q3ZT31
E	505	MET	-	initiating methionine	UNP Q3ZT31
E	625	LEU	-	expression tag	UNP Q3ZT31
E	626	GLU	-	expression tag	UNP Q3ZT31
E	627	HIS	-	expression tag	UNP Q3ZT31
E	628	HIS	-	expression tag	UNP Q3ZT31
E	629	HIS	-	expression tag	UNP Q3ZT31
E	630	HIS	-	expression tag	UNP Q3ZT31
E	631	HIS	-	expression tag	UNP Q3ZT31
E	632	HIS	-	expression tag	UNP Q3ZT31

- Molecule 2 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆) (labeled as "Ligand of Interest" by depositor).



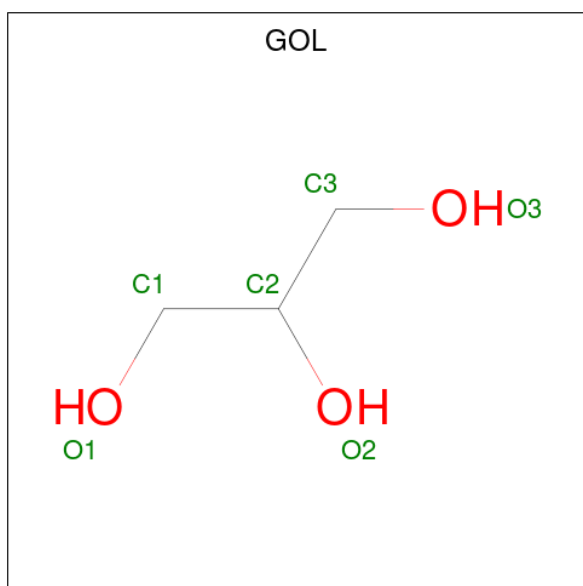
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			13	8	5		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			13	8	5		
2	B	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			9	6	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



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

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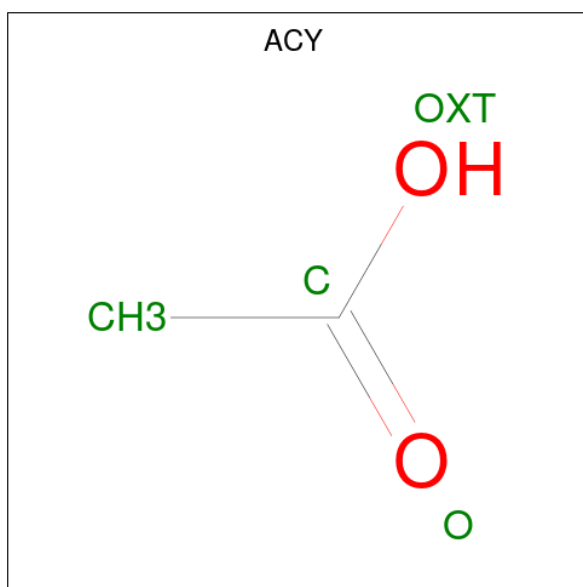
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0
4	B	1	Total Cl 1 1	0	0
4	C	1	Total Cl 1 1	0	0
4	D	1	Total Cl 1 1	0	0
4	E	1	Total Cl 1 1	0	0

- Molecule 5 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 6 is water.

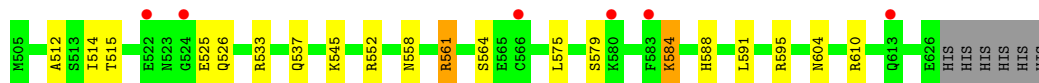
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	43	Total	O	0	0
			43	43		
6	B	30	Total	O	0	0
			30	30		
6	C	23	Total	O	0	0
			23	23		
6	D	21	Total	O	0	0
			21	21		
6	E	17	Total	O	0	0
			17	17		

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.

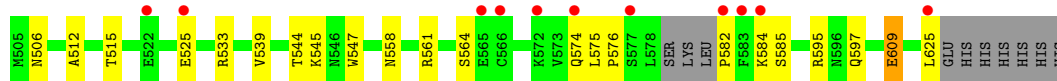
• Molecule 1: Sorting nexin-25

Chain A: 



• Molecule 1: Sorting nexin-25

Chain B: 



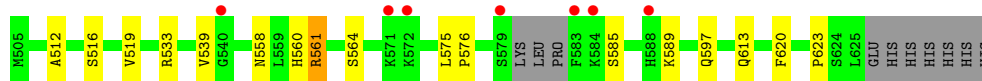
• Molecule 1: Sorting nexin-25

Chain C: 



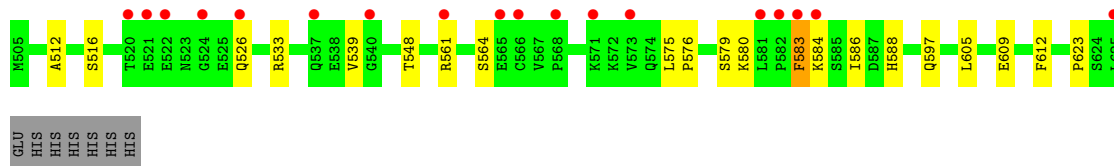
• Molecule 1: Sorting nexin-25

Chain D: 



• Molecule 1: Sorting nexin-25

Chain E: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	92.68Å 92.68Å 449.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.00 – 2.40 39.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.00-2.40) 99.8 (39.00-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.199 , 0.242 0.202 , 0.244	Depositor DCC
R_{free} test set	2319 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5209	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL, 1PE, ACY

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	1.20	3/1005 (0.3%)	1.46	4/1356 (0.3%)
1	B	1.13	2/972 (0.2%)	1.43	4/1310 (0.3%)
1	C	1.13	0/1005	1.45	1/1356 (0.1%)
1	D	1.10	1/970 (0.1%)	1.39	2/1307 (0.2%)
1	E	1.10	0/996	1.41	2/1344 (0.1%)
All	All	1.13	6/4948 (0.1%)	1.43	13/6673 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	515	THR	C-O	-6.75	1.15	1.24
1	D	623	PRO	C-O	-5.95	1.16	1.23
1	B	515	THR	C-O	-5.63	1.16	1.24
1	B	506	ASN	C-O	5.15	1.29	1.23
1	A	514	ILE	C-O	-5.13	1.18	1.24
1	A	588	HIS	CE1-NE2	5.12	1.37	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	583	PHE	CB-CA-C	7.55	125.44	110.42
1	A	595	ARG	CB-CG-CD	6.47	126.18	111.30
1	B	539	VAL	CA-C-N	-6.08	114.77	122.19
1	B	539	VAL	C-N-CA	-6.08	114.77	122.19
1	A	588	HIS	CA-CB-CG	5.78	119.58	113.80
1	C	597	GLN	CB-CG-CD	-5.73	102.86	112.60
1	B	539	VAL	N-CA-C	-5.66	101.51	109.21
1	A	552	ARG	CB-CG-CD	5.48	123.91	111.30
1	A	595	ARG	CD-NE-CZ	5.17	131.64	124.40
1	D	539	VAL	N-CA-C	-5.17	101.02	108.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	620	PHE	CA-C-O	-5.13	115.11	120.55
1	E	539	VAL	N-CA-C	-5.13	101.08	108.87
1	B	625	LEU	CA-C-O	5.03	129.35	120.80

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	985	0	993	12	0
1	B	953	0	957	9	0
1	C	985	0	993	19	0
1	D	952	0	954	7	0
1	E	976	0	987	17	0
2	A	31	0	39	1	0
2	B	45	0	58	4	0
2	C	9	0	11	1	0
2	D	28	0	35	1	0
2	E	14	0	17	4	0
3	A	30	0	40	0	0
3	C	30	0	40	8	0
3	D	6	0	8	1	0
3	E	18	0	24	6	0
4	A	1	0	0	1	0
4	B	1	0	0	0	0
4	C	1	0	0	1	0
4	D	1	0	0	0	0
4	E	1	0	0	3	0
5	C	4	0	3	0	0
5	D	4	0	3	0	0
6	A	43	0	0	1	0
6	B	30	0	0	1	0
6	C	23	0	0	1	0
6	D	21	0	0	0	0
6	E	17	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5209	0	5162	62	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 6.

All (62) 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:557:GLN:HG3	1:C:578:LEU:HD23	1.56	0.85
1:C:569:SER:HB3	3:C:702:GOL:H11	1.59	0.84
1:C:599:ASN:HD21	3:C:705:GOL:H32	1.44	0.82
1:E:576:PRO:HG3	1:E:597:GLN:HE21	1.48	0.78
1:B:576:PRO:HG3	1:B:597:GLN:HE21	1.47	0.78
1:D:576:PRO:HG3	1:D:597:GLN:HE21	1.48	0.77
1:E:588:HIS:HE1	3:E:703:GOL:H32	1.55	0.71
1:B:544:THR:HA	2:B:701:1PE:H261	1.73	0.69
1:E:516:SER:HB2	3:E:704:GOL:H31	1.74	0.68
1:E:584:LYS:HA	4:E:706:CL:CL	2.30	0.68
1:E:576:PRO:HG3	1:E:597:GLN:NE2	2.08	0.68
1:C:569:SER:CB	3:C:702:GOL:H11	2.23	0.67
1:B:576:PRO:HG3	1:B:597:GLN:NE2	2.10	0.67
1:E:588:HIS:HE1	3:E:703:GOL:C3	2.10	0.65
1:D:576:PRO:HG3	1:D:597:GLN:NE2	2.11	0.64
1:E:548:THR:OG1	2:E:701:1PE:H132	1.98	0.63
1:C:599:ASN:ND2	3:C:705:GOL:H32	2.14	0.60
1:B:609:GLU:OE2	1:D:613:GLN:NE2	2.31	0.60
1:A:526:GLN:NE2	6:A:801:HOH:O	2.22	0.60
1:C:557:GLN:OE1	1:C:557:GLN:HA	2.03	0.57
1:E:583:PHE:O	4:E:706:CL:CL	2.60	0.57
1:A:579:SER:HB3	1:A:584:LYS:HB3	1.88	0.54
1:C:623:PRO:HG2	1:E:623:PRO:HG2	1.93	0.51
1:C:595:ARG:HD2	6:C:803:HOH:O	2.11	0.50
1:E:609:GLU:HG3	1:E:612:PHE:CE2	2.46	0.50
1:A:610:ARG:HD3	1:C:585:SER:OG	2.11	0.50
1:E:588:HIS:CE1	3:E:703:GOL:C3	2.94	0.49
1:A:558:ASN:OD1	1:A:561:ARG:NH1	2.45	0.49
1:E:579:SER:OG	4:E:706:CL:CL	2.66	0.49
1:A:579:SER:HB3	1:A:584:LYS:CB	2.43	0.49
4:C:707:CL:CL	2:E:701:1PE:H232	2.50	0.49
1:E:588:HIS:CE1	3:E:703:GOL:H32	2.43	0.48
1:A:604:ASN:HB3	1:C:583:PHE:CG	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:560:HIS:CE1	3:D:705:GOL:H2	2.48	0.48
1:B:558:ASN:OD1	1:B:561:ARG:NH2	2.47	0.48
1:C:569:SER:OG	3:C:702:GOL:H12	2.14	0.47
1:C:599:ASN:HD21	3:C:705:GOL:C3	2.22	0.47
1:B:547:TRP:C	2:B:702:1PE:H141	2.40	0.47
1:D:558:ASN:OD1	1:D:561:ARG:NH2	2.48	0.46
2:E:701:1PE:C15	6:E:813:HOH:O	2.63	0.46
1:C:581:LEU:N	1:C:582:PRO:CD	2.79	0.46
1:C:557:GLN:HG3	1:C:578:LEU:CD2	2.38	0.45
1:E:526:GLN:HB3	1:E:586:ILE:HD12	1.97	0.45
1:D:516:SER:HB2	2:D:704:1PE:H141	1.99	0.44
1:C:512:ALA:HA	1:C:533:ARG:O	2.18	0.44
1:A:545:LYS:HB2	2:B:702:1PE:H162	2.00	0.43
2:A:703:1PE:H231	2:A:703:1PE:H141	1.99	0.43
1:B:533:ARG:HD3	6:B:824:HOH:O	2.19	0.43
1:C:569:SER:OG	3:C:702:GOL:C1	2.68	0.42
1:A:512:ALA:HA	1:A:533:ARG:O	2.20	0.42
1:A:591:LEU:HD23	1:A:591:LEU:HA	1.85	0.42
1:E:588:HIS:CE1	3:E:703:GOL:H31	2.55	0.42
1:C:569:SER:CB	3:C:702:GOL:C1	2.96	0.42
1:A:584:LYS:HA	1:A:584:LYS:HD2	1.83	0.41
1:A:604:ASN:HB3	1:C:583:PHE:CD2	2.55	0.41
1:E:512:ALA:HA	1:E:533:ARG:O	2.19	0.41
1:B:512:ALA:HA	1:B:533:ARG:O	2.21	0.41
1:D:512:ALA:HA	1:D:533:ARG:O	2.20	0.41
1:B:545:LYS:HG3	2:B:701:1PE:H262	2.02	0.41
1:E:548:THR:OG1	2:E:701:1PE:C13	2.66	0.41
1:C:547:TRP:C	2:C:701:1PE:H141	2.46	0.41
1:A:584:LYS:C	4:A:710:CL:CL	3.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	120/128 (94%)	116 (97%)	4 (3%)	0	100	100
1	B	114/128 (89%)	109 (96%)	5 (4%)	0	100	100
1	C	120/128 (94%)	115 (96%)	4 (3%)	1 (1%)	16	25
1	D	114/128 (89%)	111 (97%)	3 (3%)	0	100	100
1	E	119/128 (93%)	113 (95%)	6 (5%)	0	100	100
All	All	587/640 (92%)	564 (96%)	22 (4%)	1 (0%)	43	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	523	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	112/118 (95%)	106 (95%)	6 (5%)	20	35
1	B	108/118 (92%)	99 (92%)	9 (8%)	10	17
1	C	112/118 (95%)	105 (94%)	7 (6%)	16	29
1	D	108/118 (92%)	102 (94%)	6 (6%)	19	33
1	E	111/118 (94%)	106 (96%)	5 (4%)	24	42
All	All	551/590 (93%)	518 (94%)	33 (6%)	17	31

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	525	GLU
1	A	537	GLN
1	A	561	ARG
1	A	564	SER
1	A	575	LEU
1	A	584	LYS
1	B	525	GLU

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Mol	Chain	Res	Type
1	B	564	SER
1	B	574	GLN
1	B	575	LEU
1	B	582	PRO
1	B	584	LYS
1	B	585	SER
1	B	595	ARG
1	B	609	GLU
1	C	522	GLU
1	C	561	ARG
1	C	564	SER
1	C	575	LEU
1	C	593	LYS
1	C	605	LEU
1	C	609	GLU
1	D	519	VAL
1	D	561	ARG
1	D	564	SER
1	D	575	LEU
1	D	585	SER
1	D	589	LYS
1	E	561	ARG
1	E	564	SER
1	E	575	LEU
1	E	580	LYS
1	E	605	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	597	GLN
1	C	597	GLN
1	D	523	ASN
1	D	546	ASN
1	D	597	GLN
1	D	603	GLN
1	E	588	HIS
1	E	597	GLN
1	E	603	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 38 ligands modelled in this entry, 5 are monoatomic - leaving 33 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	1PE	B	703	-	9,9,15	0.47	0	8,8,14	0.44	0
3	GOL	E	704	-	5,5,5	0.30	0	5,5,5	0.67	0
2	1PE	E	702	-	3,3,15	0.34	0	2,2,14	0.18	0
2	1PE	B	706	-	3,3,15	0.20	0	2,2,14	0.36	0
2	1PE	B	704	-	3,3,15	0.28	0	2,2,14	0.24	0
2	1PE	B	705	-	3,3,15	0.47	0	2,2,14	0.26	0
3	GOL	A	705	-	5,5,5	0.19	0	5,5,5	0.45	0
3	GOL	D	705	-	5,5,5	0.20	0	5,5,5	0.41	0
2	1PE	A	703	-	12,12,15	0.53	0	11,11,14	0.41	0
2	1PE	C	701	-	8,8,15	0.81	0	7,7,14	0.39	0
2	1PE	D	702	-	6,6,15	0.17	0	5,5,14	0.35	0
2	1PE	D	701	-	6,6,15	1.03	0	5,5,14	0.73	0
2	1PE	E	701	-	9,9,15	0.57	0	8,8,14	0.44	0
3	GOL	A	706	-	5,5,5	0.33	0	5,5,5	0.70	0
2	1PE	B	701	-	12,12,15	0.65	0	11,11,14	0.50	0
3	GOL	C	702	-	5,5,5	0.05	0	5,5,5	0.46	0
3	GOL	E	705	-	5,5,5	0.13	0	5,5,5	0.39	0
2	1PE	A	701	-	9,9,15	0.35	0	8,8,14	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	E	703	-	5,5,5	0.18	0	5,5,5	0.65	0
3	GOL	A	707	-	5,5,5	0.14	0	5,5,5	0.52	0
2	1PE	B	702	-	9,9,15	0.70	0	8,8,14	0.33	0
2	1PE	D	703	-	3,3,15	0.40	0	2,2,14	0.15	0
3	GOL	C	706	-	5,5,5	0.22	0	5,5,5	0.64	0
2	1PE	A	702	-	3,3,15	0.49	0	2,2,14	0.27	0
3	GOL	A	709	-	5,5,5	0.20	0	5,5,5	0.62	0
2	1PE	A	704	-	3,3,15	0.43	0	2,2,14	0.31	0
2	1PE	D	704	-	9,9,15	0.43	0	8,8,14	0.46	0
5	ACY	D	707	-	3,3,3	1.28	0	3,3,3	0.69	0
3	GOL	C	704	-	5,5,5	0.17	0	5,5,5	0.28	0
3	GOL	C	705	-	5,5,5	0.19	0	5,5,5	0.43	0
5	ACY	C	708	-	3,3,3	1.15	0	3,3,3	0.93	0
3	GOL	C	703	-	5,5,5	0.13	0	5,5,5	0.33	0
3	GOL	A	708	-	5,5,5	0.11	0	5,5,5	0.36	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	1PE	B	703	-	-	6/7/7/13	-
3	GOL	E	704	-	-	4/4/4/4	-
2	1PE	E	702	-	-	1/1/1/13	-
2	1PE	B	706	-	-	0/1/1/13	-
2	1PE	B	704	-	-	0/1/1/13	-
2	1PE	B	705	-	-	0/1/1/13	-
3	GOL	A	705	-	-	4/4/4/4	-
3	GOL	D	705	-	-	0/4/4/4	-
2	1PE	A	703	-	-	7/10/10/13	-
2	1PE	C	701	-	-	5/6/6/13	-
2	1PE	D	702	-	-	2/4/4/13	-
2	1PE	D	701	-	-	2/4/4/13	-
2	1PE	E	701	-	-	4/7/7/13	-
3	GOL	A	706	-	-	4/4/4/4	-
2	1PE	B	701	-	-	8/10/10/13	-
3	GOL	C	702	-	-	4/4/4/4	-
3	GOL	E	705	-	-	2/4/4/4	-
2	1PE	A	701	-	-	1/7/7/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	E	703	-	-	0/4/4/4	-
3	GOL	A	707	-	-	3/4/4/4	-
2	1PE	B	702	-	-	5/7/7/13	-
2	1PE	D	703	-	-	1/1/1/13	-
3	GOL	C	706	-	-	4/4/4/4	-
2	1PE	A	702	-	-	1/1/1/13	-
3	GOL	A	709	-	-	0/4/4/4	-
2	1PE	A	704	-	-	0/1/1/13	-
2	1PE	D	704	-	-	4/7/7/13	-
3	GOL	C	704	-	-	0/4/4/4	-
3	GOL	C	705	-	-	4/4/4/4	-
3	GOL	C	703	-	-	2/4/4/4	-
3	GOL	A	708	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (79) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	706	GOL	O1-C1-C2-C3
3	A	706	GOL	C1-C2-C3-O3
3	A	706	GOL	O2-C2-C3-O3
3	C	702	GOL	O1-C1-C2-C3
3	C	702	GOL	C1-C2-C3-O3
3	C	705	GOL	C1-C2-C3-O3
3	C	706	GOL	C1-C2-C3-O3
3	E	704	GOL	O1-C1-C2-C3
3	E	705	GOL	C1-C2-C3-O3
2	B	703	1PE	C25-C15-OH6-C26
2	B	701	1PE	OH6-C15-C25-OH5
2	A	703	1PE	OH5-C14-C24-OH4
2	D	704	1PE	OH5-C14-C24-OH4
2	B	701	1PE	OH5-C14-C24-OH4
2	E	701	1PE	OH6-C15-C25-OH5
2	A	703	1PE	C12-C22-OH3-C23
2	B	701	1PE	C23-C13-OH4-C24
3	E	704	GOL	O2-C2-C3-O3
2	A	703	1PE	OH4-C13-C23-OH3

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Mol	Chain	Res	Type	Atoms
2	C	701	1PE	OH7-C16-C26-OH6
2	B	703	1PE	C15-C25-OH5-C14
2	B	703	1PE	OH6-C15-C25-OH5
3	A	705	GOL	O1-C1-C2-C3
3	A	705	GOL	C1-C2-C3-O3
3	C	703	GOL	C1-C2-C3-O3
3	C	705	GOL	O1-C1-C2-C3
3	E	704	GOL	C1-C2-C3-O3
2	B	702	1PE	OH7-C16-C26-OH6
2	D	701	1PE	OH2-C12-C22-OH3
2	D	704	1PE	OH4-C13-C23-OH3
2	B	702	1PE	OH6-C15-C25-OH5
3	A	705	GOL	O1-C1-C2-O2
3	A	706	GOL	O1-C1-C2-O2
3	C	702	GOL	O1-C1-C2-O2
3	C	702	GOL	O2-C2-C3-O3
3	C	705	GOL	O2-C2-C3-O3
3	C	706	GOL	O2-C2-C3-O3
3	E	705	GOL	O2-C2-C3-O3
2	D	702	1PE	OH6-C15-C25-OH5
2	B	701	1PE	OH4-C13-C23-OH3
2	B	703	1PE	OH5-C14-C24-OH4
3	C	703	GOL	O2-C2-C3-O3
3	C	705	GOL	O1-C1-C2-O2
3	E	704	GOL	O1-C1-C2-O2
2	E	701	1PE	OH5-C14-C24-OH4
2	A	702	1PE	OH6-C15-C25-OH5
2	D	703	1PE	OH7-C16-C26-OH6
2	E	702	1PE	OH7-C16-C26-OH6
2	A	703	1PE	OH6-C15-C25-OH5
3	C	706	GOL	O1-C1-C2-O2
2	B	701	1PE	C15-C25-OH5-C14
2	B	702	1PE	C16-C26-OH6-C15
2	A	703	1PE	C15-C25-OH5-C14
2	B	703	1PE	C24-C14-OH5-C25
3	A	707	GOL	O1-C1-C2-C3
2	E	701	1PE	OH4-C13-C23-OH3
2	C	701	1PE	OH6-C15-C25-OH5
2	A	701	1PE	OH5-C14-C24-OH4
2	D	704	1PE	C23-C13-OH4-C24
2	C	701	1PE	C16-C26-OH6-C15
2	C	701	1PE	C24-C14-OH5-C25

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Mol	Chain	Res	Type	Atoms
2	B	702	1PE	C24-C14-OH5-C25
2	D	702	1PE	C16-C26-OH6-C15
2	B	703	1PE	C16-C26-OH6-C15
2	B	701	1PE	C24-C14-OH5-C25
2	D	701	1PE	C12-C22-OH3-C23
3	A	707	GOL	C1-C2-C3-O3
3	C	706	GOL	O1-C1-C2-C3
3	A	707	GOL	O1-C1-C2-O2
2	E	701	1PE	C14-C24-OH4-C13
2	D	704	1PE	OH6-C15-C25-OH5
2	C	701	1PE	C25-C15-OH6-C26
3	A	705	GOL	O2-C2-C3-O3
2	A	703	1PE	C24-C14-OH5-C25
2	B	701	1PE	C14-C24-OH4-C13
3	A	708	GOL	O2-C2-C3-O3
2	B	702	1PE	OH5-C14-C24-OH4
2	B	701	1PE	C25-C15-OH6-C26
2	A	703	1PE	C23-C13-OH4-C24

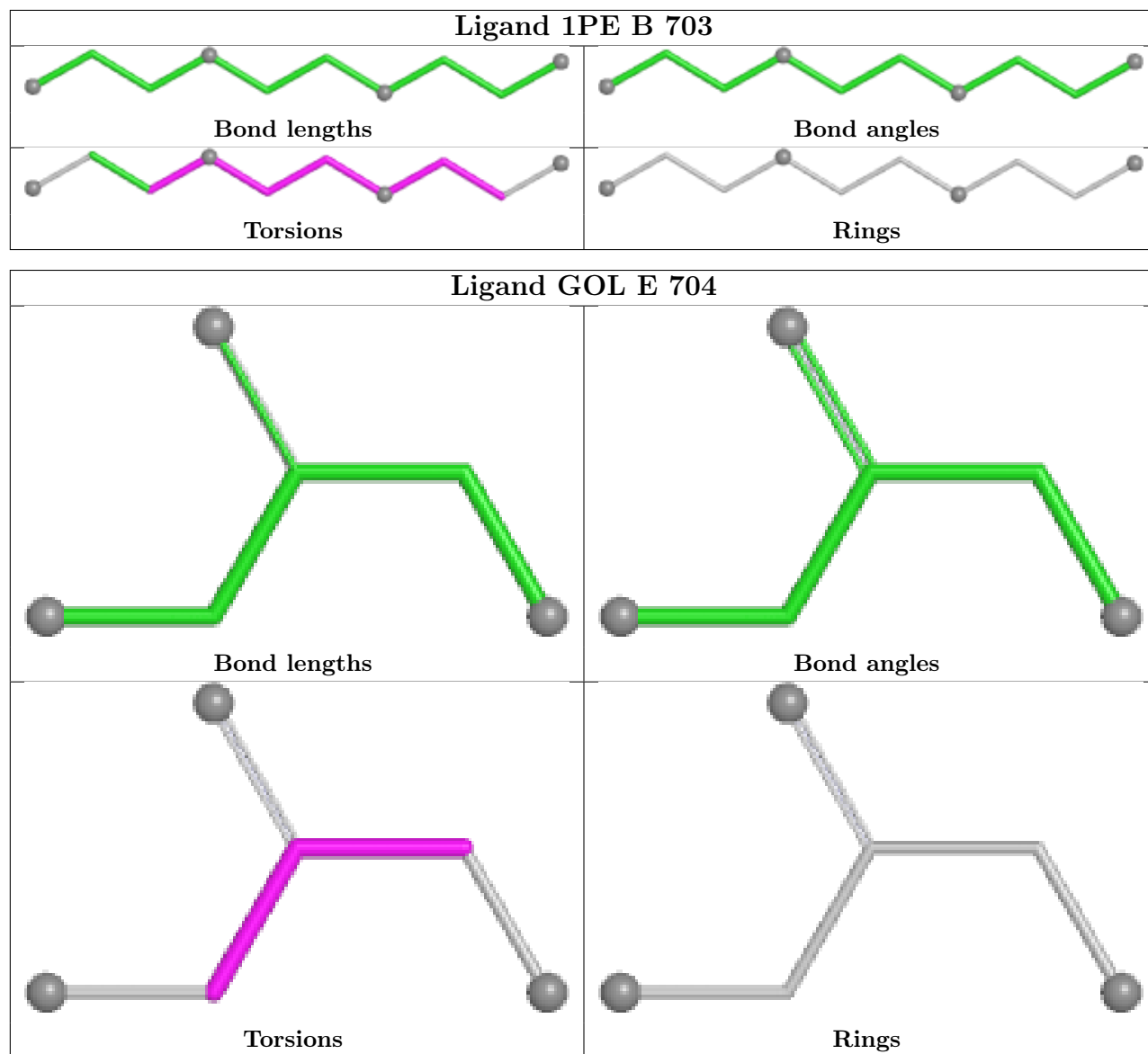
There are no ring outliers.

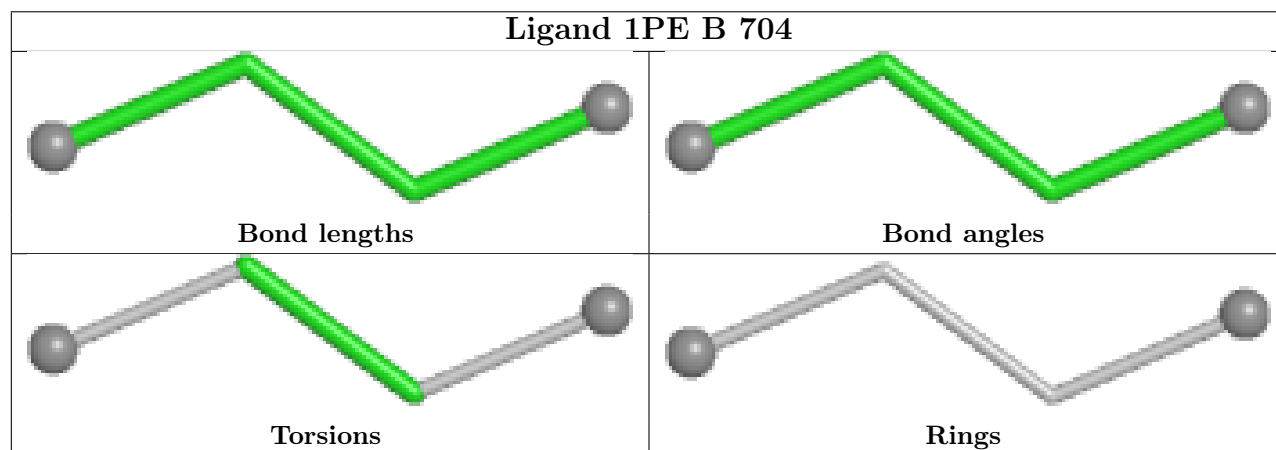
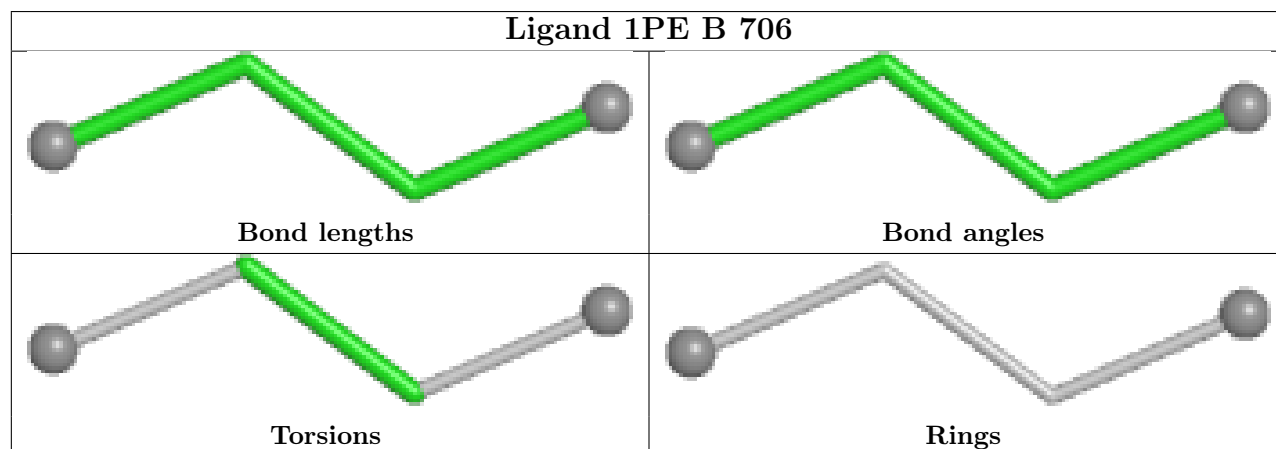
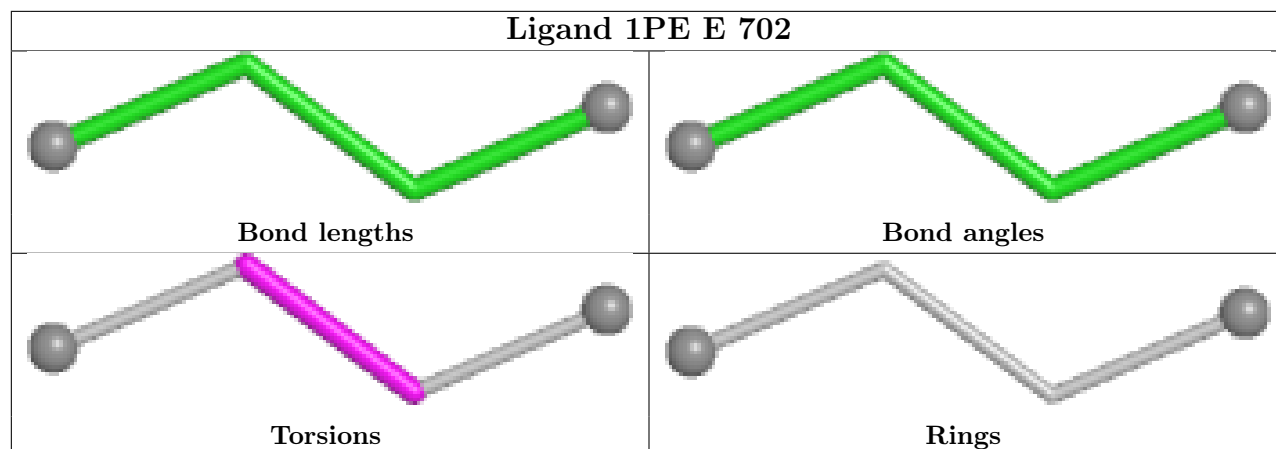
11 monomers are involved in 26 short contacts:

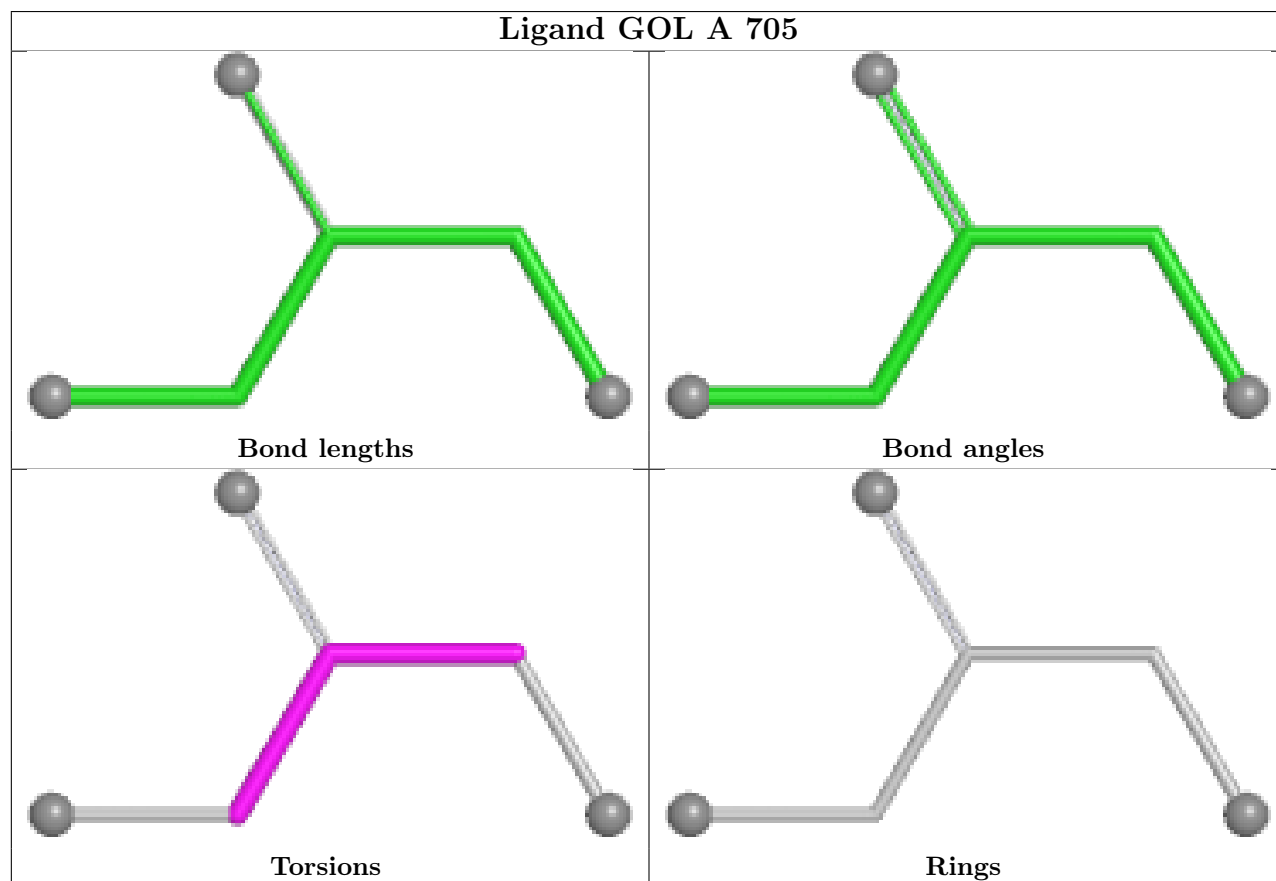
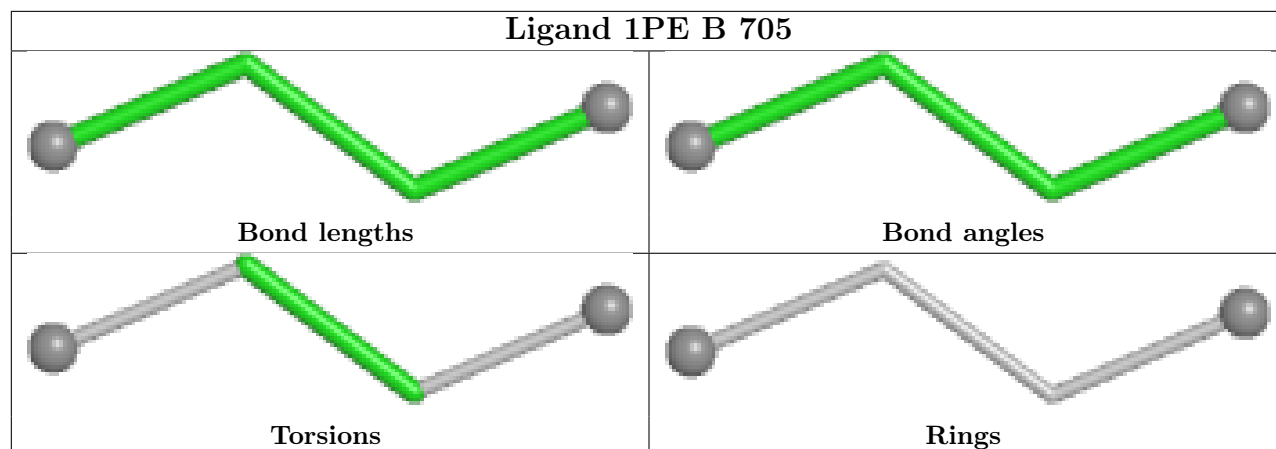
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	704	GOL	1	0
3	D	705	GOL	1	0
2	A	703	1PE	1	0
2	C	701	1PE	1	0
2	E	701	1PE	4	0
2	B	701	1PE	2	0
3	C	702	GOL	5	0
3	E	703	GOL	5	0
2	B	702	1PE	2	0
2	D	704	1PE	1	0
3	C	705	GOL	3	0

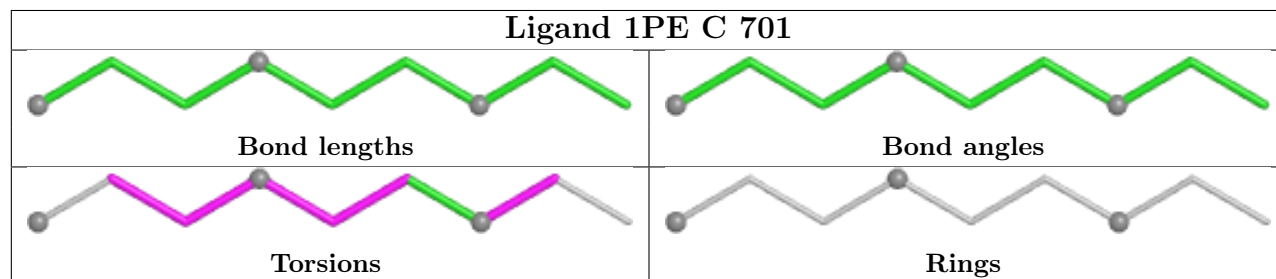
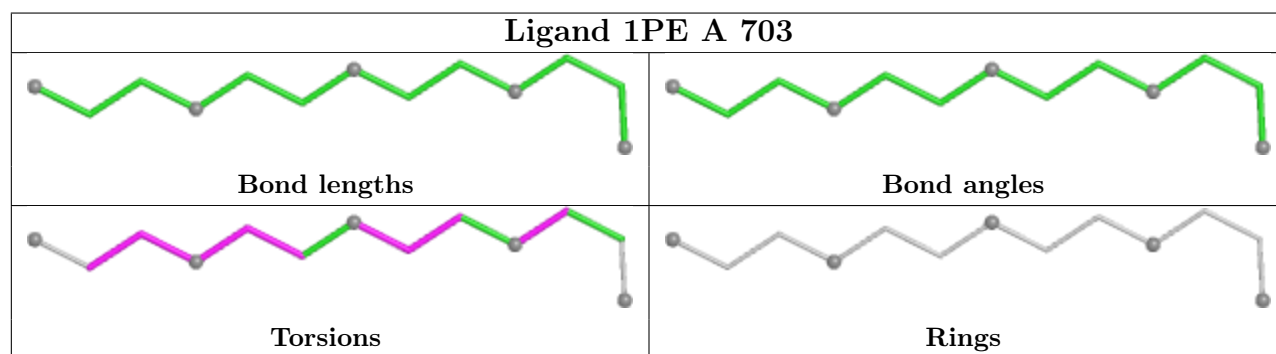
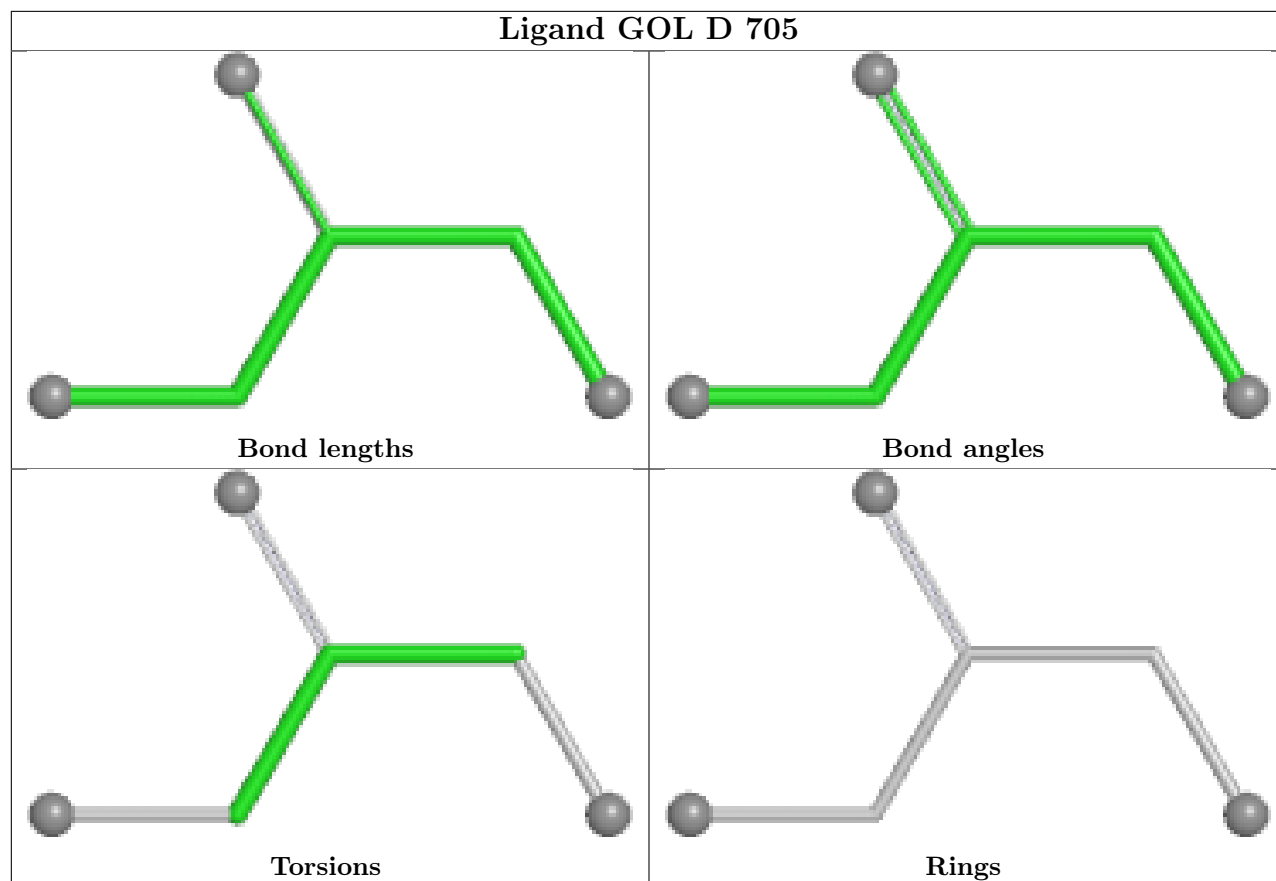
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

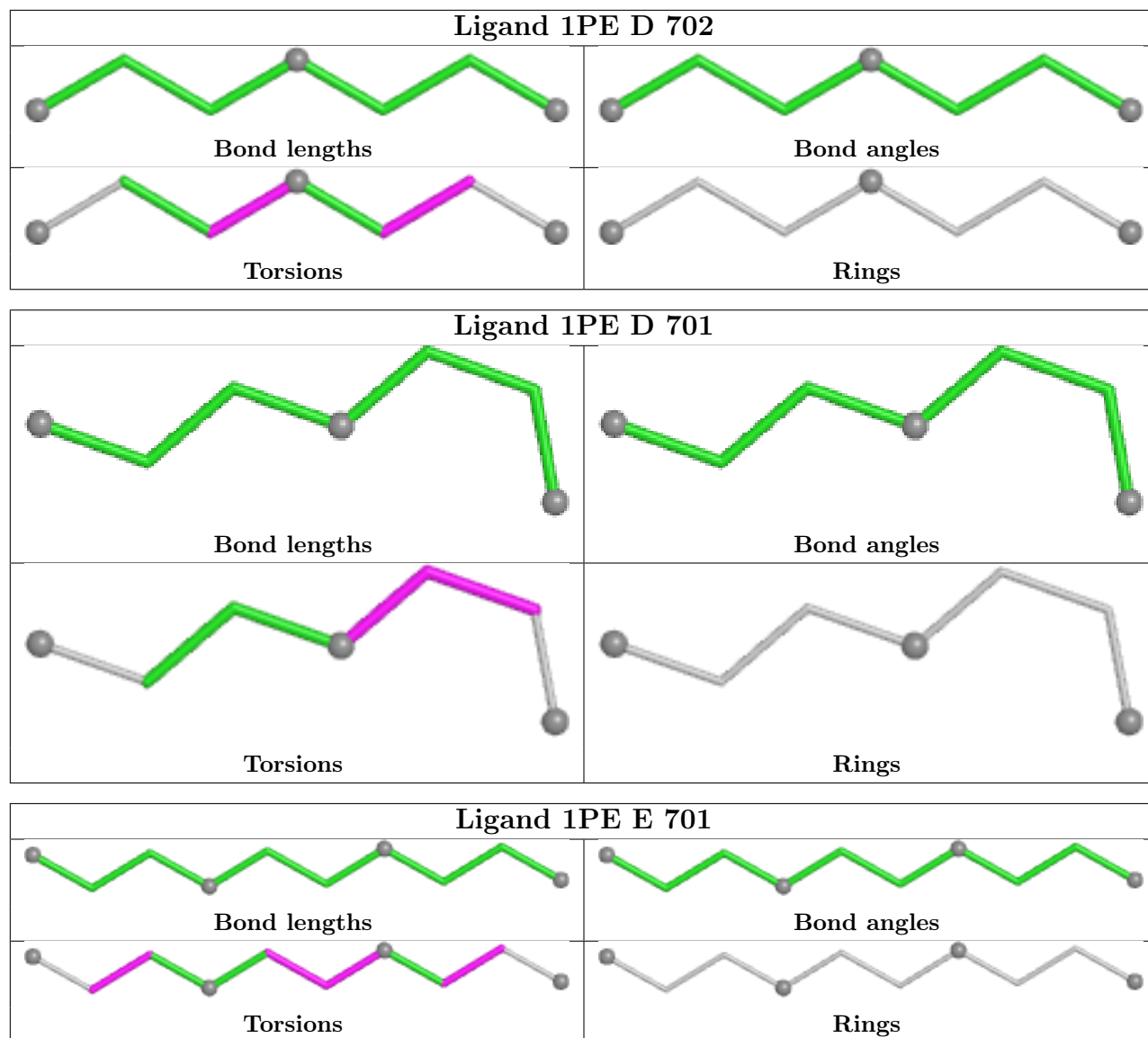
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

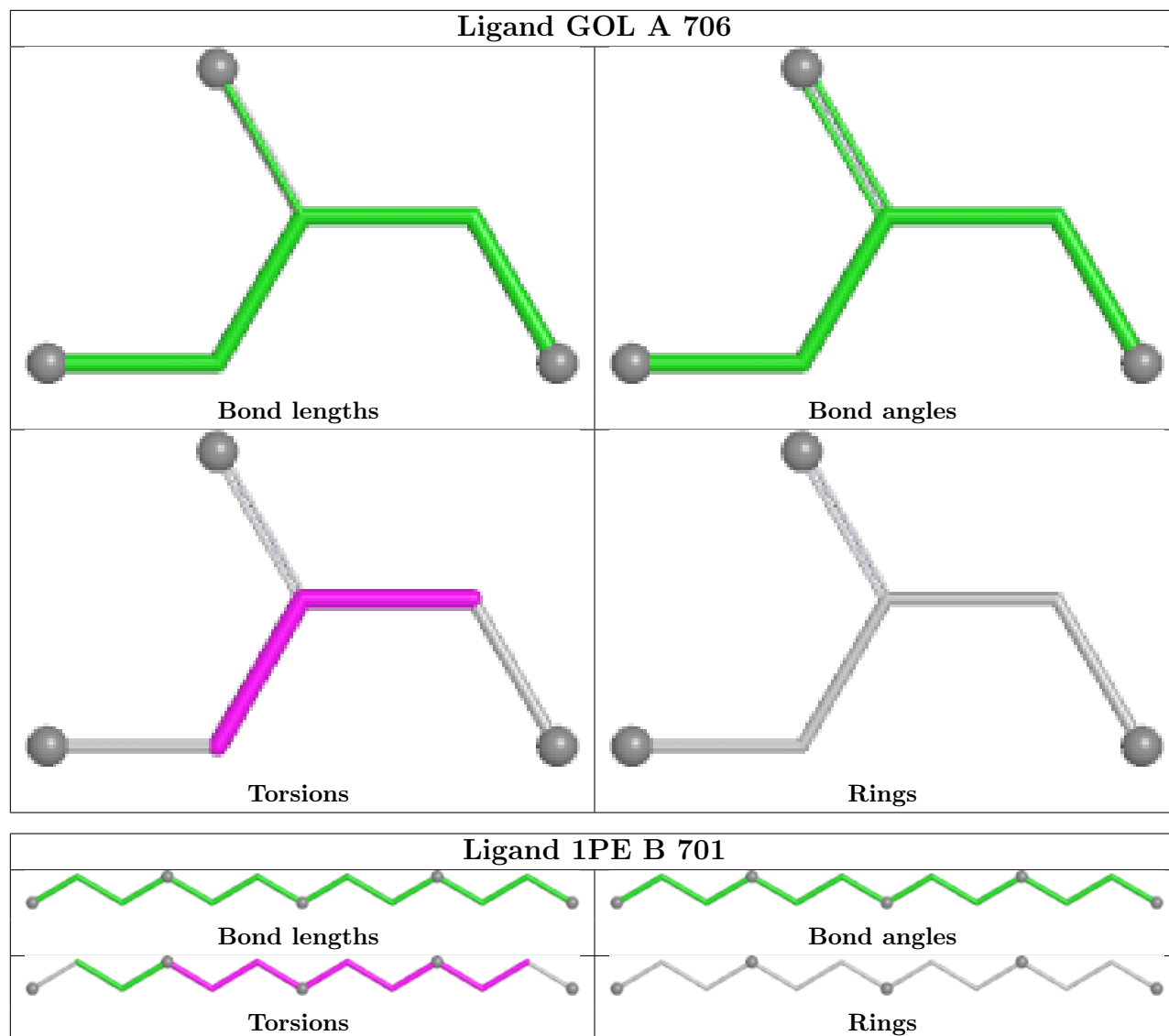


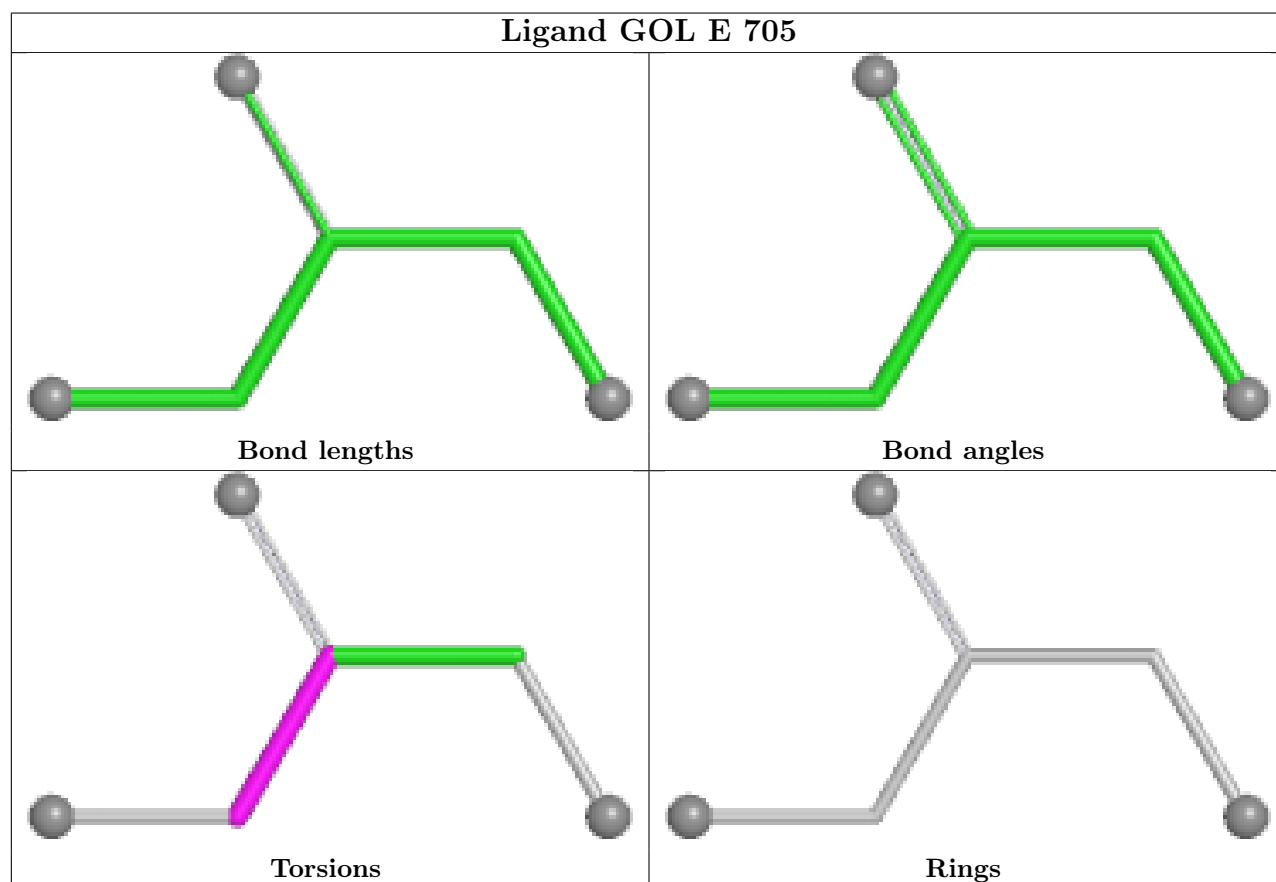
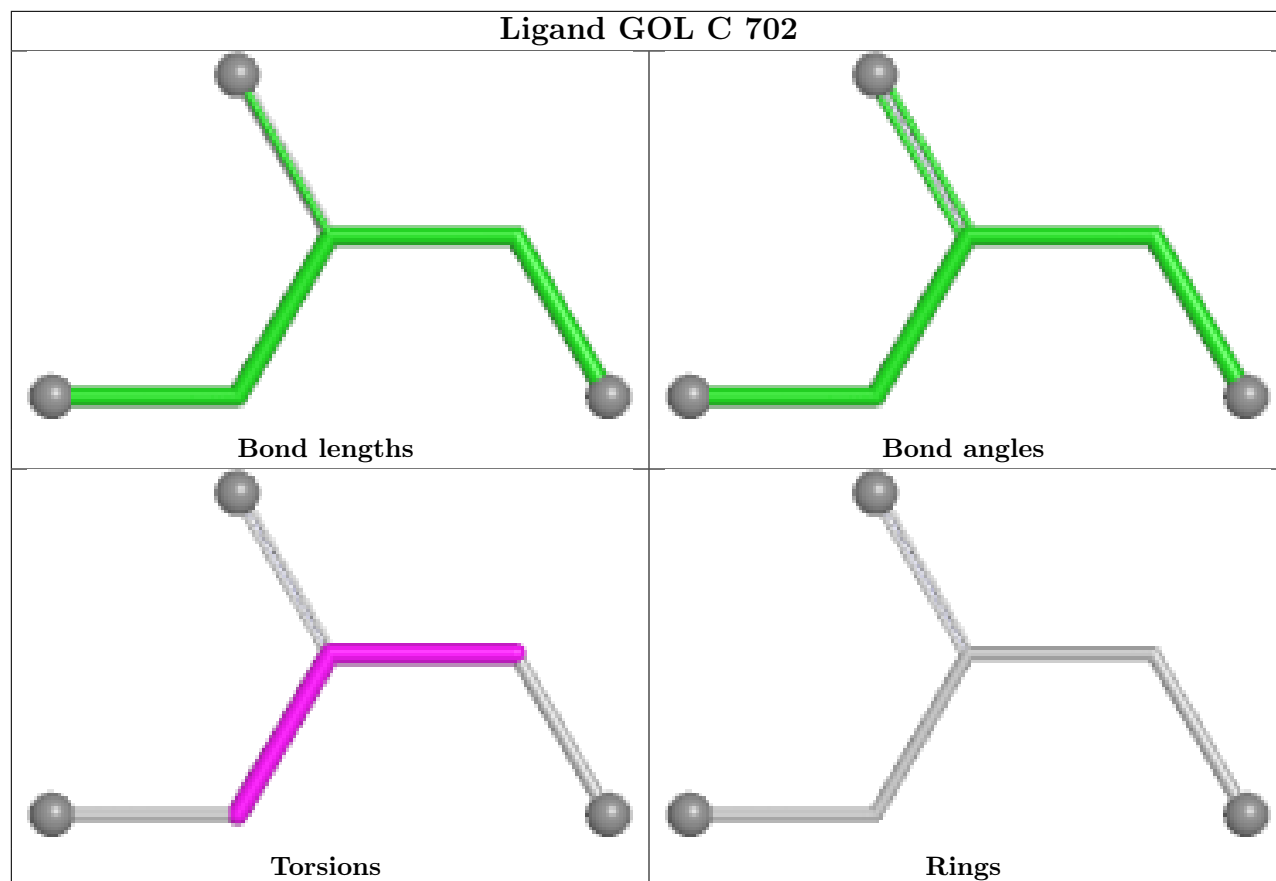


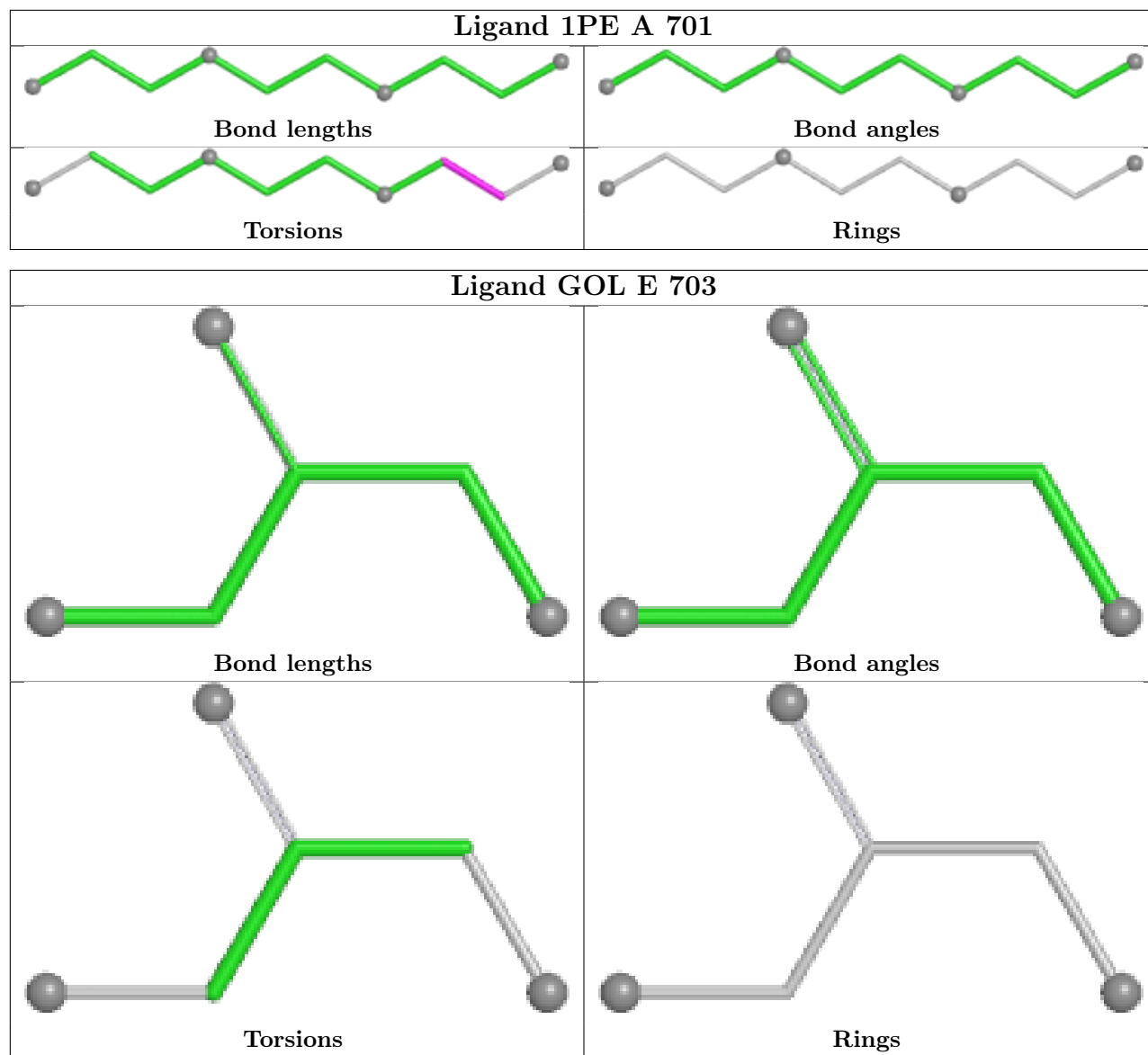


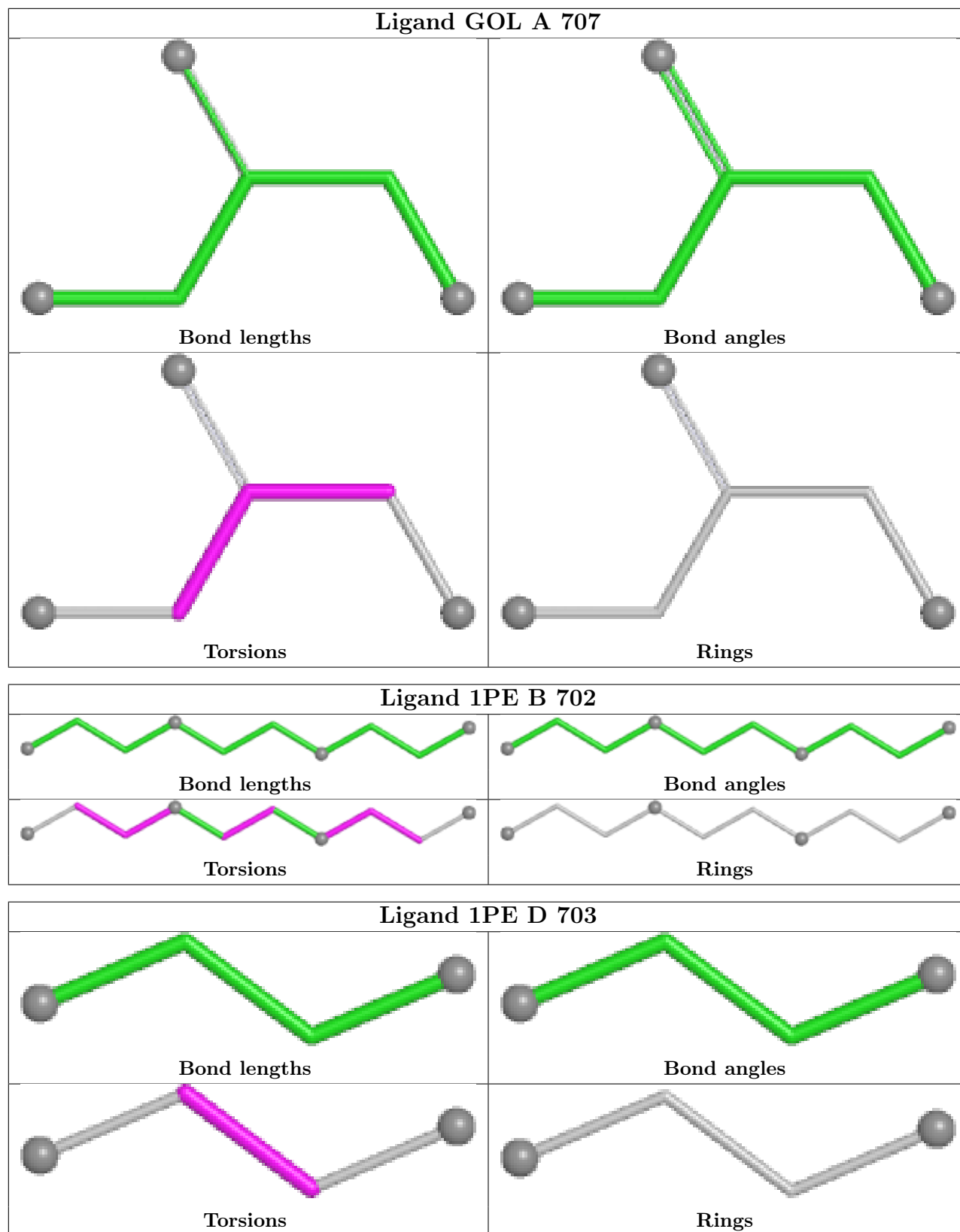


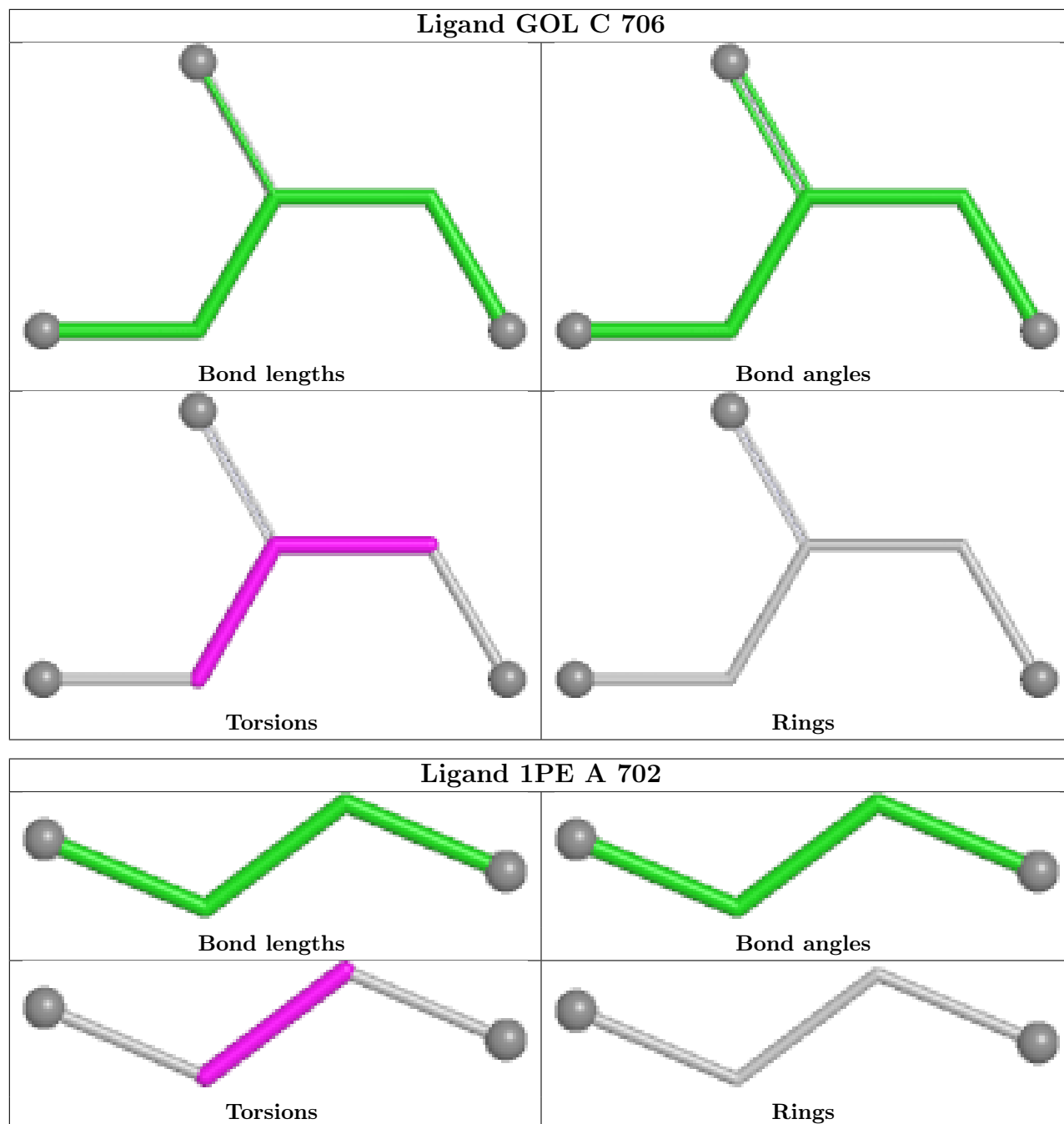


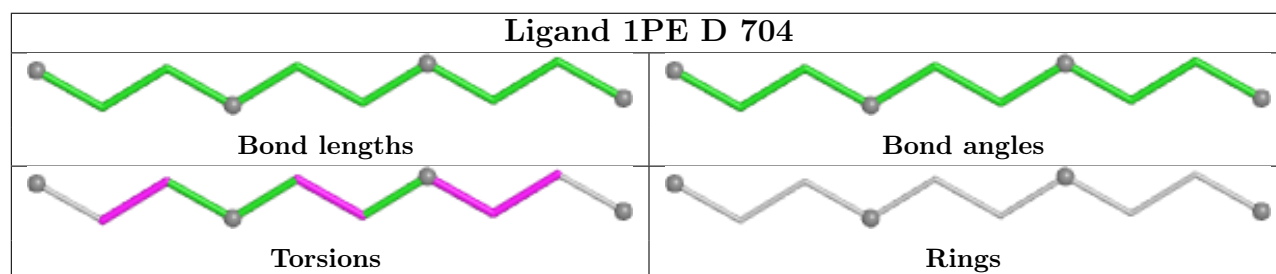
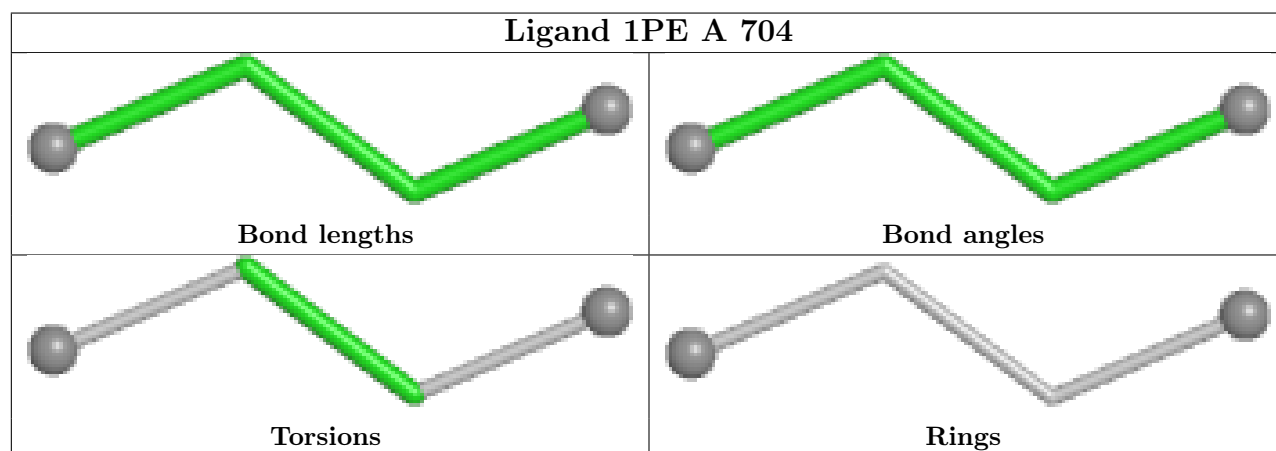
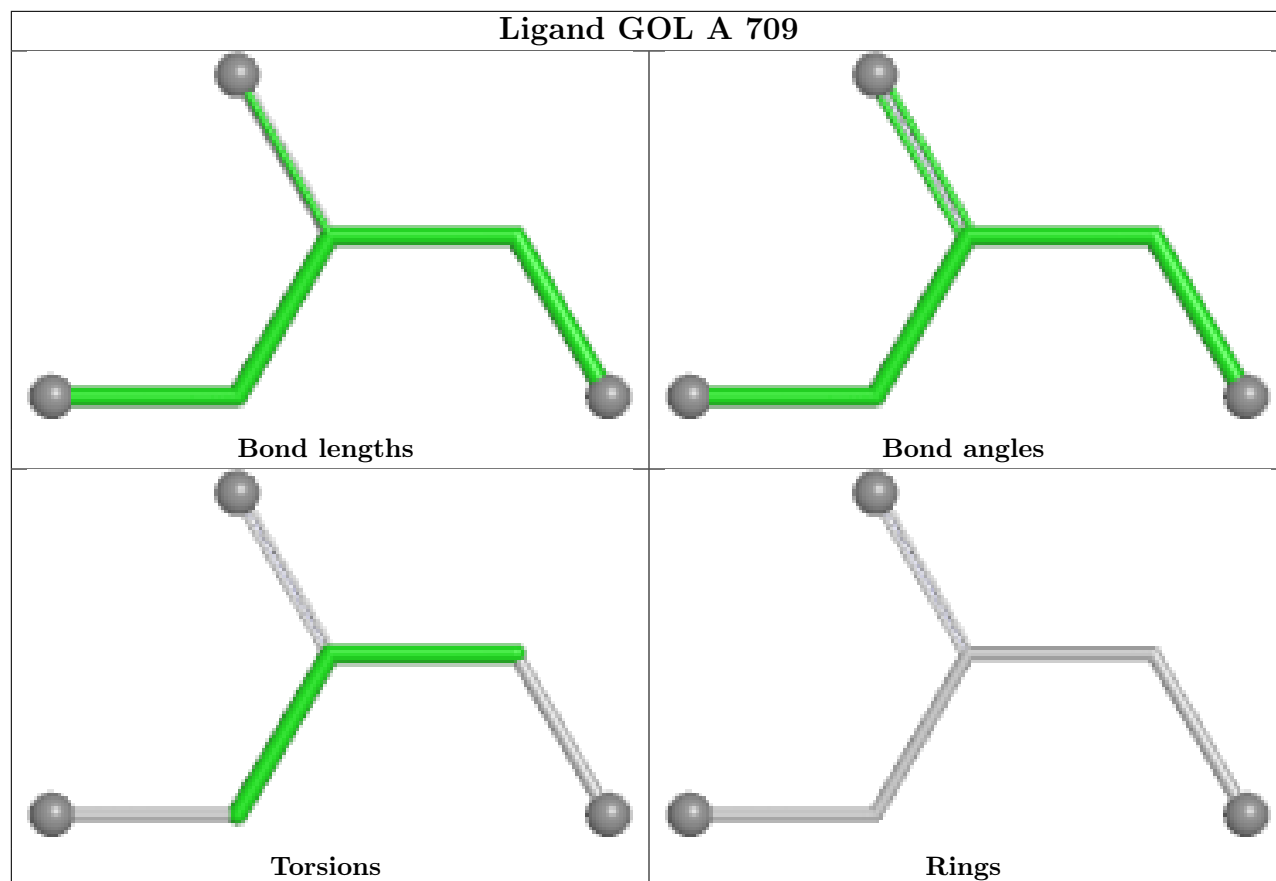


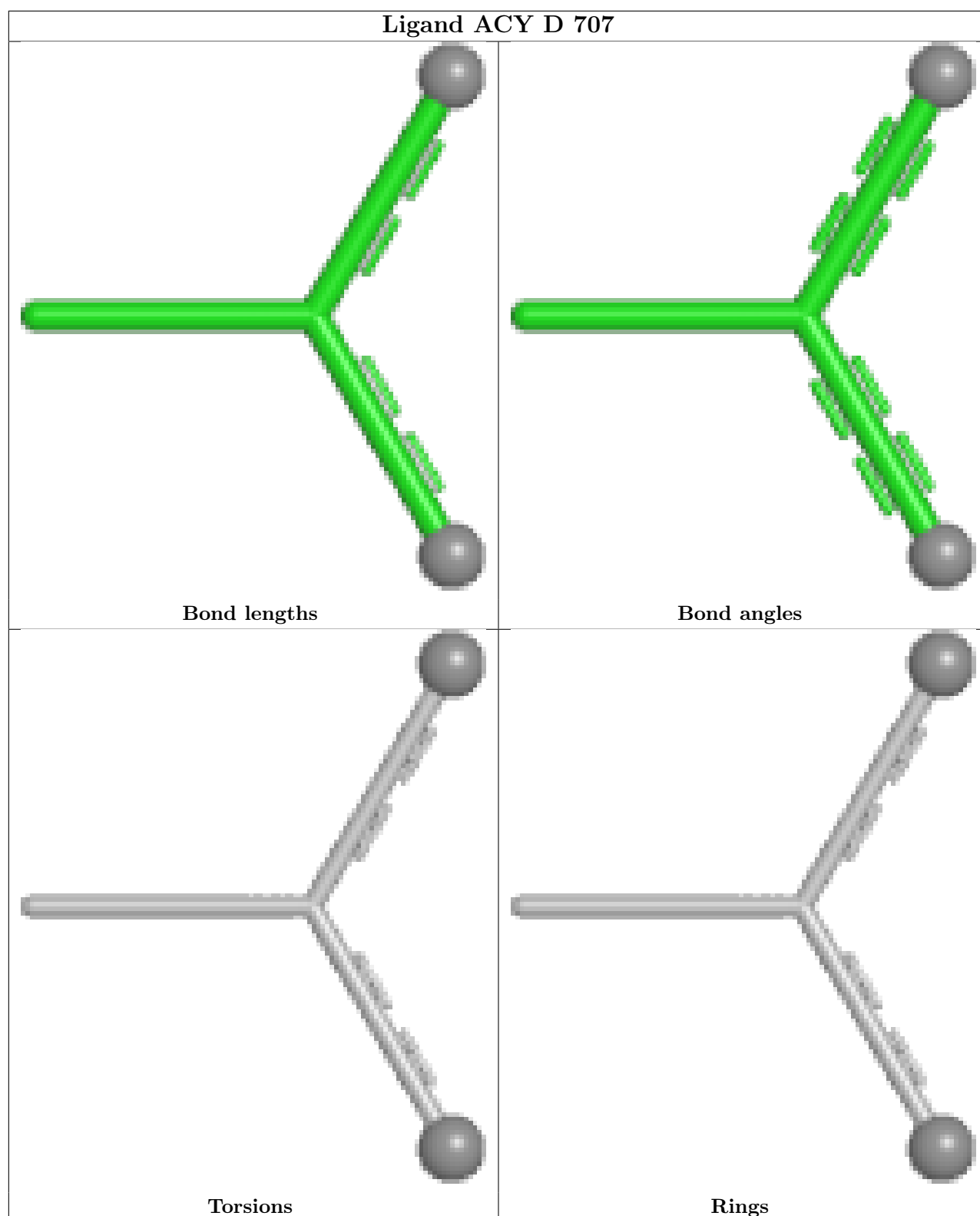


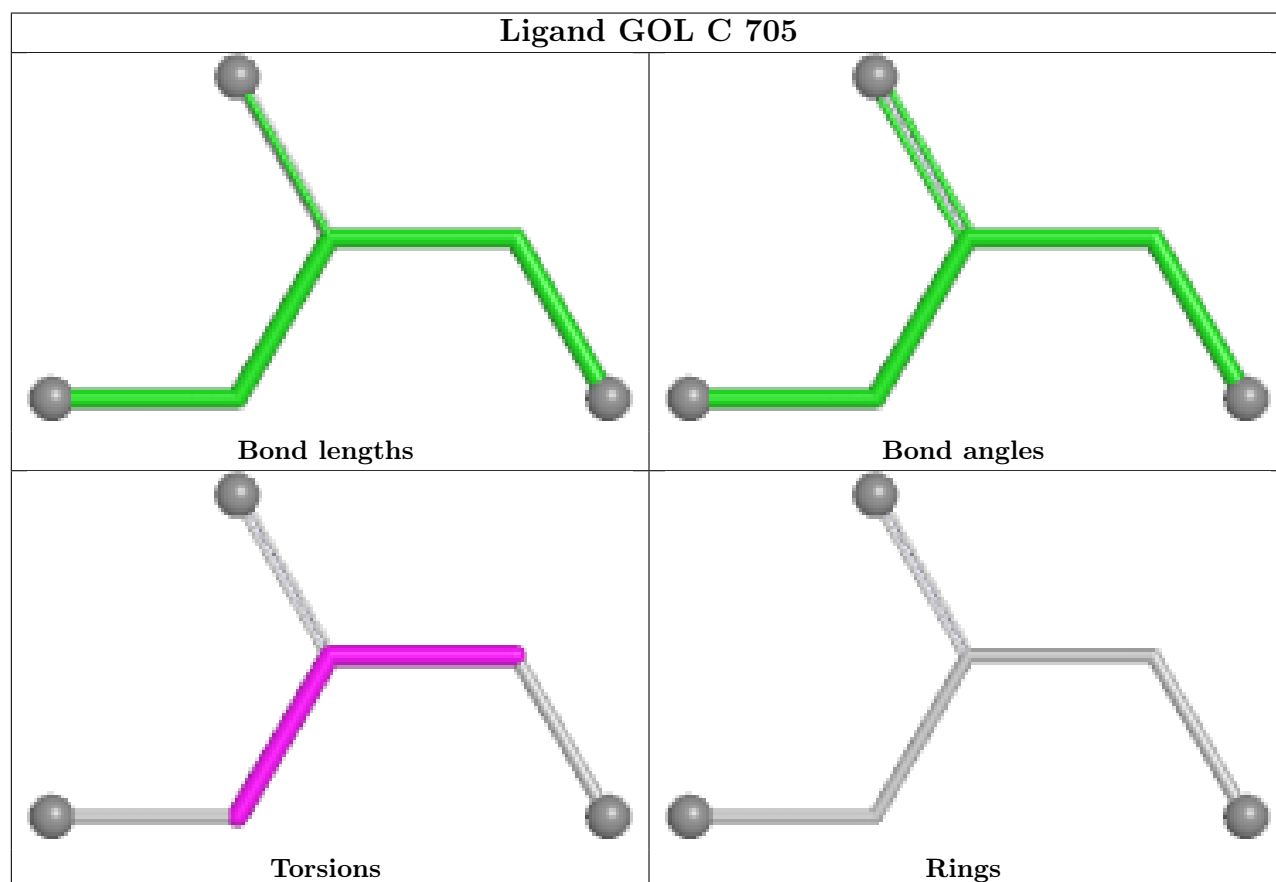
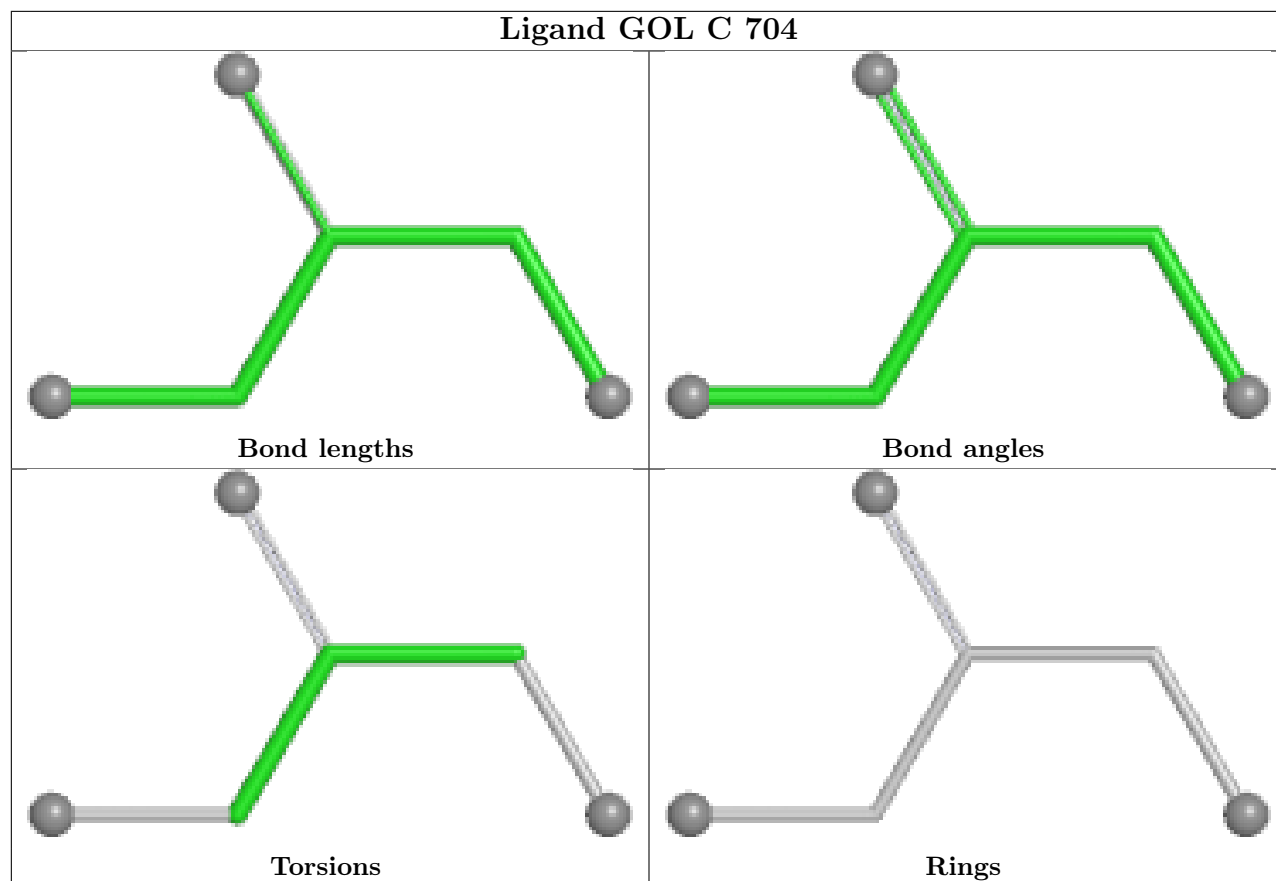


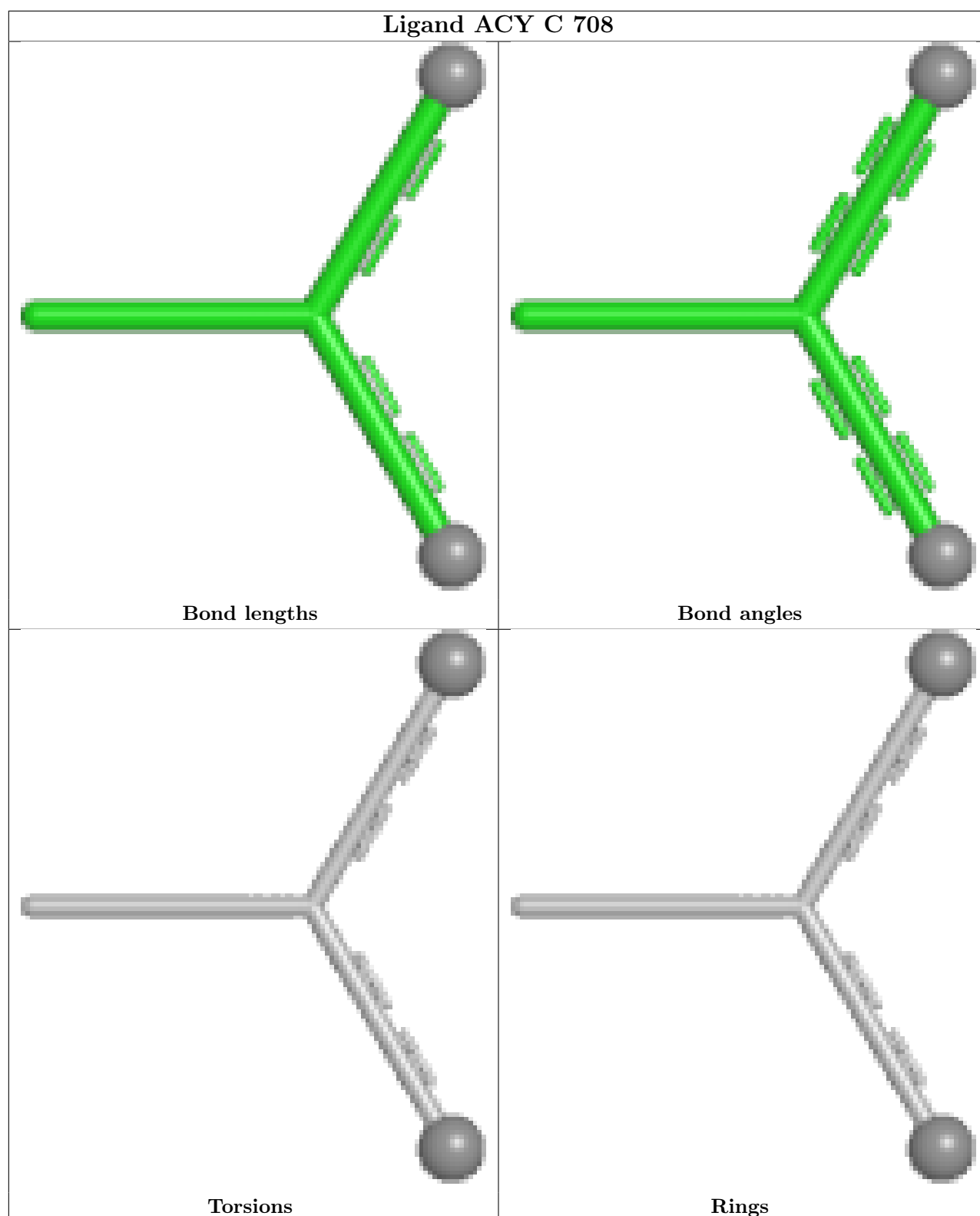


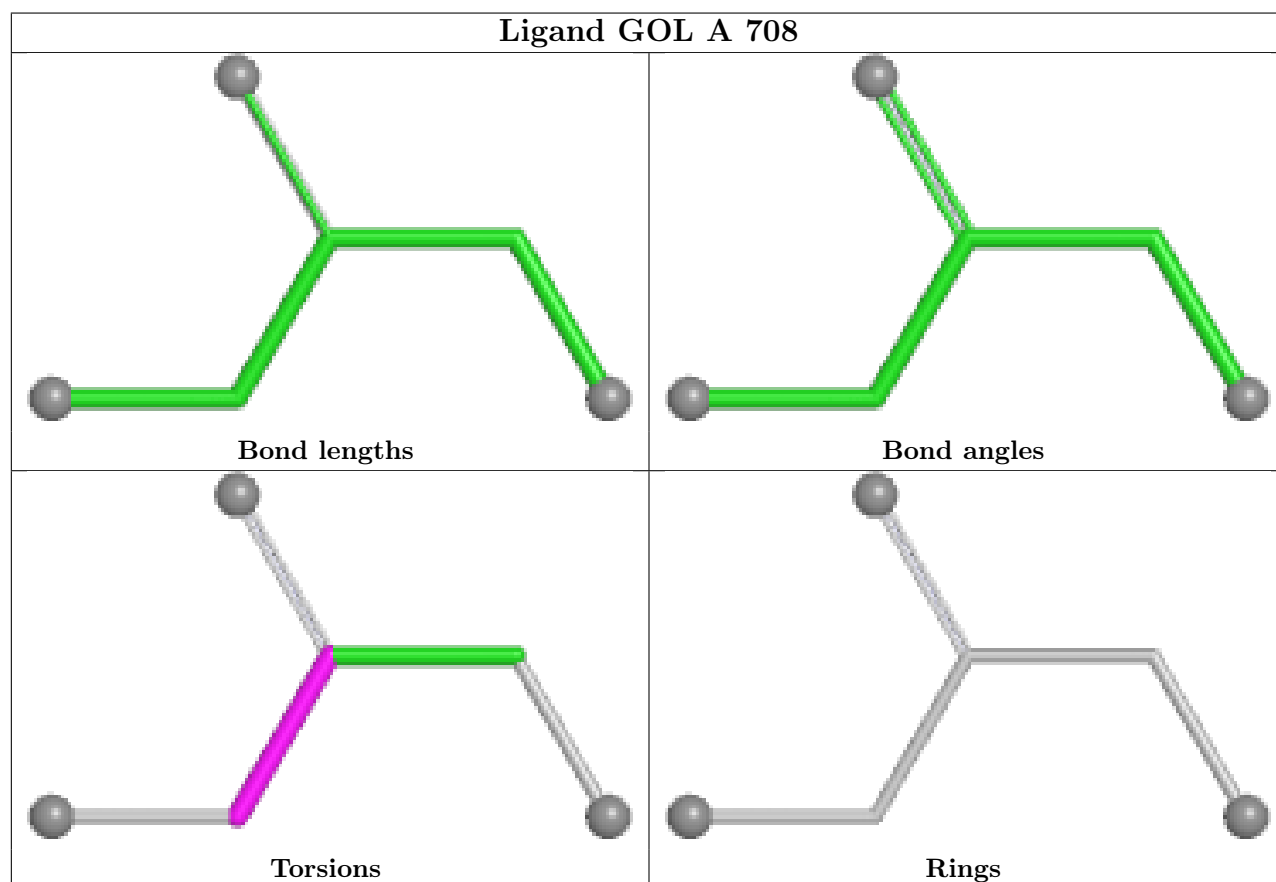
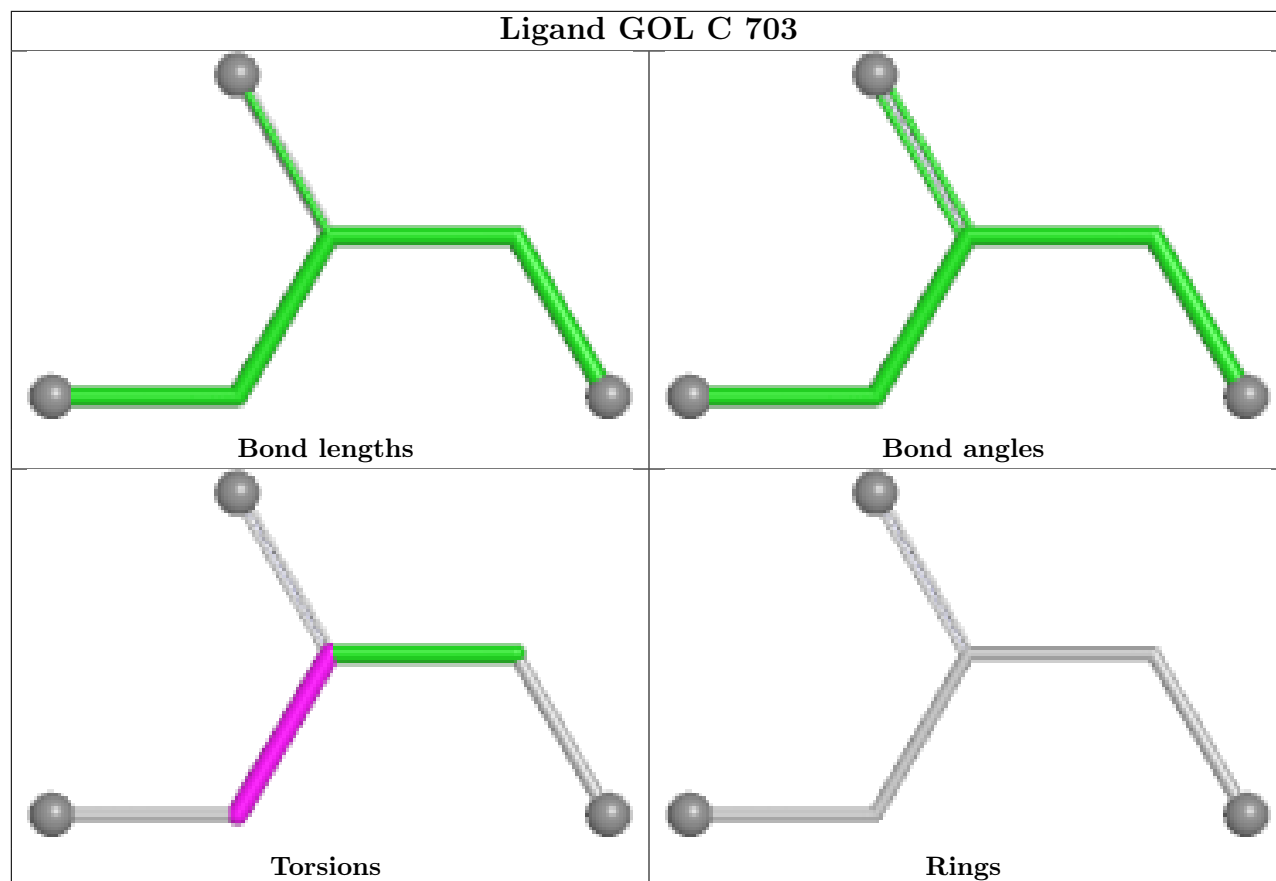












5.7 Other polymers [i](#)

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	A	122/128 (95%)	0.24	6 (4%) 35 31	28, 44, 93, 117	0
1	B	118/128 (92%)	0.26	11 (9%) 14 11	30, 46, 104, 134	0
1	C	122/128 (95%)	0.40	8 (6%) 24 20	34, 53, 97, 117	0
1	D	118/128 (92%)	0.35	7 (5%) 28 24	34, 54, 109, 132	0
1	E	121/128 (94%)	0.80	18 (14%) 5 4	38, 59, 105, 125	0
All	All	601/640 (93%)	0.41	50 (8%) 17 14	28, 52, 103, 134	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	583	PHE	5.8
1	B	583	PHE	5.5
1	E	583	PHE	4.8
1	B	582	PRO	4.4
1	A	583	PHE	4.3
1	B	584	LYS	4.2
1	E	524	GLY	4.1
1	C	566	CYS	4.1
1	E	582	PRO	3.9
1	D	572	LYS	3.6
1	A	580	LYS	3.5
1	E	565	GLU	3.4
1	D	579	SER	3.2
1	E	581	LEU	3.2
1	E	537	GLN	3.1
1	D	584	LYS	3.1
1	E	540	GLY	3.1
1	D	588	HIS	3.0
1	E	526	GLN	3.0
1	E	521	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	568	PRO	2.8
1	E	584	LYS	2.8
1	E	522	GLU	2.7
1	D	540	GLY	2.7
1	E	561	ARG	2.7
1	C	540	GLY	2.7
1	C	626	GLU	2.7
1	A	566	CYS	2.6
1	A	524	GLY	2.6
1	C	521	GLU	2.5
1	E	625	LEU	2.5
1	B	577	SER	2.5
1	E	566	CYS	2.5
1	C	524	GLY	2.5
1	B	525	GLU	2.5
1	E	520	THR	2.5
1	C	593	LYS	2.4
1	E	571	LYS	2.4
1	E	568	PRO	2.4
1	B	574	GLN	2.3
1	B	566	CYS	2.3
1	B	625	LEU	2.3
1	B	565	GLU	2.3
1	A	522	GLU	2.2
1	D	571	LYS	2.2
1	A	613	GLN	2.1
1	C	505	MET	2.1
1	E	573	VAL	2.1
1	B	572	LYS	2.0
1	B	522	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 ⓘ

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
2	1PE	E	702	4/16	0.61	0.32	85,95,97,104	0
2	1PE	D	703	4/16	0.71	0.29	75,76,79,85	0
2	1PE	B	705	4/16	0.74	0.32	63,76,83,91	0
2	1PE	B	704	4/16	0.76	0.23	68,73,85,87	0
5	ACY	C	708	4/4	0.76	0.23	68,76,76,90	0
3	GOL	E	704	6/6	0.77	0.20	65,82,95,97	0
4	CL	A	710	1/1	0.77	0.20	94,94,94,94	0
3	GOL	D	705	6/6	0.77	0.20	64,87,95,96	0
2	1PE	A	704	4/16	0.78	0.24	69,74,79,82	0
2	1PE	D	702	7/16	0.79	0.20	81,92,97,105	0
3	GOL	A	707	6/6	0.79	0.23	74,80,93,97	0
5	ACY	D	707	4/4	0.79	0.26	75,90,91,97	0
3	GOL	E	703	6/6	0.80	0.15	82,92,95,95	0
2	1PE	A	703	13/16	0.81	0.24	68,93,101,110	0
3	GOL	A	706	6/6	0.81	0.27	71,92,96,100	0
3	GOL	E	705	6/6	0.81	0.19	90,98,103,105	0
3	GOL	C	702	6/6	0.82	0.13	71,81,84,85	0
2	1PE	D	704	10/16	0.83	0.23	73,84,92,97	0
3	GOL	C	705	6/6	0.83	0.15	82,86,94,98	0
2	1PE	B	701	13/16	0.83	0.22	49,71,86,87	0
2	1PE	B	702	10/16	0.84	0.21	53,70,84,85	0
2	1PE	A	701	10/16	0.84	0.24	75,113,118,119	0
2	1PE	C	701	9/16	0.85	0.21	49,76,82,84	0
2	1PE	A	702	4/16	0.85	0.17	47,69,70,71	0
3	GOL	A	705	6/6	0.88	0.19	62,64,72,76	0
2	1PE	E	701	10/16	0.88	0.17	52,79,85,86	0
2	1PE	B	703	10/16	0.88	0.19	75,84,101,108	0
2	1PE	D	701	7/16	0.89	0.17	55,65,71,74	0
4	CL	E	706	1/1	0.89	0.13	89,89,89,89	0
3	GOL	C	706	6/6	0.90	0.18	71,80,94,95	0
2	1PE	B	706	4/16	0.91	0.20	75,77,80,86	0
3	GOL	C	704	6/6	0.91	0.15	78,85,93,95	0
3	GOL	A	708	6/6	0.91	0.18	69,86,93,93	0
3	GOL	C	703	6/6	0.92	0.13	63,78,82,85	0
3	GOL	A	709	6/6	0.92	0.13	65,80,90,93	0
4	CL	B	707	1/1	0.95	0.13	100,100,100,100	0
4	CL	C	707	1/1	0.96	0.10	89,89,89,89	0

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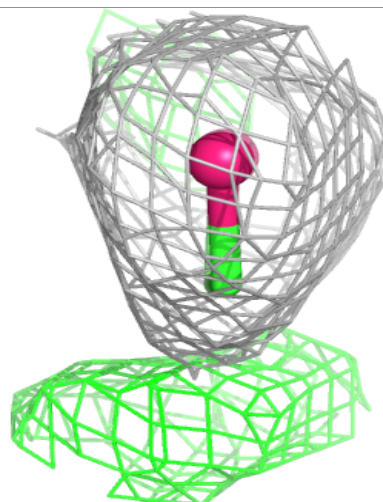
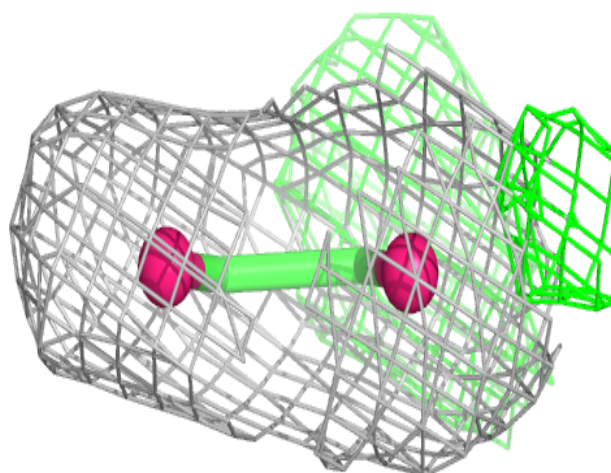
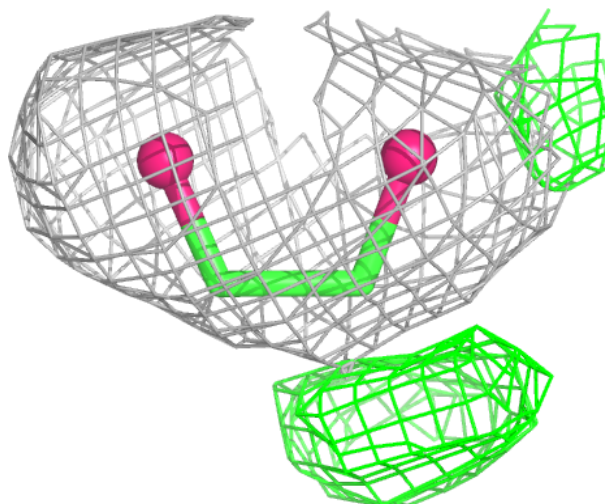
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CL	D	706	1/1	0.97	0.14	103,103,103,103	1

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.

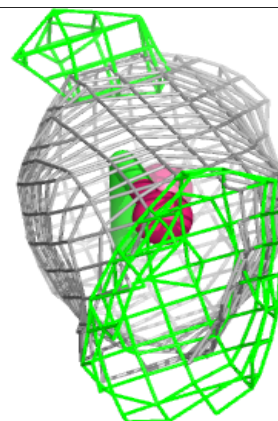
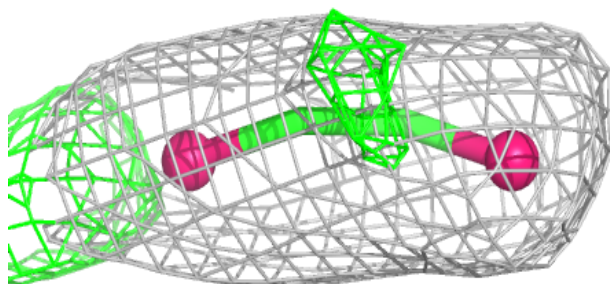
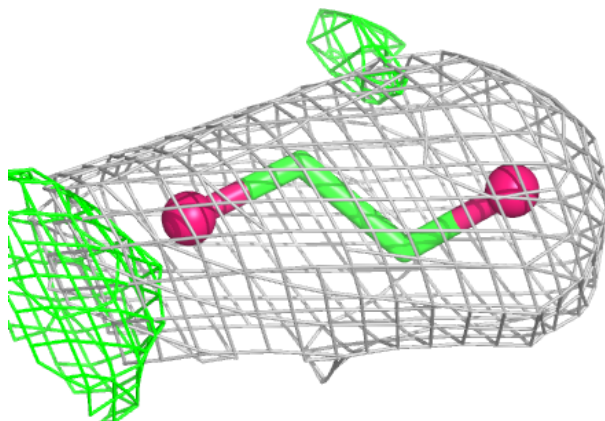
Electron density around 1PE E 702:

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



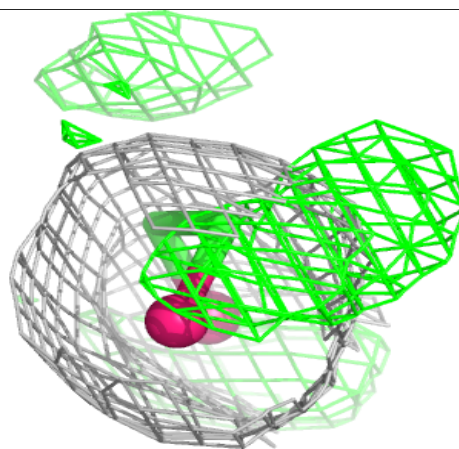
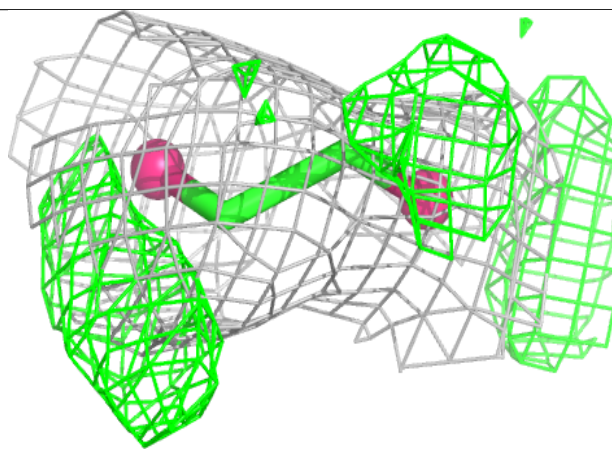
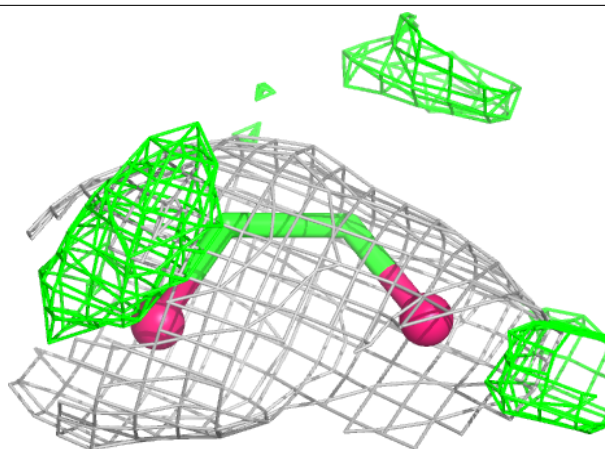
Electron density around 1PE D 703:

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



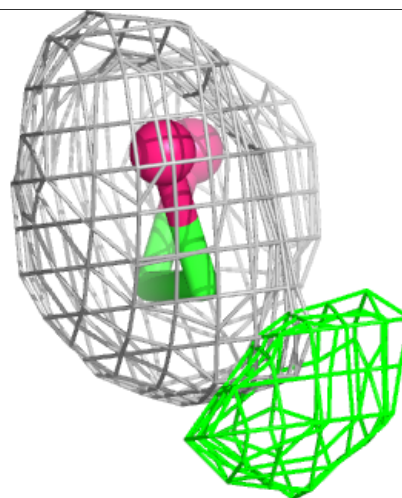
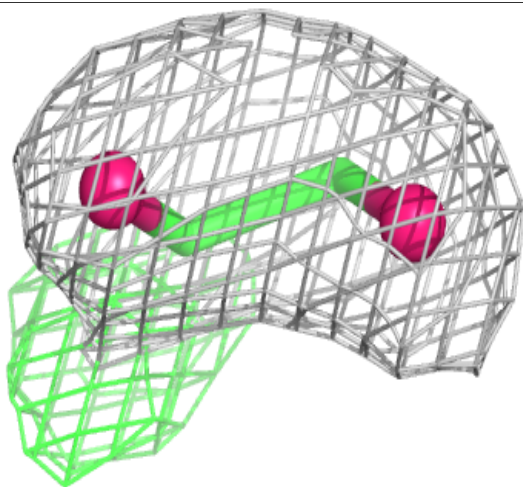
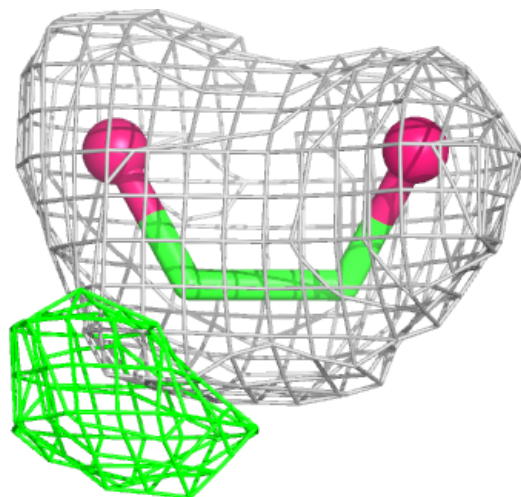
Electron density around 1PE B 705:

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and green (positive)



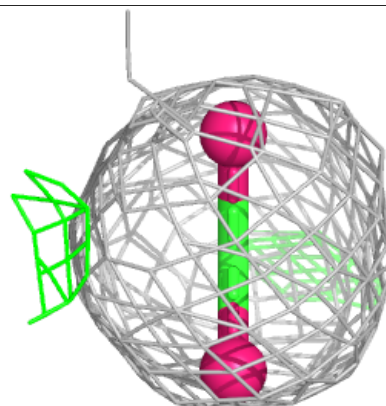
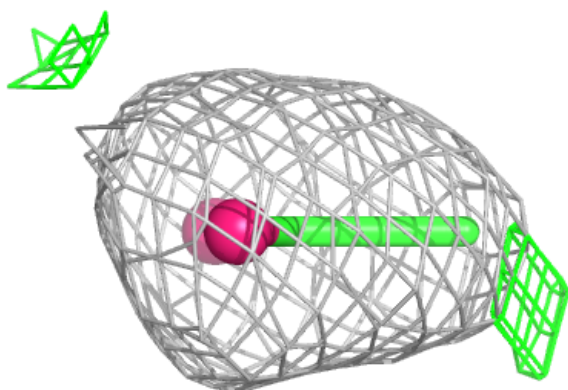
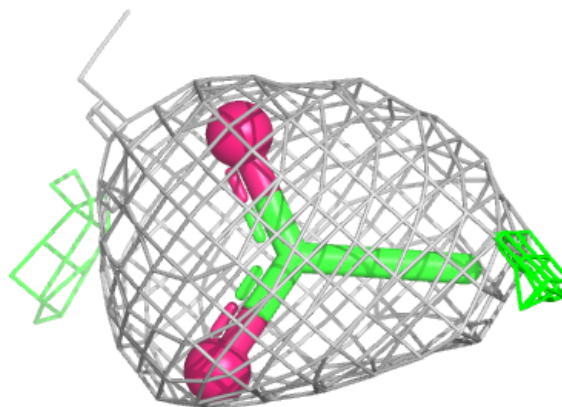
Electron density around 1PE B 704:

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



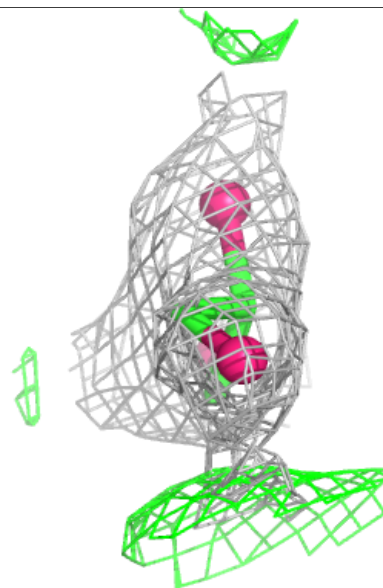
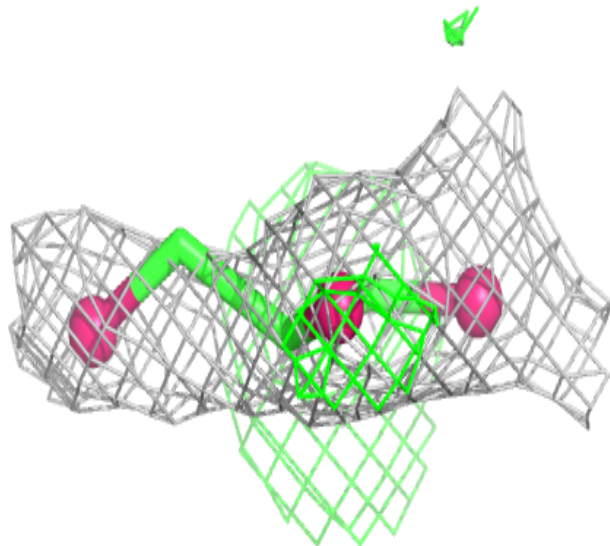
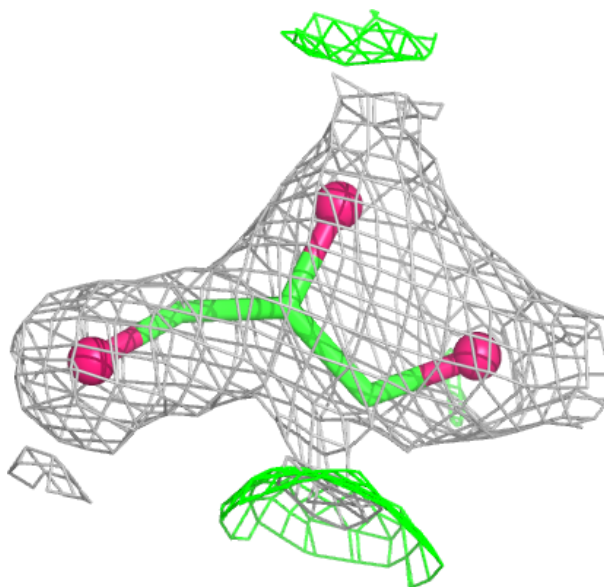
Electron density around ACY C 708:

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and green (positive)



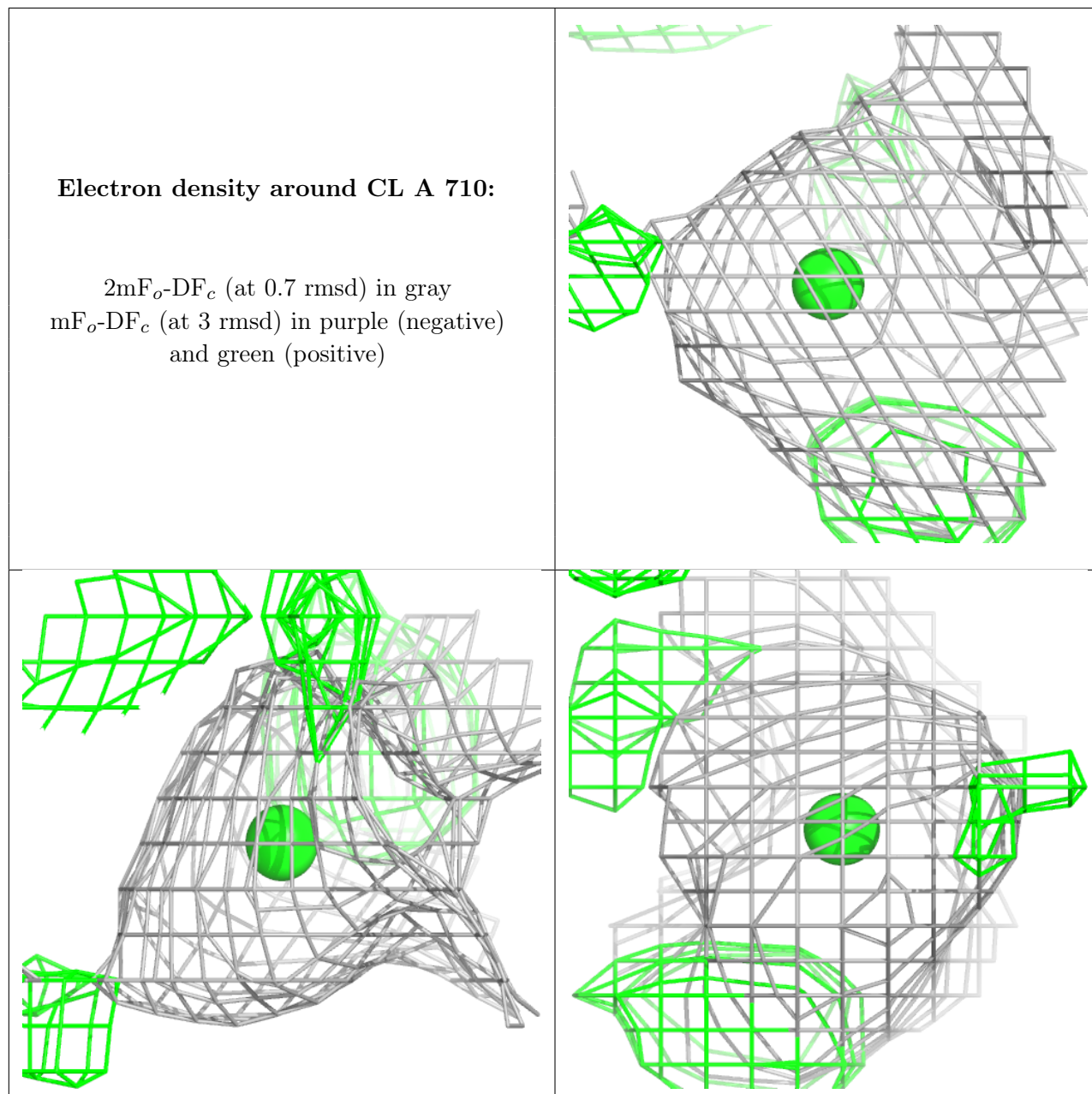
Electron density around GOL E 704:

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



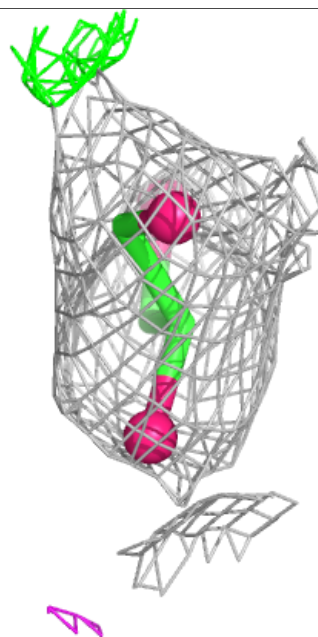
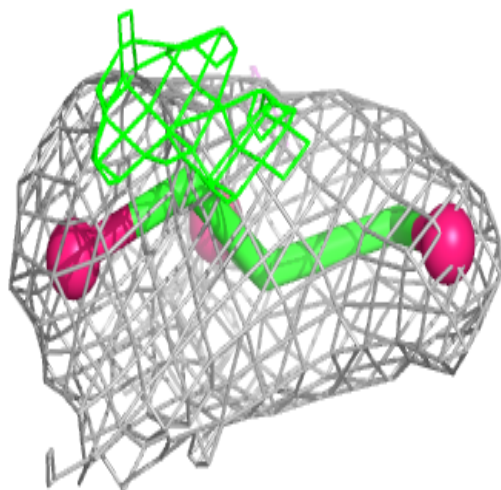
Electron density around CL A 710:

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and green (positive)



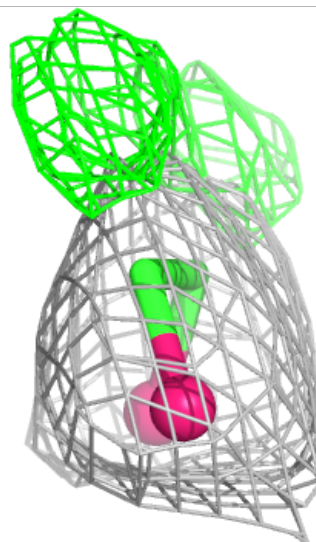
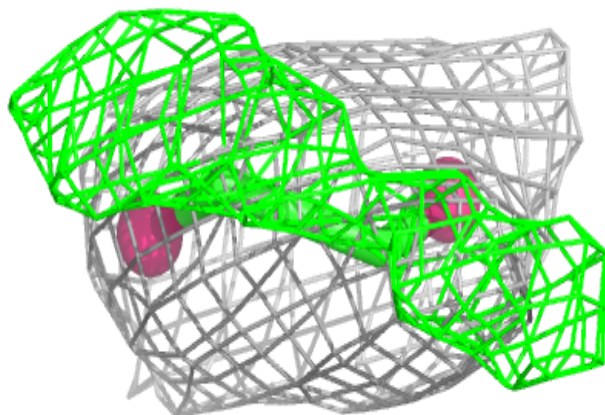
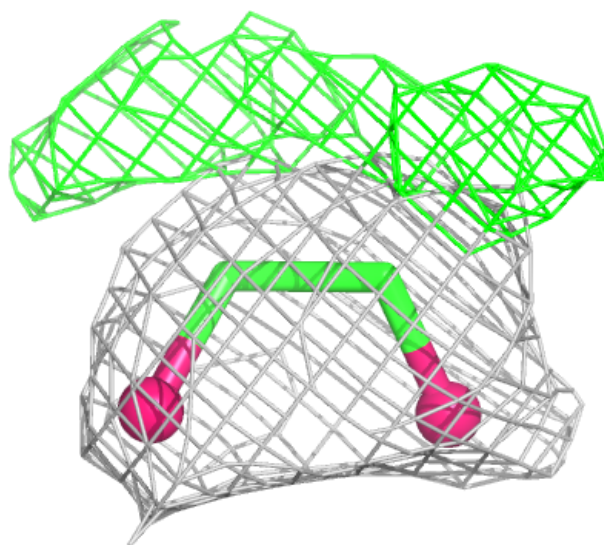
Electron density around GOL D 705:

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



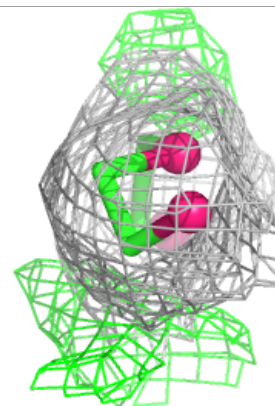
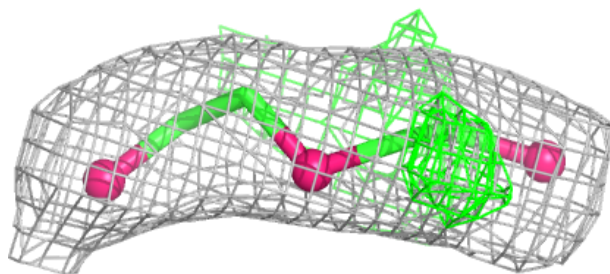
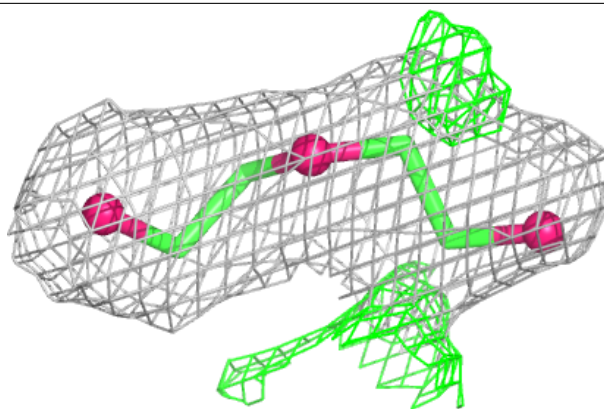
Electron density around 1PE A 704:

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and green (positive)



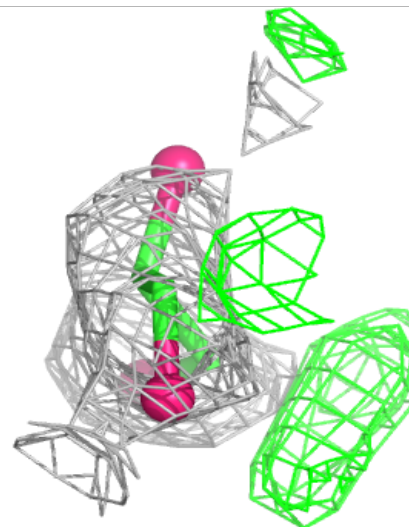
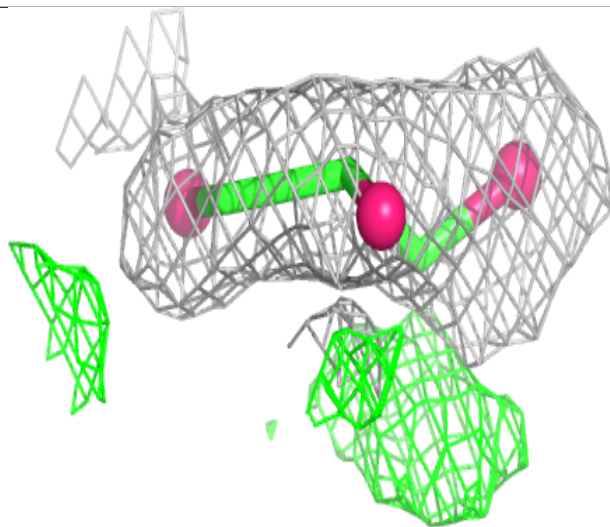
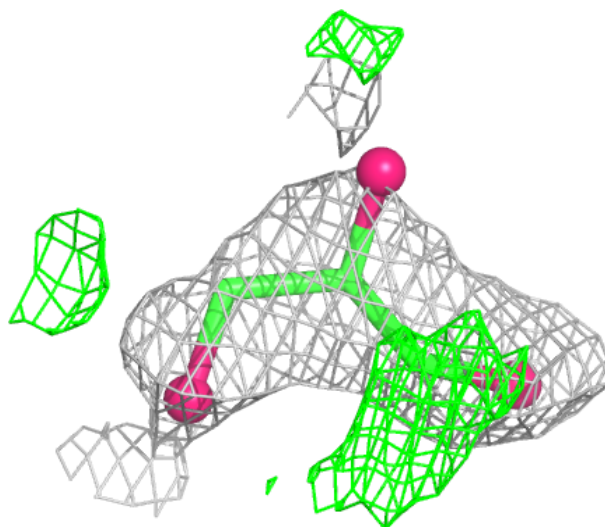
Electron density around 1PE D 702:

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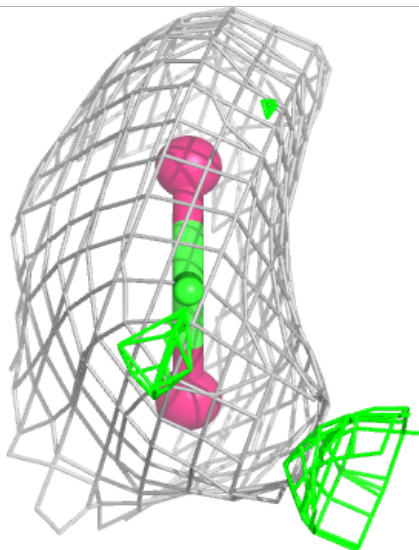
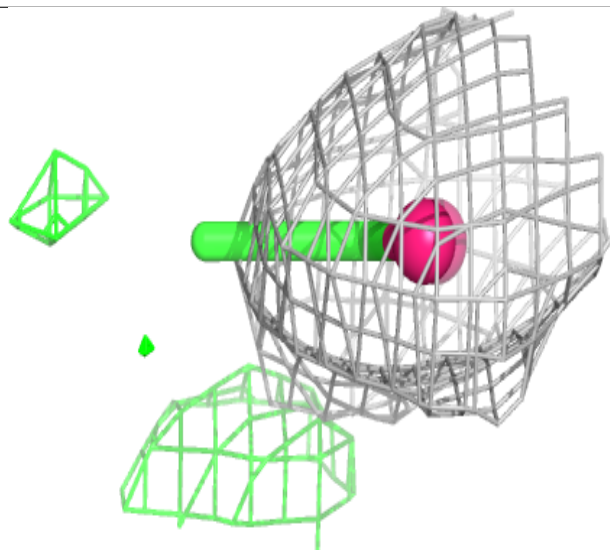
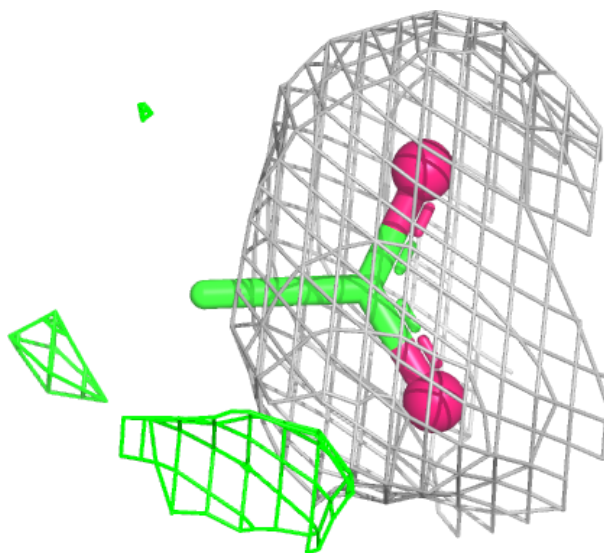
Electron density around GOL A 707:

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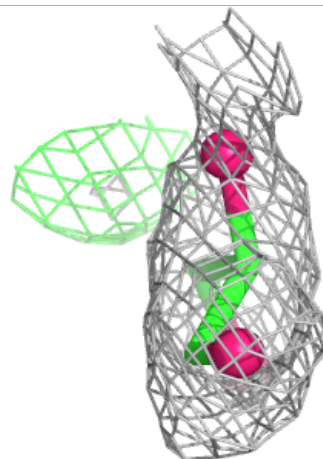
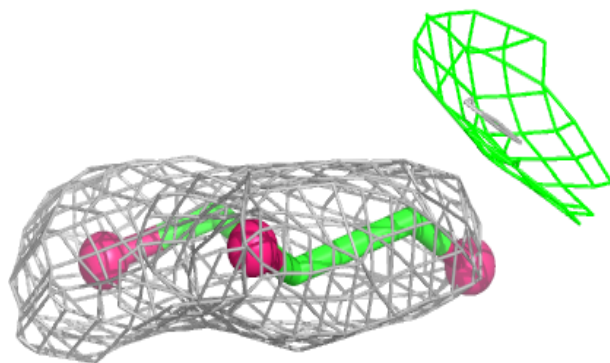
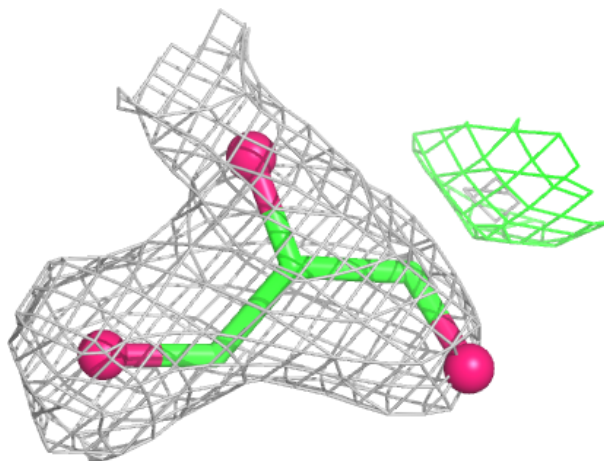
Electron density around ACY D 707:

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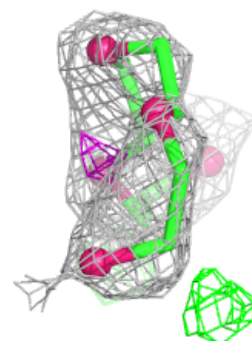
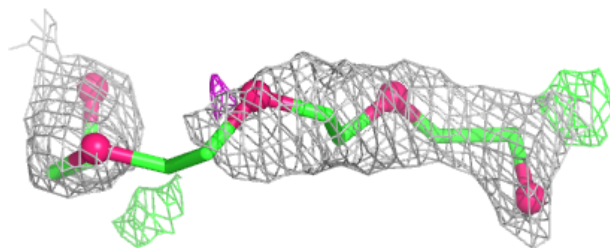
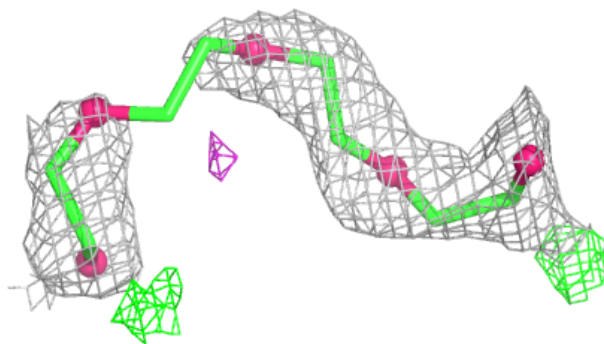
Electron density around GOL E 703:

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and green (positive)



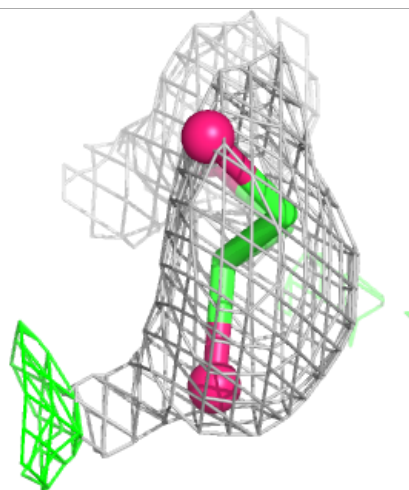
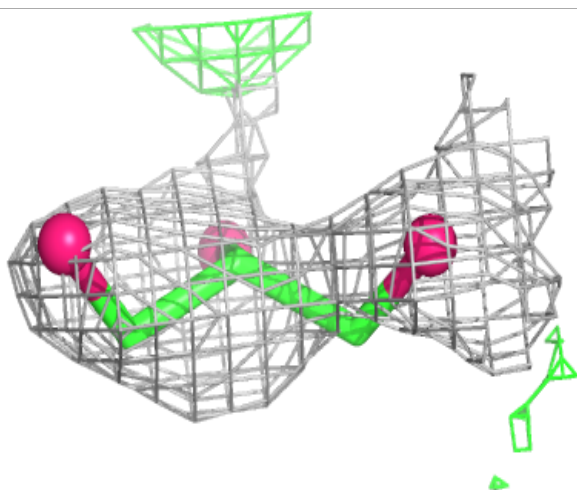
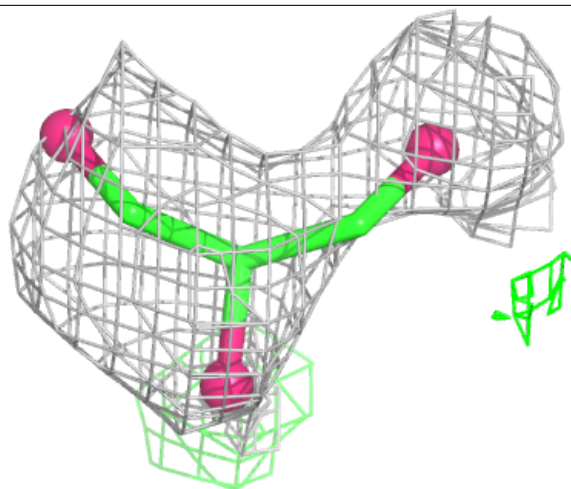
Electron density around 1PE A 703:

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and green (positive)



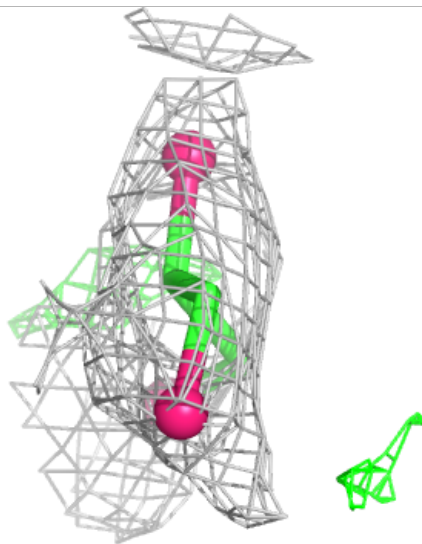
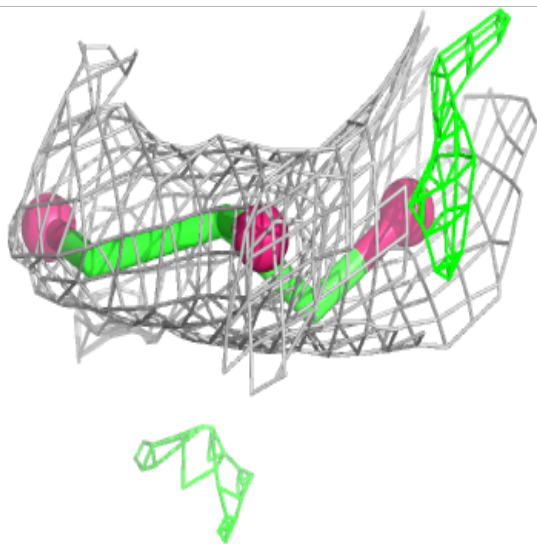
Electron density around GOL A 706:

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



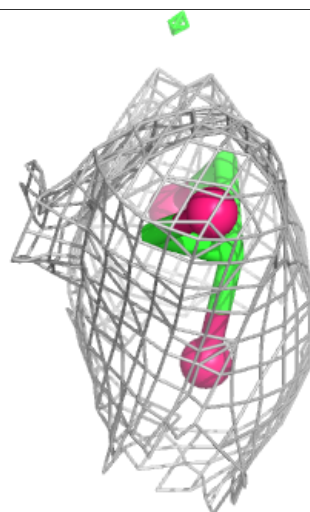
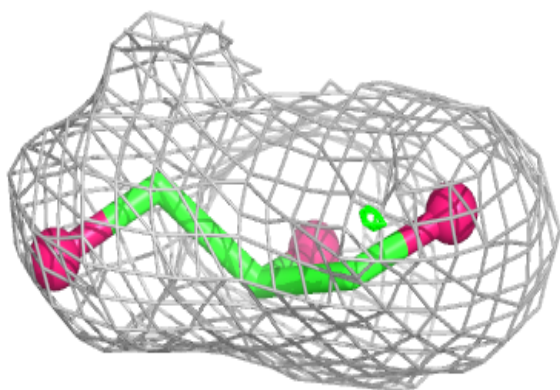
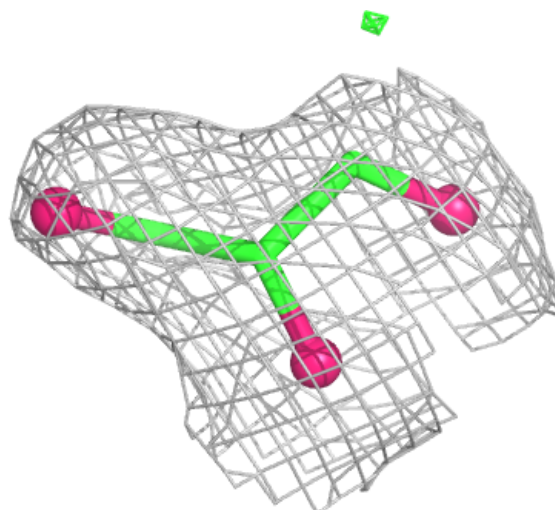
Electron density around GOL E 705:

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



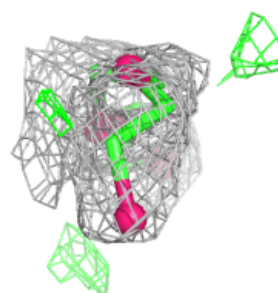
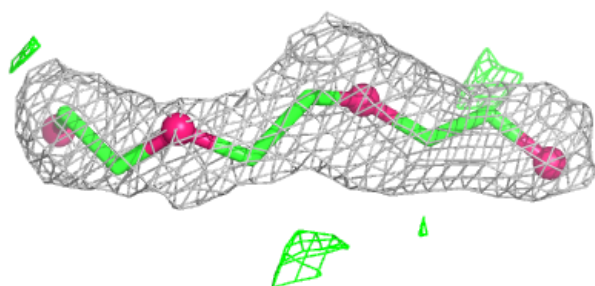
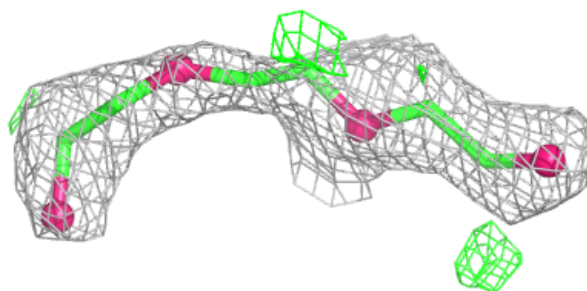
Electron density around GOL C 702:

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

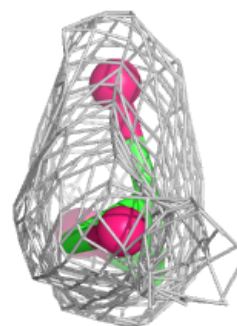
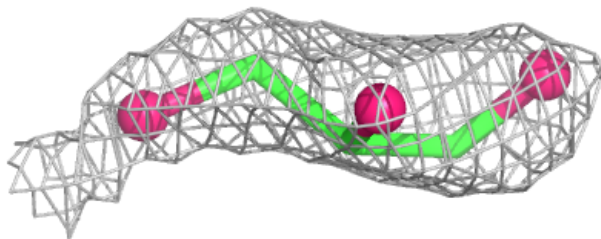
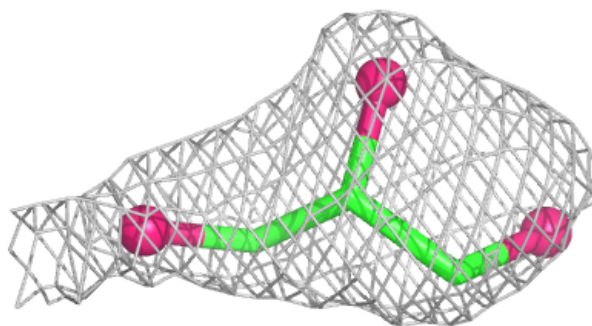


Electron density around 1PE D 704:

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

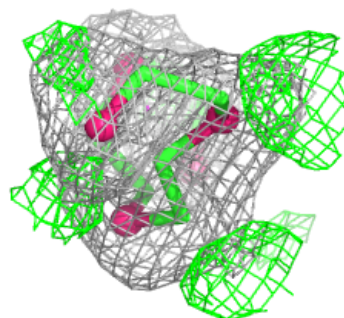
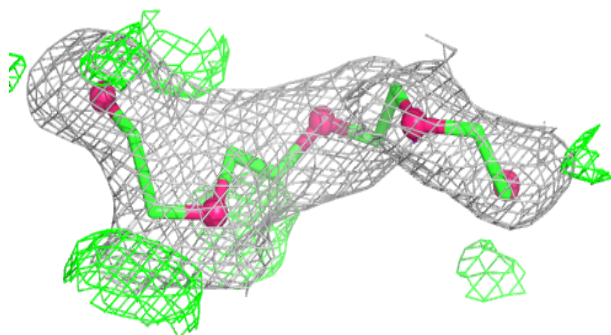
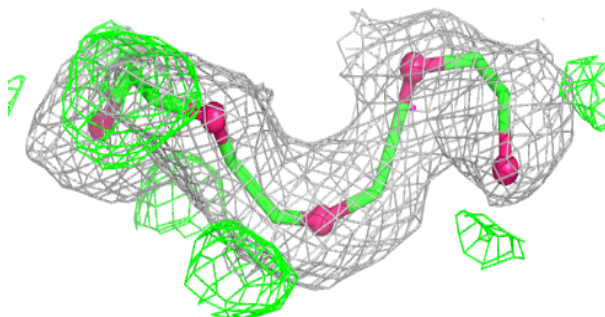
**Electron density around GOL C 705:**

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

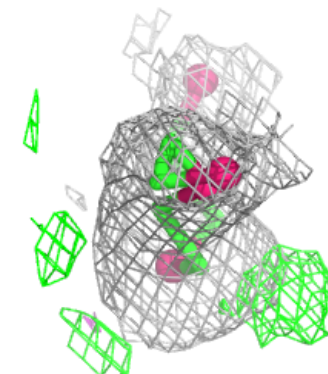
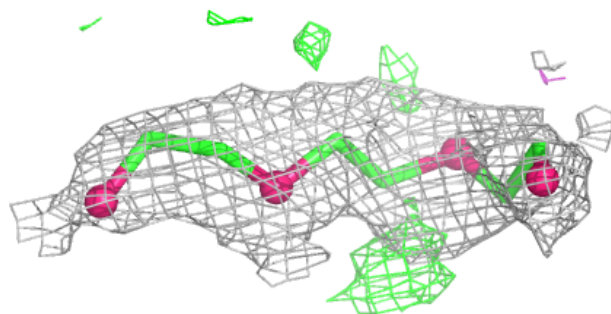
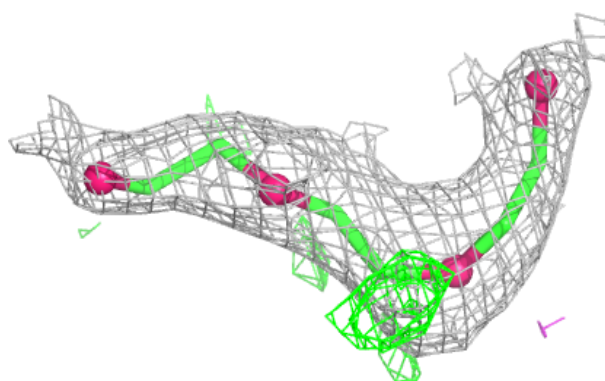


Electron density around 1PE B 701:

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

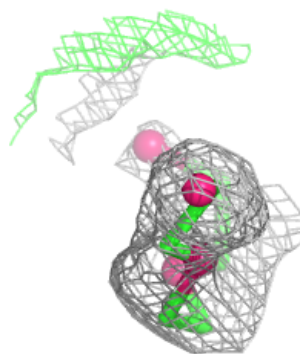
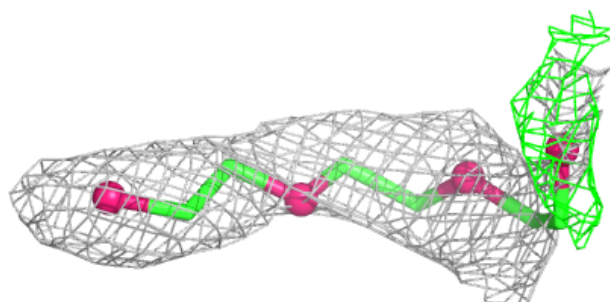
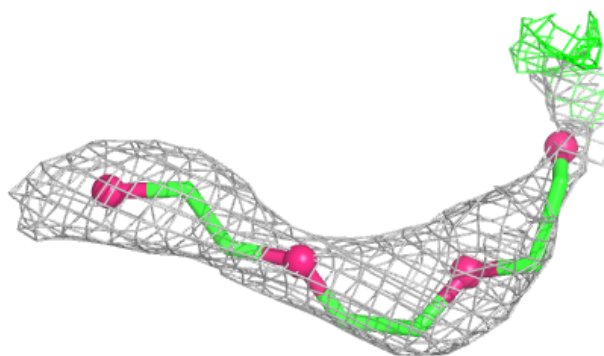
**Electron density around 1PE B 702:**

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

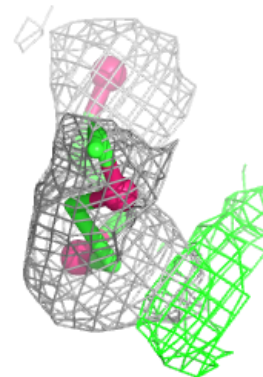
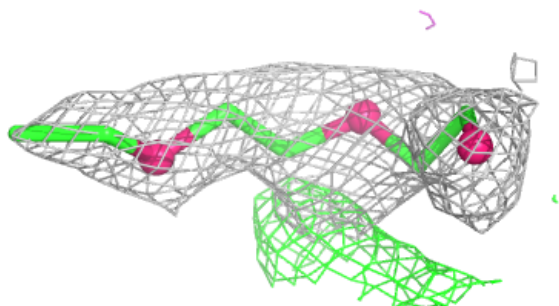
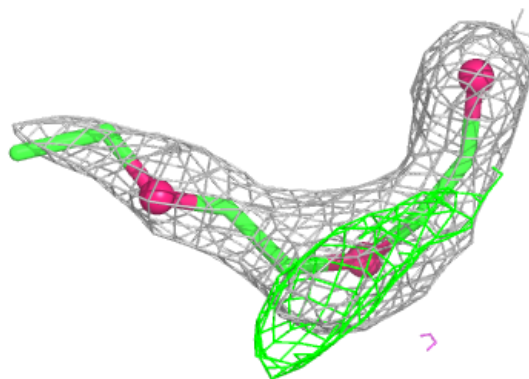


Electron density around 1PE A 701:

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

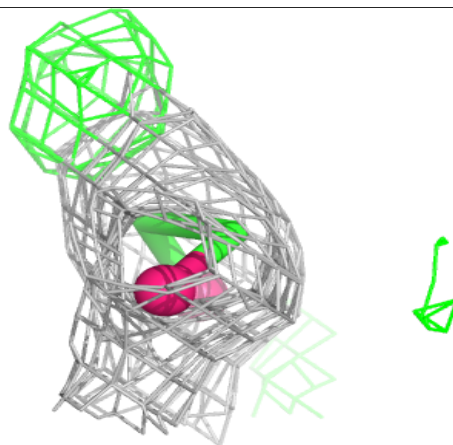
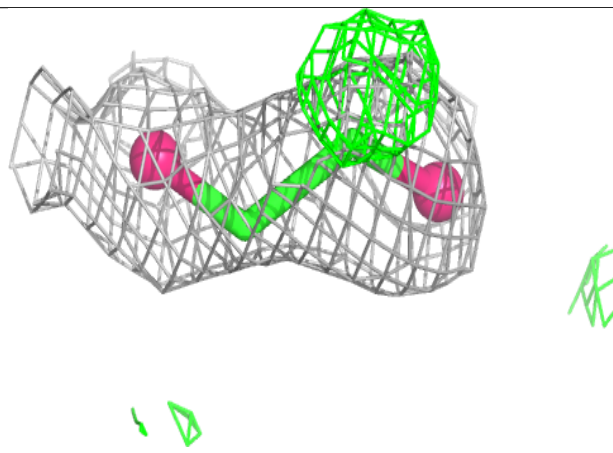
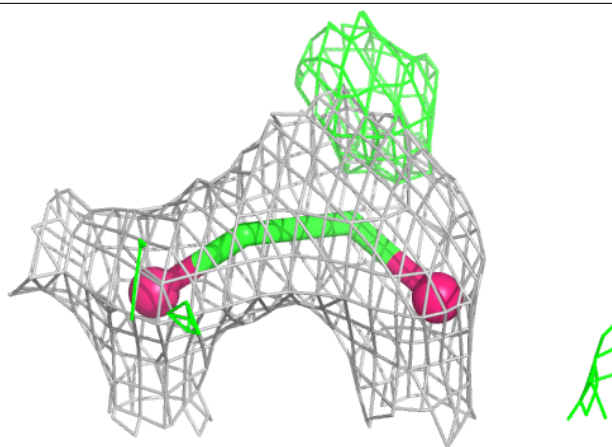
**Electron density around 1PE C 701:**

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



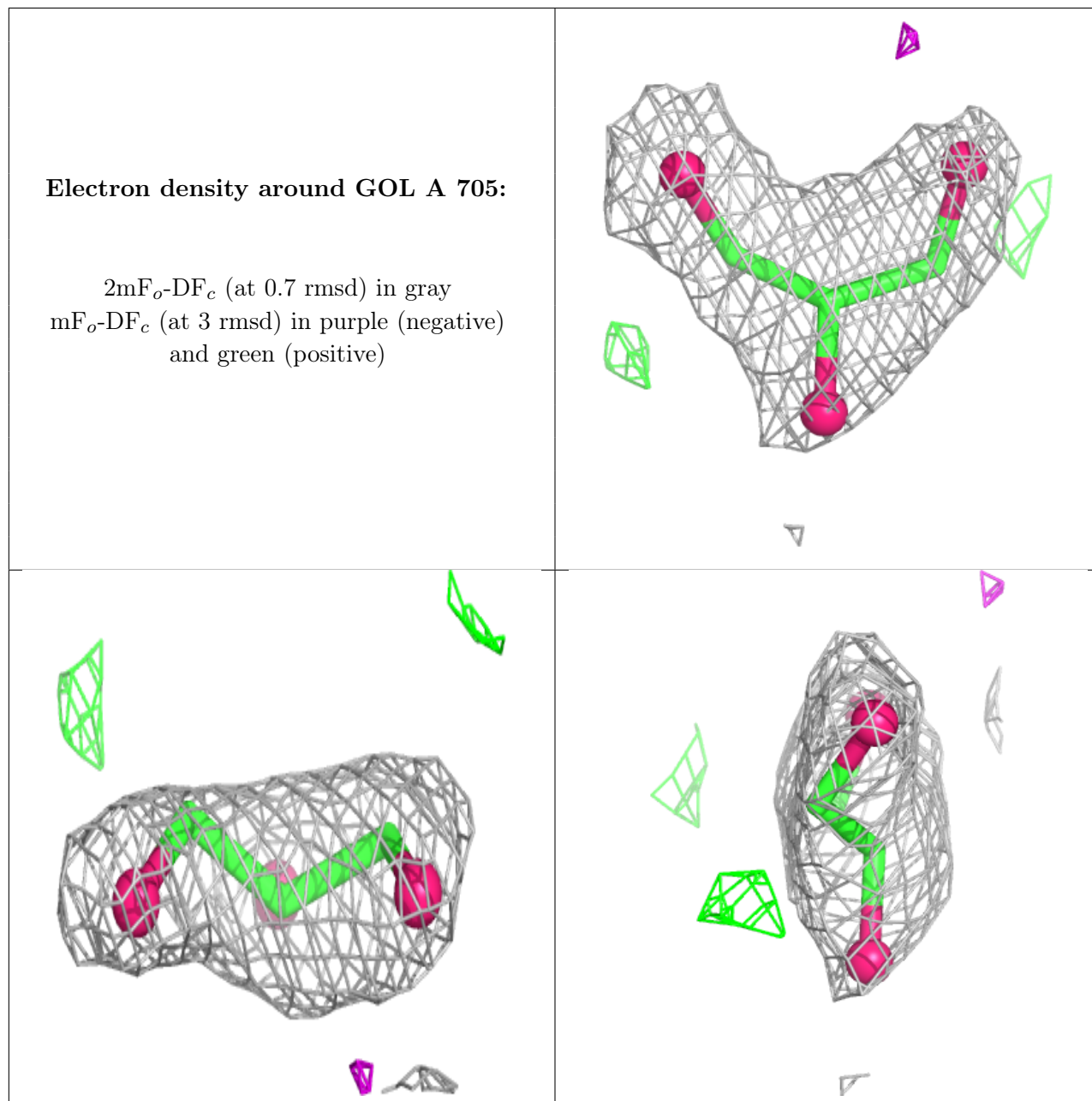
Electron density around 1PE A 702:

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



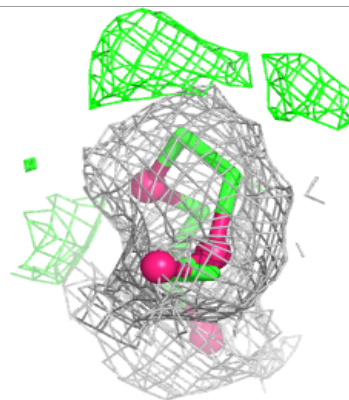
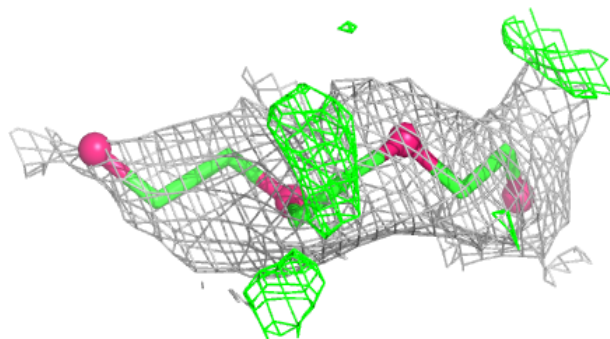
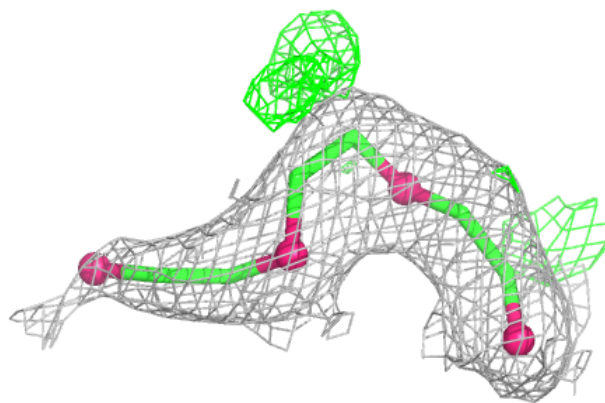
Electron density around GOL A 705:

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

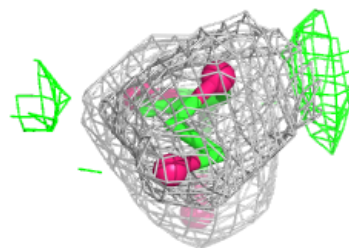
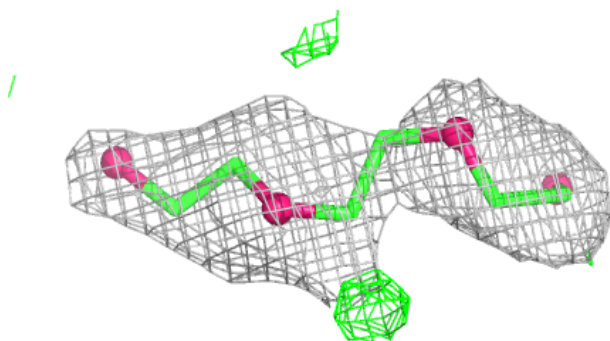
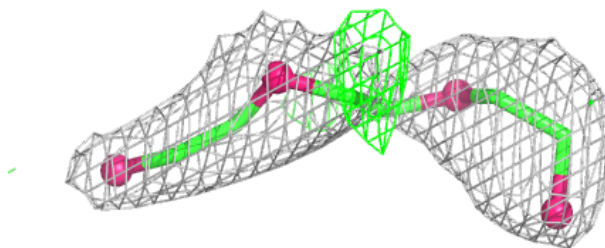


Electron density around 1PE E 701:

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

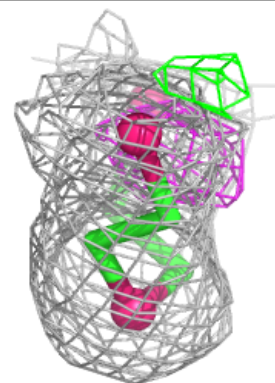
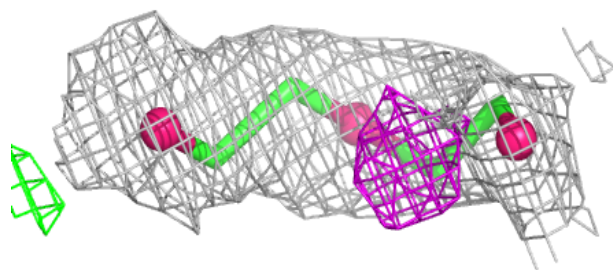
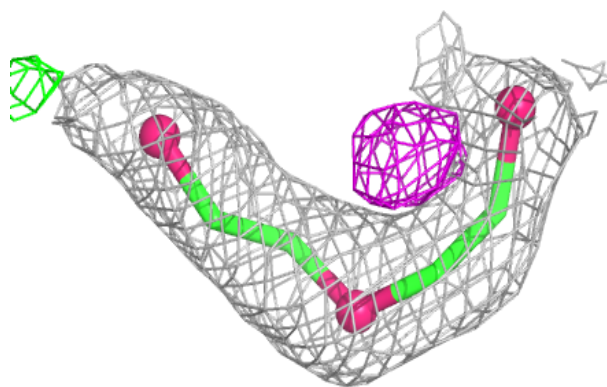
**Electron density around 1PE B 703:**

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



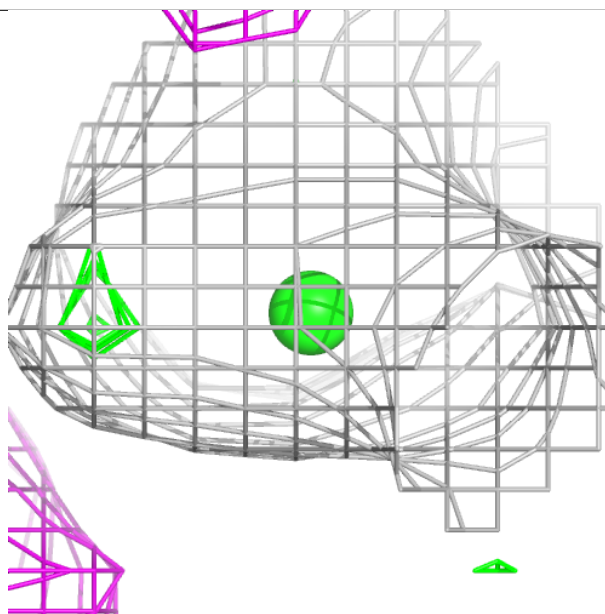
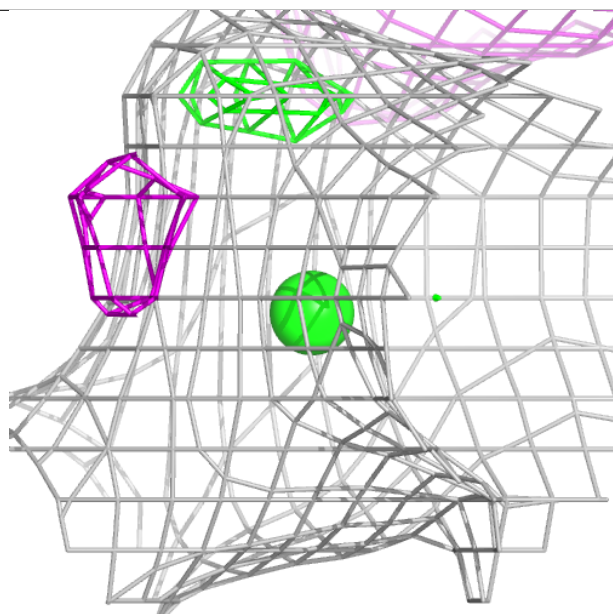
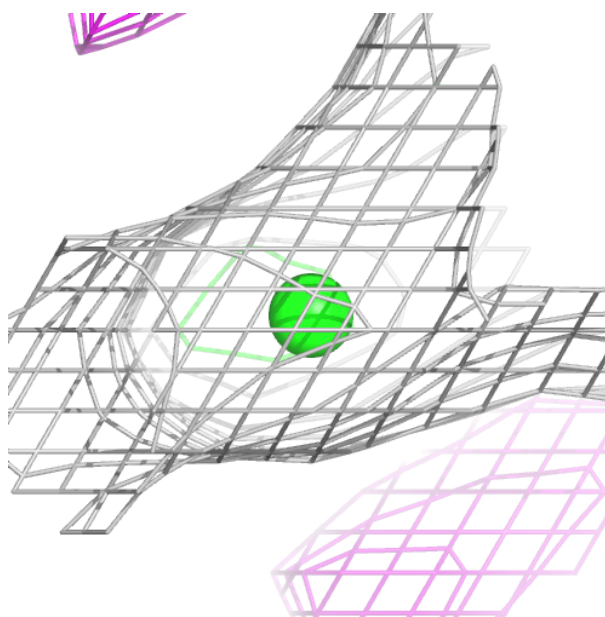
Electron density around 1PE D 701:

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



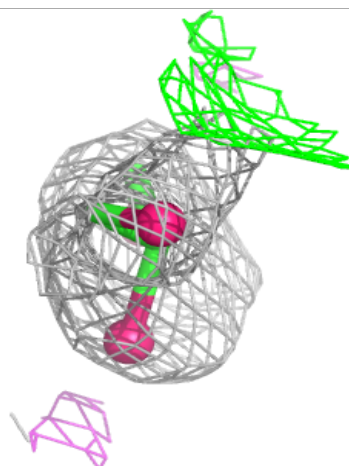
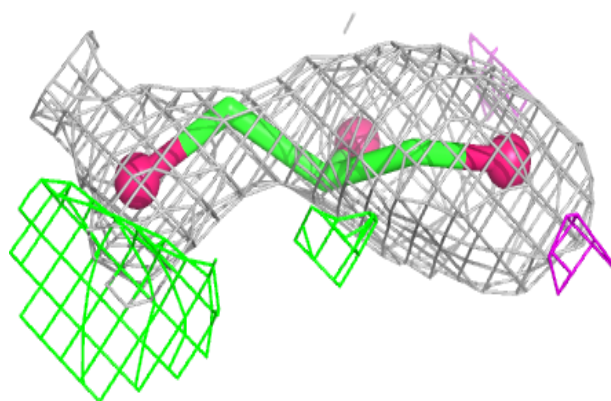
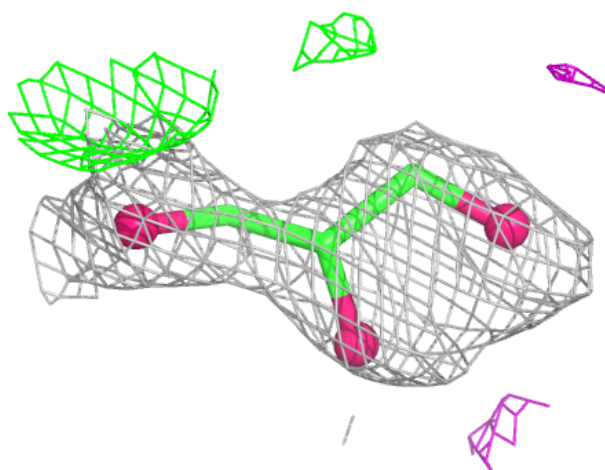
Electron density around CL E 706:

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



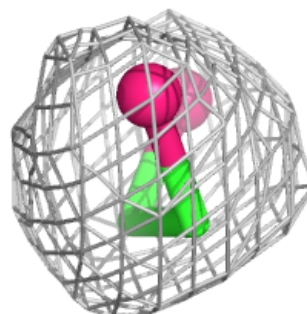
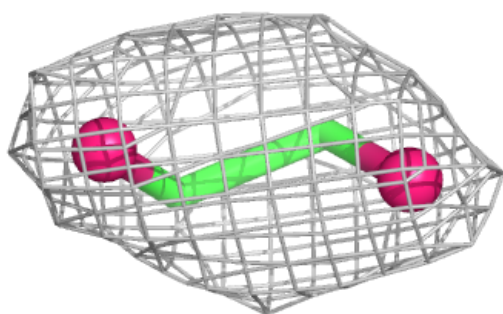
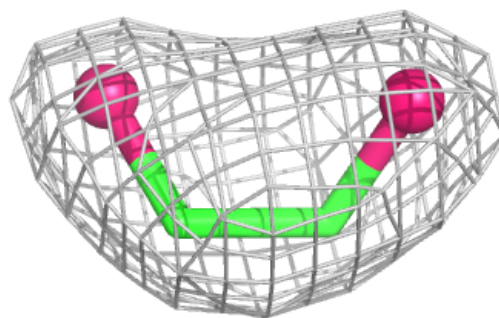
Electron density around GOL C 706:

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



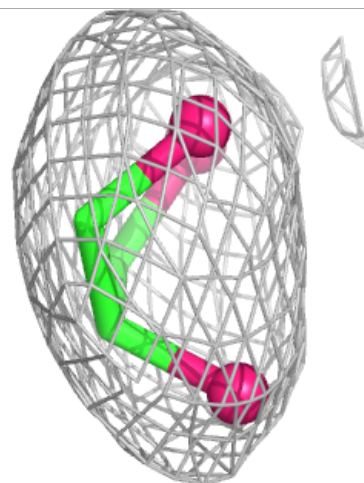
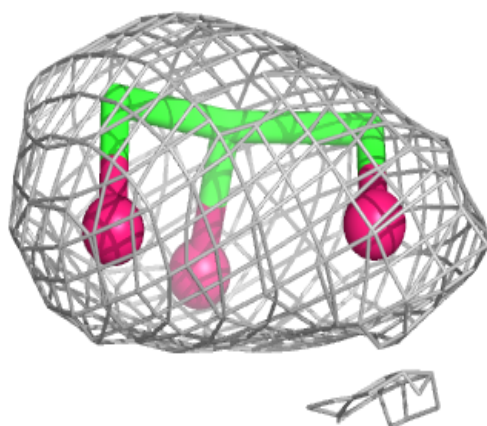
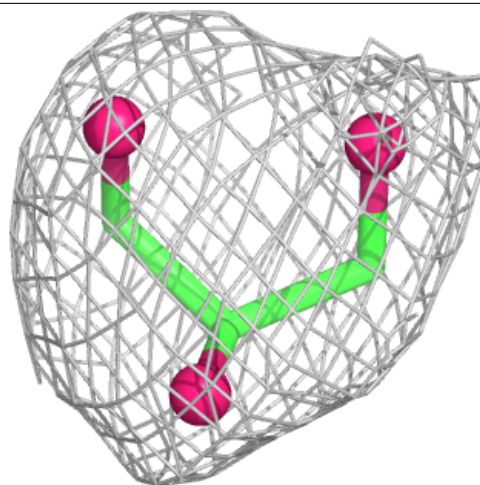
Electron density around 1PE B 706:

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



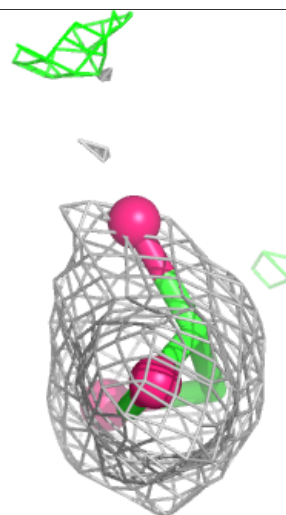
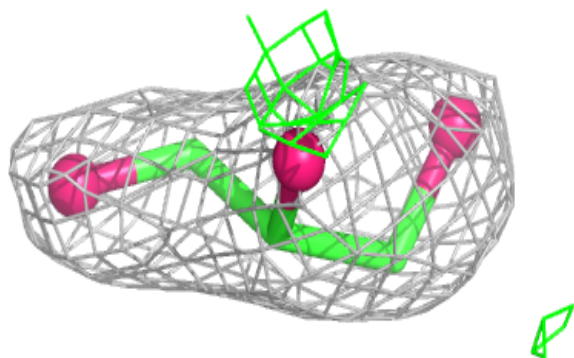
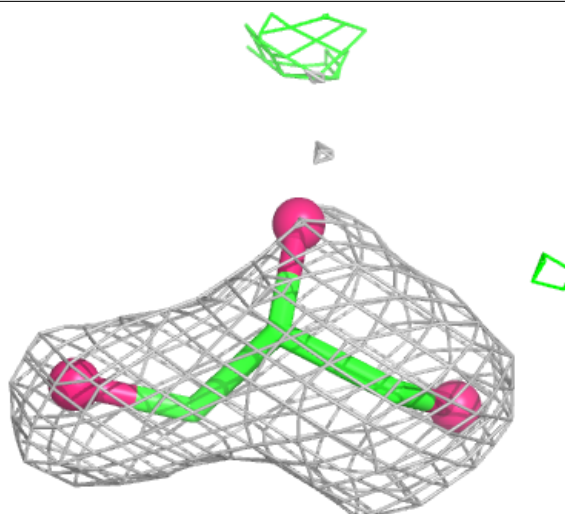
Electron density around GOL C 704:

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



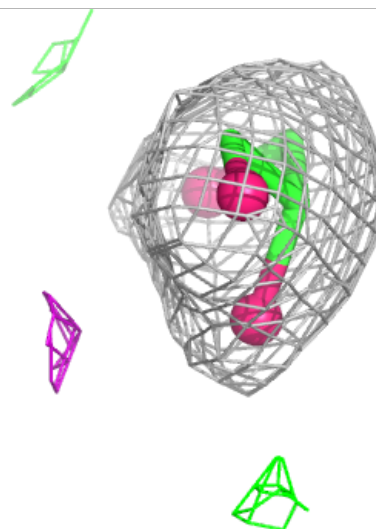
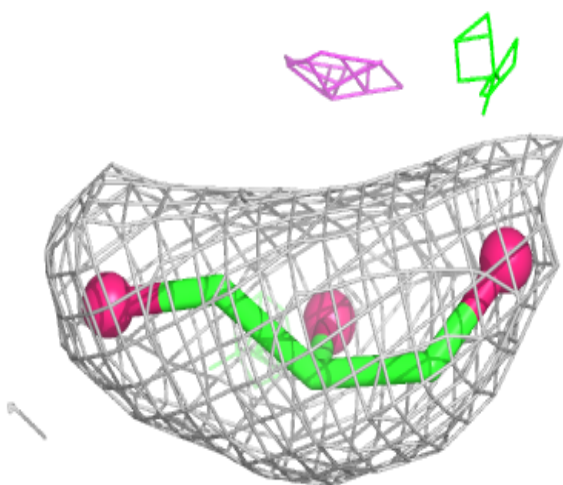
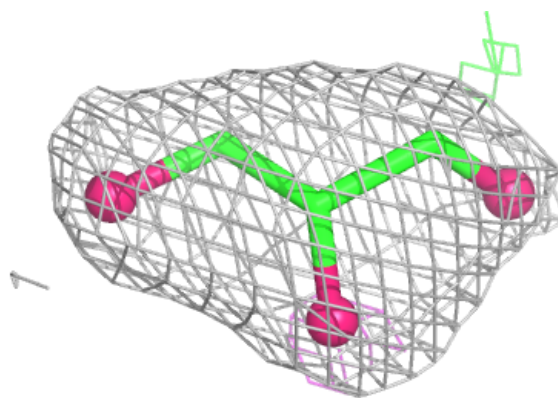
Electron density around GOL A 708:

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



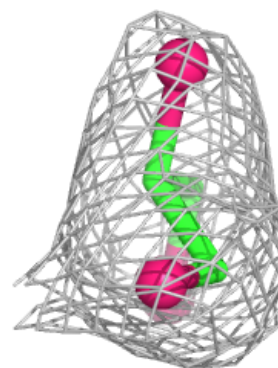
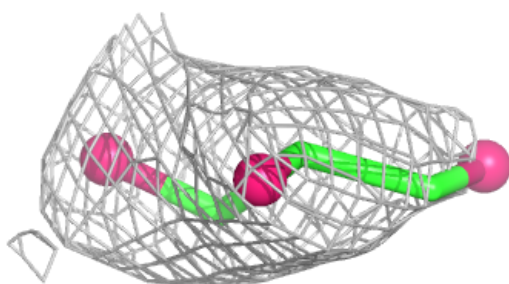
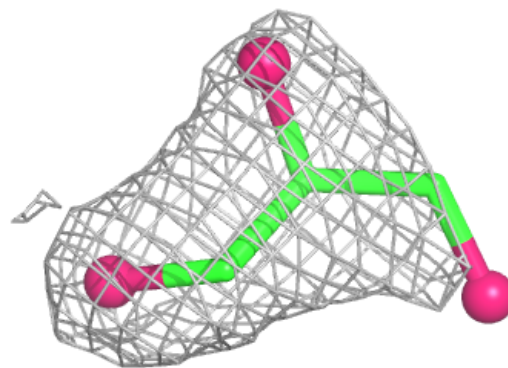
Electron density around GOL C 703:

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



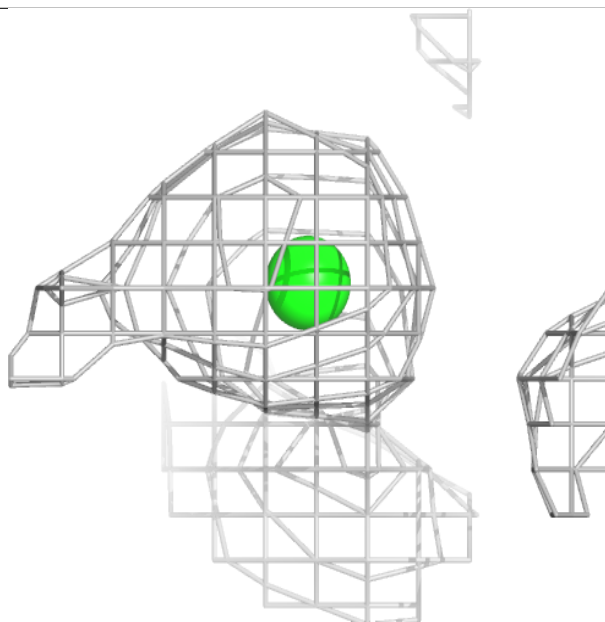
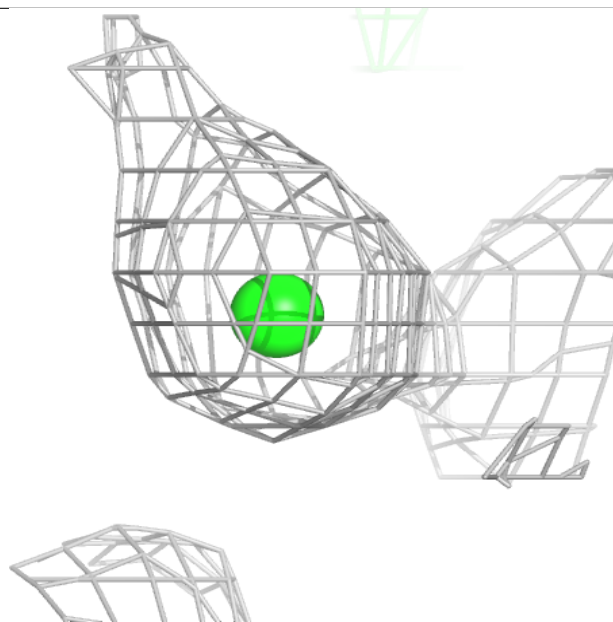
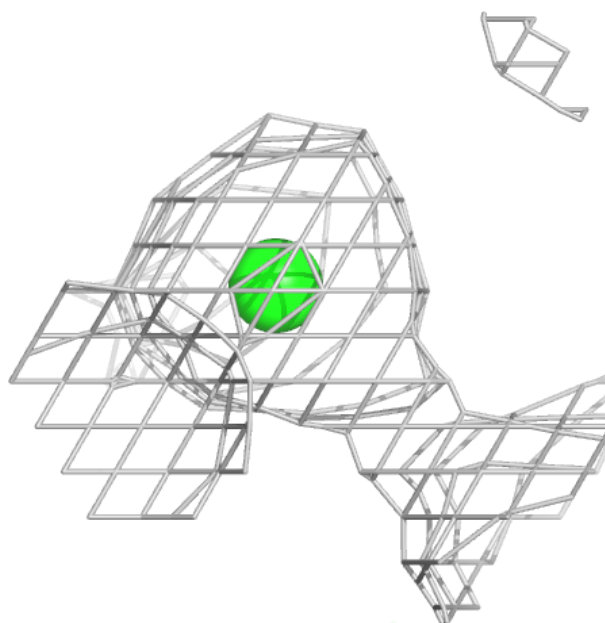
Electron density around GOL A 709:

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



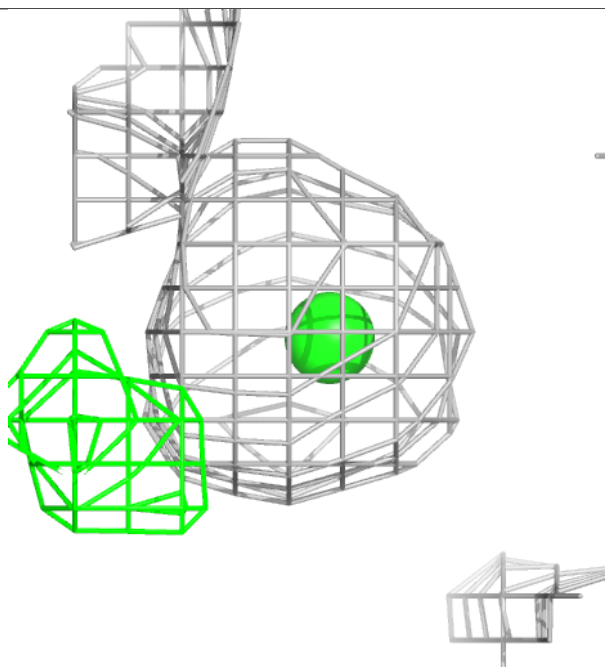
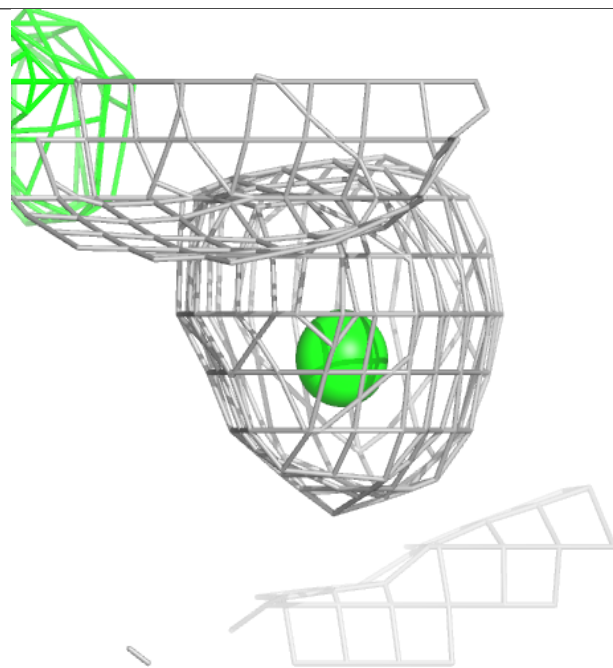
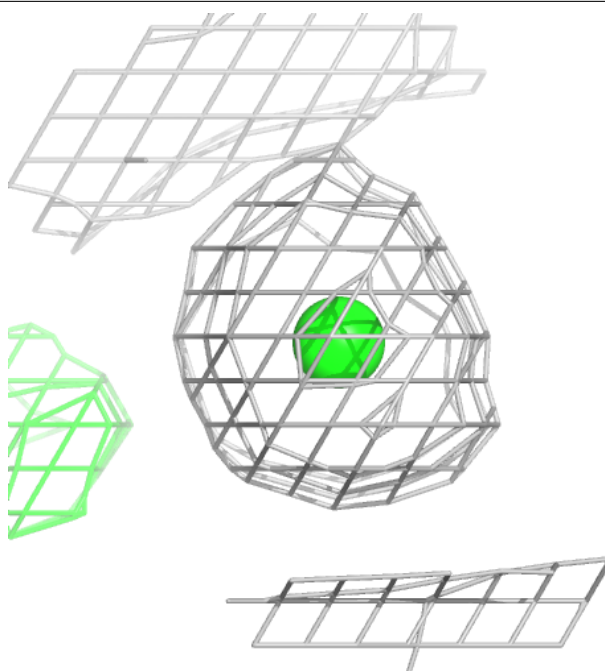
Electron density around CL B 707:

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



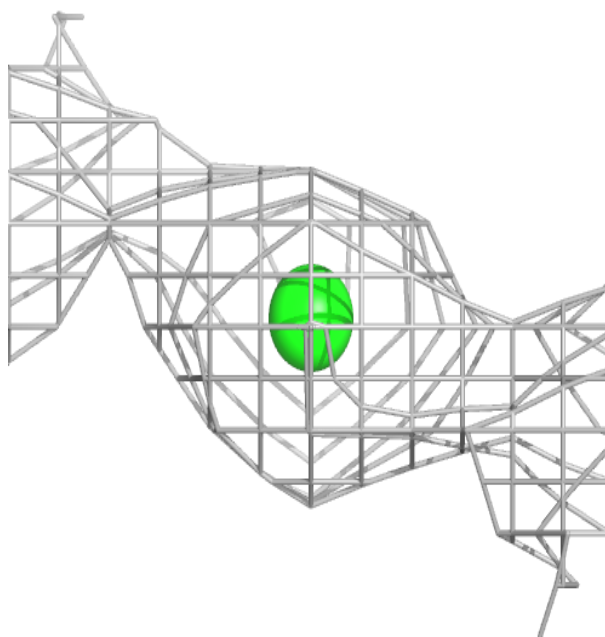
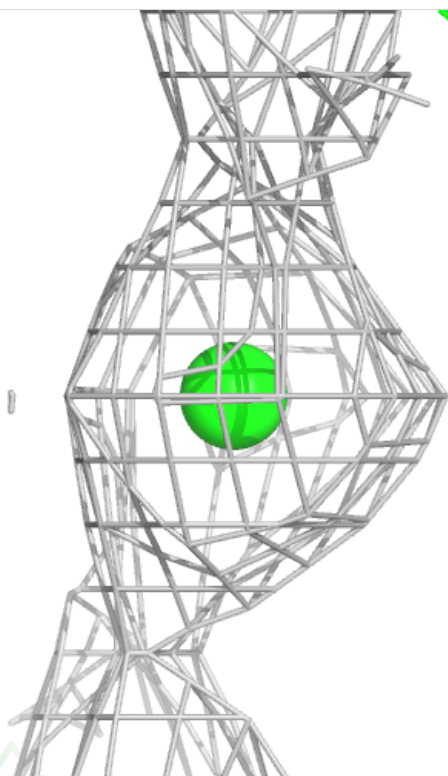
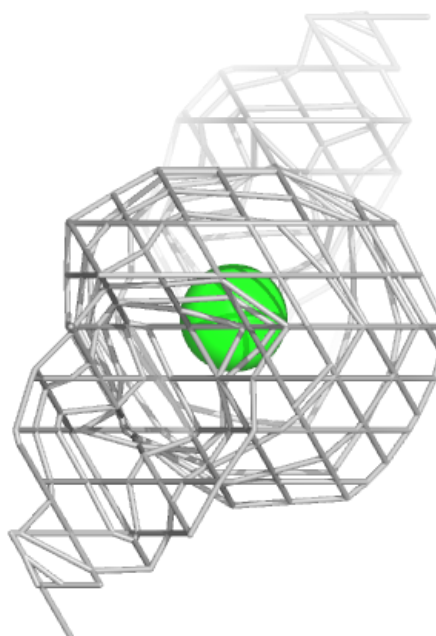
Electron density around CL C 707:

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



Electron density around CL D 706:

$2mF_o-DF_c$ (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.