



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 12, 2024 – 10:41 AM EST

PDB ID : 3FYE
Title : Catalytic core subunits (I and II) of cytochrome c oxidase from Rhodobacter sphaeroides in the reduced state
Authors : Qin, L.; Mills, D.A.; Proshlyakov, D.A.; Hiser, C.; Ferguson-Miller, S.
Deposited on : 2009-01-22
Resolution : 2.15 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

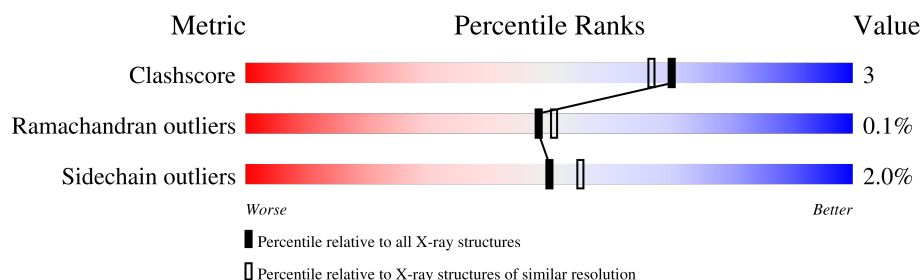
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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))
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)

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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	566	
1	C	566	
2	B	262	
2	D	262	

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
10	HTO	B	1	X	-	-	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 13611 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 Cytochrome C oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	26	1	0
			4218	2826	663	698	31			
1	C	531	Total	C	N	O	S	22	0	0
			4172	2794	656	691	31			

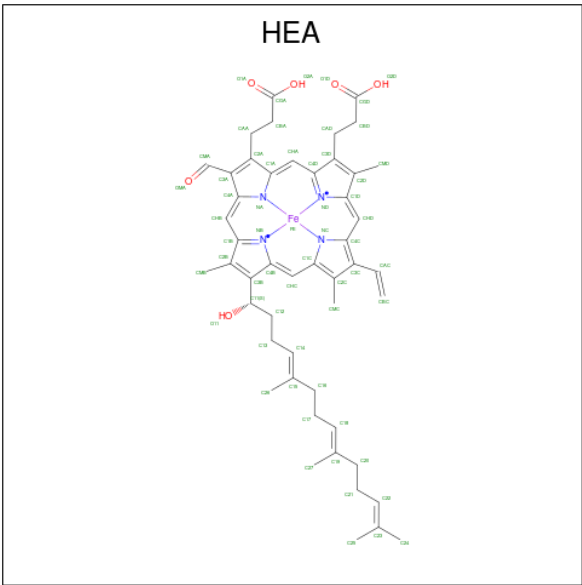
- Molecule 2 is a protein called Cytochrome C oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	256	Total	C	N	O	S	7	1	0
			2031	1325	333	367	6			
2	D	256	Total	C	N	O	S	9	1	0
			2031	1325	333	367	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	282	HIS	-	expression tag	UNP Q03736
B	283	HIS	-	expression tag	UNP Q03736
B	284	HIS	-	expression tag	UNP Q03736
B	285	HIS	-	expression tag	UNP Q03736
B	286	HIS	-	expression tag	UNP Q03736
B	287	HIS	-	expression tag	UNP Q03736
D	282	HIS	-	expression tag	UNP Q03736
D	283	HIS	-	expression tag	UNP Q03736
D	284	HIS	-	expression tag	UNP Q03736
D	285	HIS	-	expression tag	UNP Q03736
D	286	HIS	-	expression tag	UNP Q03736
D	287	HIS	-	expression tag	UNP Q03736

- Molecule 3 is HEME-A (three-letter code: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
3	A	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
3	C	1	Total 60	C 49	Fe 1	N 4	O 6	0	0
3	C	1	Total 60	C 49	Fe 1	N 4	O 6	0	0

- Molecule 4 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	Mg	0	0
			1	1		

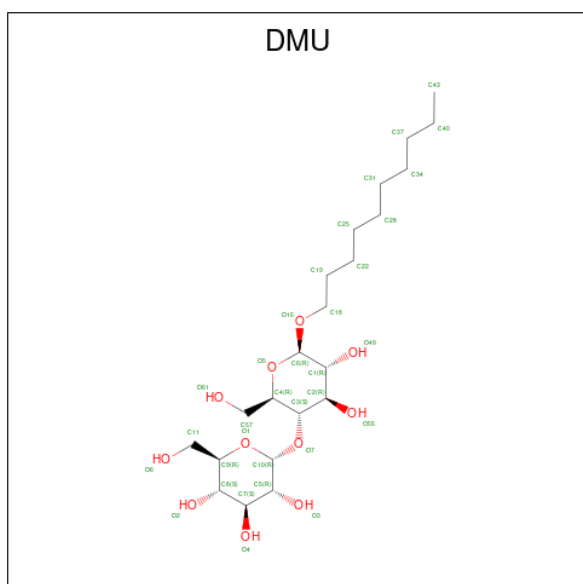
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 7 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	X	0	0
			1	1		
7	C	1	Total	X	0	0
			1	1		

- Molecule 8 is DECYL-BETA-D-MALTOPYRANOSIDE (three-letter code: DMU) (formula: C₂₂H₄₂O₁₁).



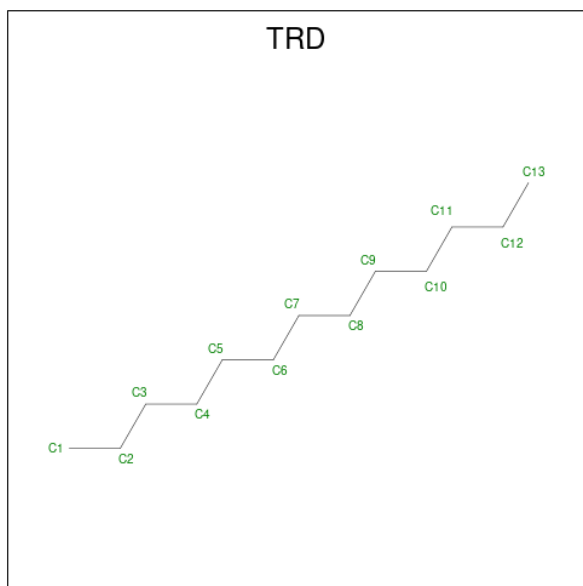
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			33	22	11		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			33	22	11		
8	A	1	Total	C	O	0	0
			22	16	6		
8	A	1	Total	C	O	0	0
			33	22	11		
8	B	1	Total	C	O	0	0
			33	22	11		
8	B	1	Total	C	O	0	0
			23	12	11		
8	C	1	Total	C	O	0	0
			23	12	11		
8	C	1	Total	C	O	0	0
			33	22	11		
8	D	1	Total	C	O	0	0
			33	22	11		
8	D	1	Total	C	O	0	0
			23	12	11		

- Molecule 9 is TRIDECANE (three-letter code: TRD) (formula: $C_{13}H_{28}$).



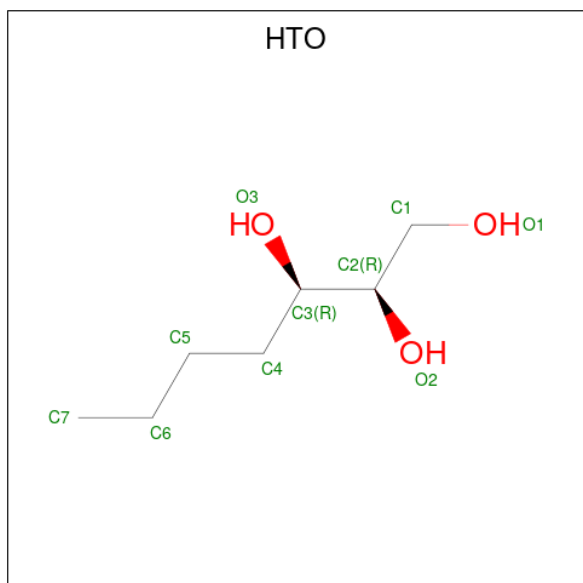
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	C	0	0
			13	13		
9	A	1	Total	C	0	0
			13	13		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C 7 7	0	0
9	A	1	Total C 13 13	0	0
9	A	1	Total C 9 9	0	0
9	B	1	Total C 7 7	0	0
9	C	1	Total C 13 13	0	0
9	C	1	Total C 13 13	0	0
9	C	1	Total C 7 7	0	0
9	C	1	Total C 9 9	0	0
9	D	1	Total C 13 13	0	0
9	D	1	Total C 7 7	0	0

- Molecule 10 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: $C_7H_{16}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total C O 10 7 3	0	0

- Molecule 11 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	2	Total 2	Cd 2	0	0
11	D	2	Total 2	Cd 2	0	0

- Molecule 12 is water.

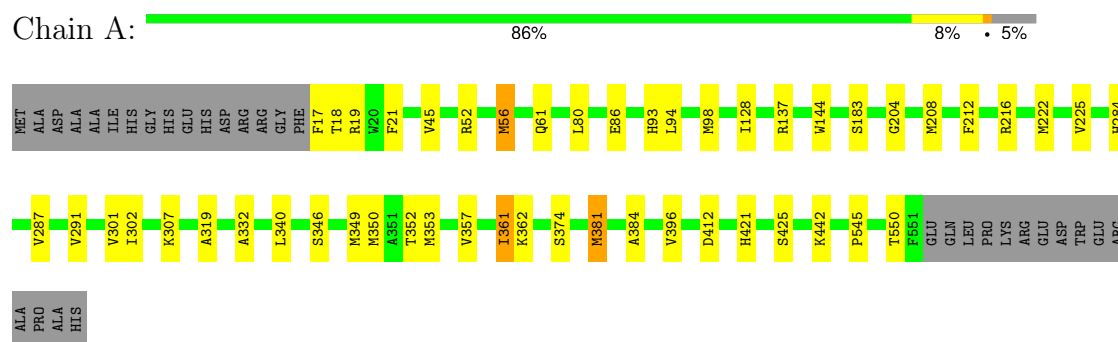
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	129	Total 129	O 129	0	0
12	B	134	Total 134	O 134	0	0
12	C	97	Total 97	O 97	0	0
12	D	120	Total 120	O 120	0	0

3 Residue-property plots

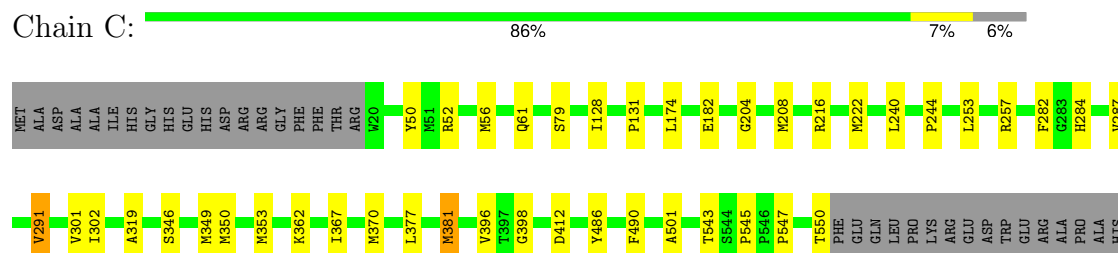
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

Note EDS failed to run properly.

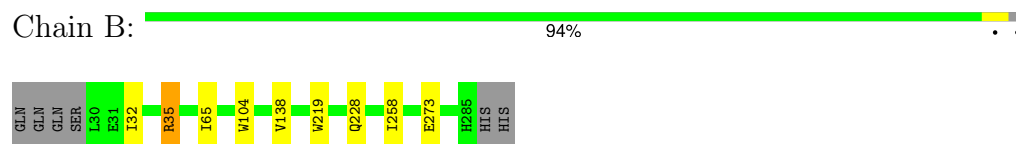
• Molecule 1: Cytochrome C oxidase subunit 1



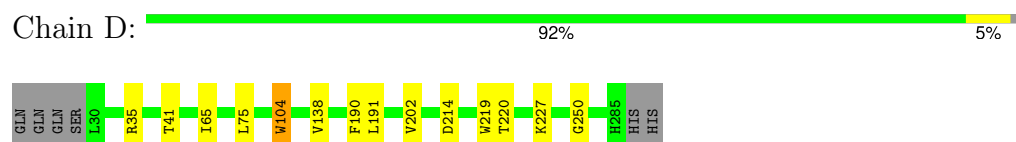
• Molecule 1: Cytochrome C oxidase subunit 1



• Molecule 2: Cytochrome C oxidase subunit 2



• Molecule 2: Cytochrome C oxidase subunit 2



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	124.61Å 131.47Å 176.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15	Depositor
% Data completeness (in resolution range)	99.1 (50.00-2.15)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.221	Depositor
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.034	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	13611	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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: CU1, UNX, CD, MG, DMU, TRD, HTO, CA, HEA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/4377	0.57	0/5973
1	C	0.50	0/4326	0.54	0/5905
2	B	0.55	0/2096	0.59	0/2869
2	D	0.50	0/2096	0.57	0/2869
All	All	0.54	0/12895	0.56	0/17616

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4218	0	4139	33	0
1	C	4172	0	4095	32	0
2	B	2031	0	1988	7	0
2	D	2031	0	1988	7	0
3	A	120	0	108	8	0
3	C	120	0	108	8	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	2	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	1	0	0	1	0
7	C	1	0	0	0	0
8	A	121	0	157	2	0
8	B	56	0	63	0	0
8	C	56	0	63	1	0
8	D	56	0	63	1	0
9	A	55	0	114	1	0
9	B	7	0	13	2	0
9	C	42	0	86	1	0
9	D	20	0	41	1	0
10	B	10	0	16	0	0
11	B	2	0	0	0	0
11	D	2	0	0	0	0
12	A	129	0	0	1	0
12	B	134	0	0	3	0
12	C	97	0	0	0	0
12	D	120	0	0	0	0
All	All	13611	0	13042	87	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 3.

The worst 5 of 87 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)
2:B:228:GLN:NE2	12:B:723:HOH:O	1.92	1.03
3:C:567:HEA:HMC1	3:C:567:HEA:HBC1	1.58	0.85
1:A:21:PHE:HB3	1:A:144:TRP:HZ2	1.42	0.82
3:A:568:HEA:HBD2	3:A:568:HEA:HMD1	1.61	0.81
2:B:32:ILE:HG22	2:B:35:ARG:HD3	1.62	0.81

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	534/566 (94%)	524 (98%)	9 (2%)	1 (0%)	44	44
1	C	529/566 (94%)	523 (99%)	6 (1%)	0	100	100
2	B	255/262 (97%)	250 (98%)	5 (2%)	0	100	100
2	D	255/262 (97%)	249 (98%)	6 (2%)	0	100	100
All	All	1573/1656 (95%)	1546 (98%)	26 (2%)	1 (0%)	48	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	THR

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	436/459 (95%)	424 (97%)	12 (3%)	38	40
1	C	431/459 (94%)	424 (98%)	7 (2%)	58	64
2	B	216/221 (98%)	214 (99%)	2 (1%)	75	81
2	D	216/221 (98%)	211 (98%)	5 (2%)	45	49
All	All	1299/1360 (96%)	1273 (98%)	26 (2%)	50	55

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	61	GLN
1	C	282	PHE
2	D	214	ASP
1	C	222	MET
1	C	291	VAL

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

Mol	Chain	Res	Type
1	A	140	ASN
2	D	127	GLN
2	D	209	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 43 ligands modelled in this entry, 14 are monoatomic and 2 are unknown - leaving 27 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	$\# Z > 2$
8	DMU	B	288	-	34,34,34	0.57	0	45,45,45	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	DMU	A	576	-	22,22,34	0.57	1 (4%)	27,27,45	0.93	2 (7%)
8	DMU	A	577	-	34,34,34	0.60	1 (2%)	45,45,45	0.95	1 (2%)
9	TRD	A	581	-	12,12,12	0.25	0	11,11,11	0.52	0
3	HEA	C	568	1	58,67,67	1.60	6 (10%)	63,103,103	1.66	16 (25%)
9	TRD	C	1006	-	12,12,12	0.28	0	11,11,11	0.51	0
9	TRD	A	579	-	12,12,12	0.28	0	11,11,11	0.43	0
8	DMU	A	575	-	34,34,34	0.58	1 (2%)	45,45,45	0.99	3 (6%)
3	HEA	C	567	1	58,67,67	1.42	8 (13%)	63,103,103	1.07	2 (3%)
9	TRD	C	1010	-	8,8,12	0.29	0	7,7,11	0.39	0
8	DMU	C	1005	-	34,34,34	0.59	1 (2%)	45,45,45	0.85	1 (2%)
10	HTO	B	1	-	9,9,9	0.44	0	10,10,10	0.67	0
3	HEA	A	567	1	58,67,67	1.44	6 (10%)	63,103,103	1.22	7 (11%)
9	TRD	B	289	-	6,6,12	0.31	0	5,5,11	0.29	0
3	HEA	A	568	1	58,67,67	1.45	8 (13%)	63,103,103	1.68	17 (26%)
8	DMU	C	1002	-	24,24,34	0.51	0	35,35,45	0.66	0
9	TRD	D	1008	-	6,6,12	0.28	0	5,5,11	0.34	0
9	TRD	A	578	-	12,12,12	0.27	0	11,11,11	0.49	0
8	DMU	D	1011	-	24,24,34	0.51	0	35,35,45	0.84	0
9	TRD	D	1007	-	12,12,12	0.22	0	11,11,11	0.60	0
9	TRD	C	1001	-	12,12,12	0.28	0	11,11,11	0.45	0
9	TRD	A	582	-	8,8,12	0.27	0	7,7,11	0.46	0
8	DMU	D	1003	-	34,34,34	0.56	0	45,45,45	0.59	0
8	DMU	B	11	-	24,24,34	0.50	0	35,35,45	0.84	0
9	TRD	A	580	-	6,6,12	0.25	0	5,5,11	0.42	0
8	DMU	A	574	-	34,34,34	0.52	0	45,45,45	1.03	3 (6%)
9	TRD	C	1009	-	6,6,12	0.29	0	5,5,11	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
8	DMU	B	288	-	-	5/19/59/59	0/2/2/2
8	DMU	A	576	-	-	9/13/33/59	0/1/1/2
8	DMU	A	577	-	-	10/19/59/59	0/2/2/2
9	TRD	A	581	-	-	6/10/10/10	-
3	HEA	C	568	1	-	5/32/76/76	-
9	TRD	C	1006	-	-	3/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	TRD	A	579	-	-	5/10/10/10	-
8	DMU	A	575	-	-	6/19/59/59	0/2/2/2
3	HEA	C	567	1	-	4/32/76/76	-
9	TRD	C	1010	-	-	4/6/6/10	-
8	DMU	C	1005	-	-	9/19/59/59	0/2/2/2
10	HTO	B	1	-	1/1/2/2	4/10/10/10	-
3	HEA	A	567	1	-	4/32/76/76	-
9	TRD	B	289	-	-	1/4/4/10	-
3	HEA	A	568	1	-	5/32/76/76	-
8	DMU	C	1002	-	-	2/8/48/59	0/2/2/2
9	TRD	D	1008	-	-	1/4/4/10	-
9	TRD	A	578	-	-	7/10/10/10	-
8	DMU	D	1011	-	-	2/8/48/59	0/2/2/2
9	TRD	D	1007	-	-	8/10/10/10	-
9	TRD	C	1001	-	-	4/10/10/10	-
9	TRD	A	582	-	-	3/6/6/10	-
8	DMU	D	1003	-	-	5/19/59/59	0/2/2/2
8	DMU	B	11	-	-	1/8/48/59	0/2/2/2
9	TRD	A	580	-	-	1/4/4/10	-
8	DMU	A	574	-	-	3/19/59/59	0/2/2/2
9	TRD	C	1009	-	-	0/4/4/10	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	568	HEA	C11-C3B	5.53	1.58	1.51
3	C	567	HEA	C3A-C2A	-5.11	1.33	1.40
3	A	567	HEA	C3A-C2A	-4.84	1.33	1.40
3	C	568	HEA	FE-NB	4.82	2.25	1.98
3	A	568	HEA	C11-C3B	4.76	1.57	1.51

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	568	HEA	CBA-CAA-C2A	-4.21	105.61	112.55
3	A	568	HEA	CMC-C2C-C1C	-4.01	122.59	128.46
8	A	575	DMU	O16-C6-C1	3.88	114.17	108.27
3	A	568	HEA	CBA-CAA-C2A	-3.53	106.73	112.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	568	HEA	C4A-CHB-C1B	3.31	126.92	122.56

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	B	1	HTO	C2

5 of 117 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	568	HEA	C2D-C3D-CAD-CBD
3	C	568	HEA	C2D-C3D-CAD-CBD
10	B	1	HTO	O1-C1-C2-C3
10	B	1	HTO	O1-C1-C2-O2
3	A	568	HEA	C4D-C3D-CAD-CBD

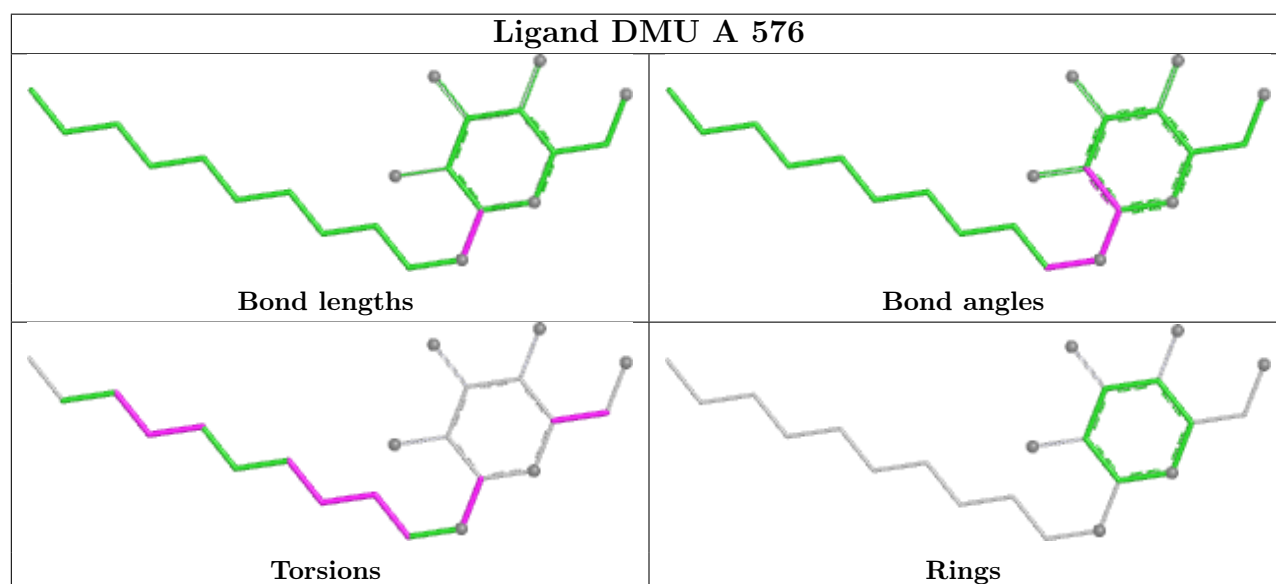
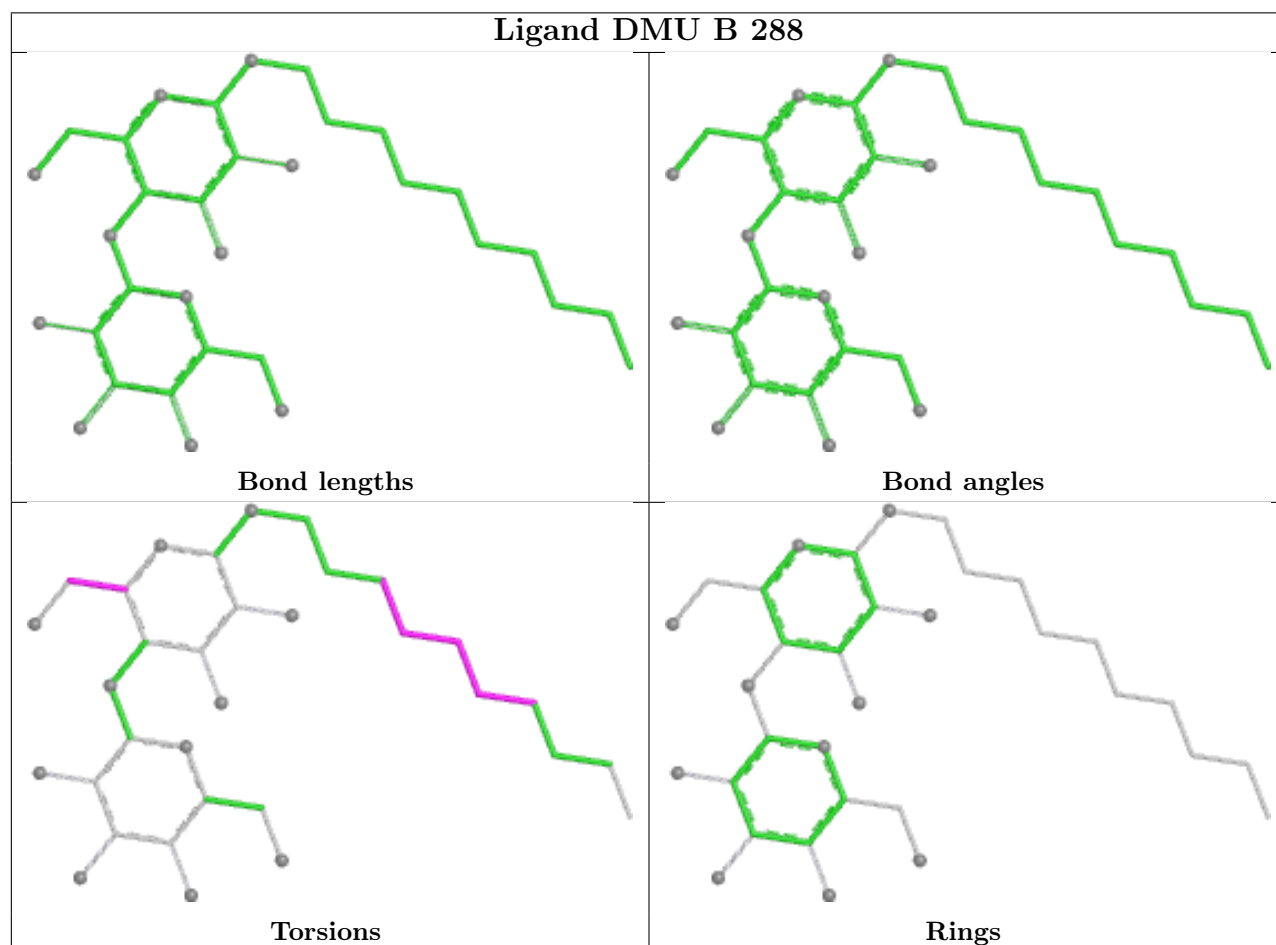
There are no ring outliers.

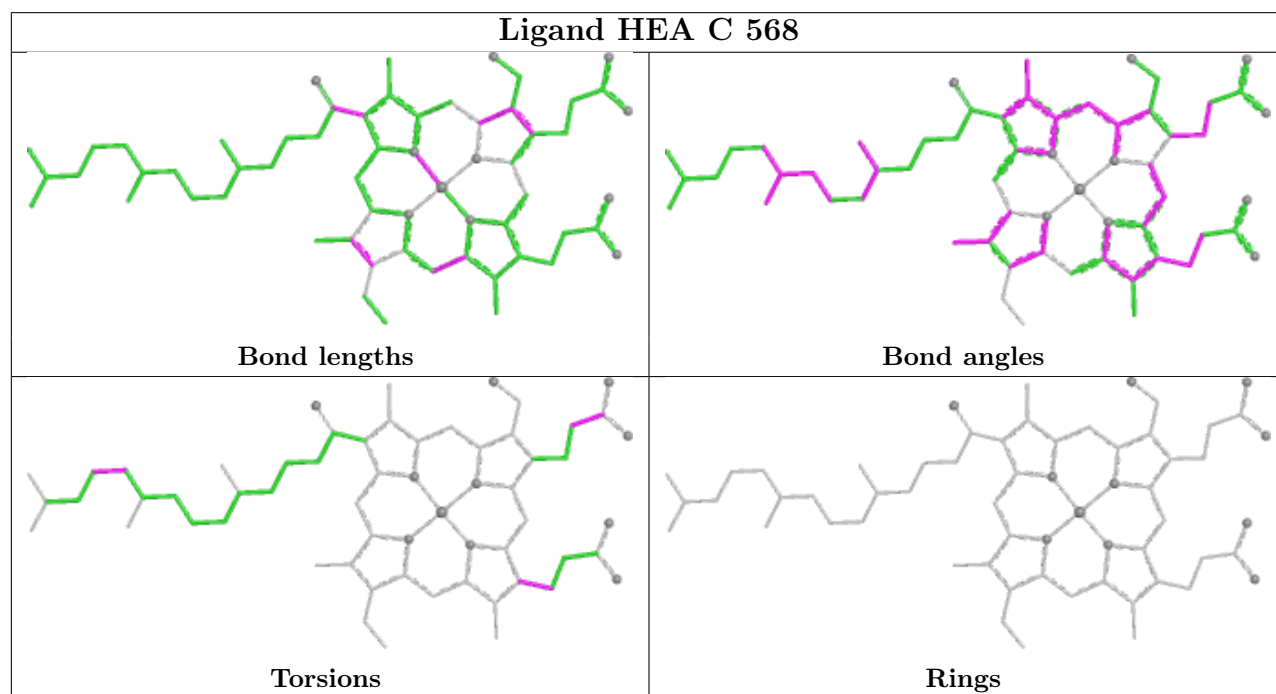
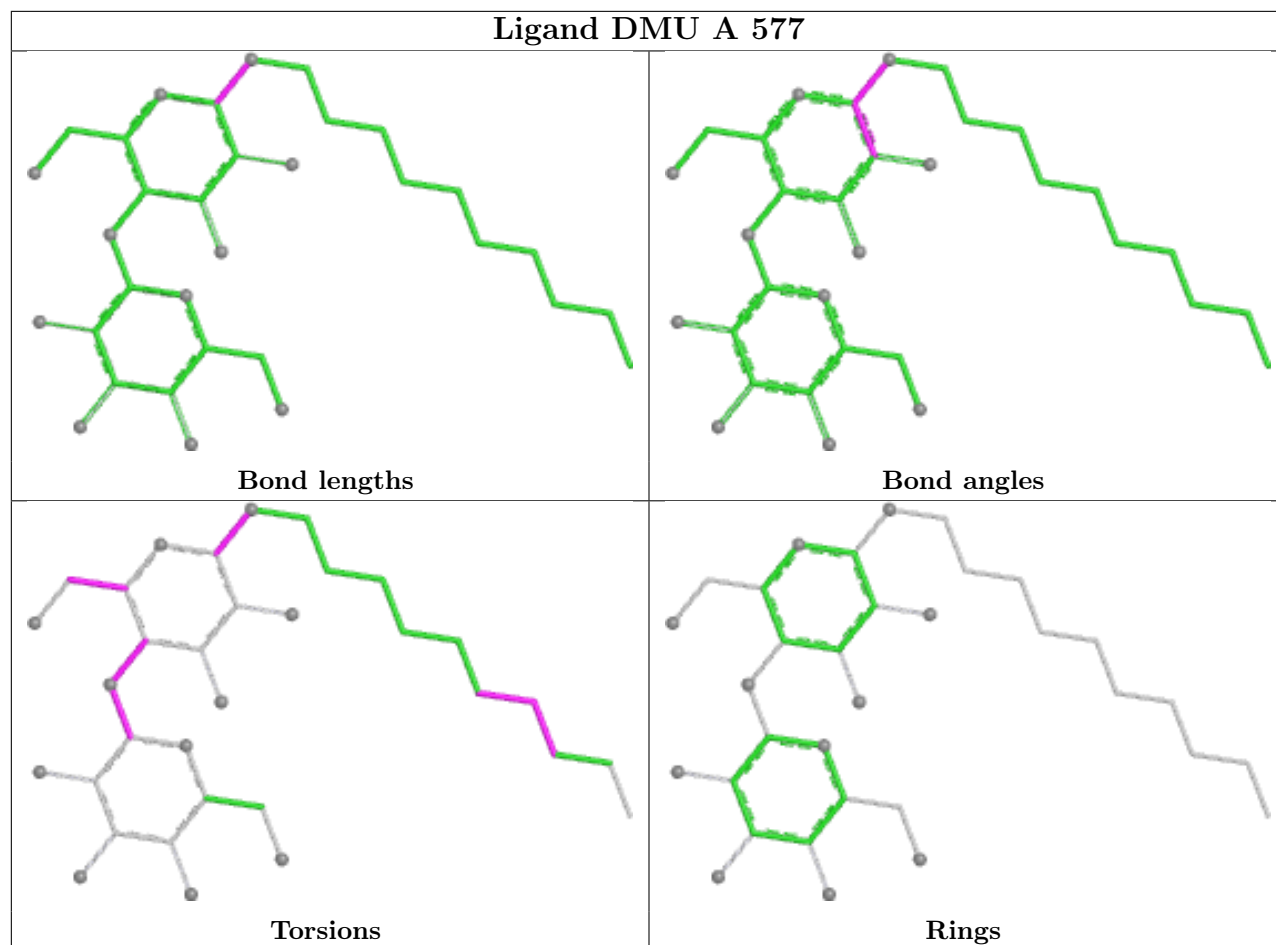
11 monomers are involved in 24 short contacts:

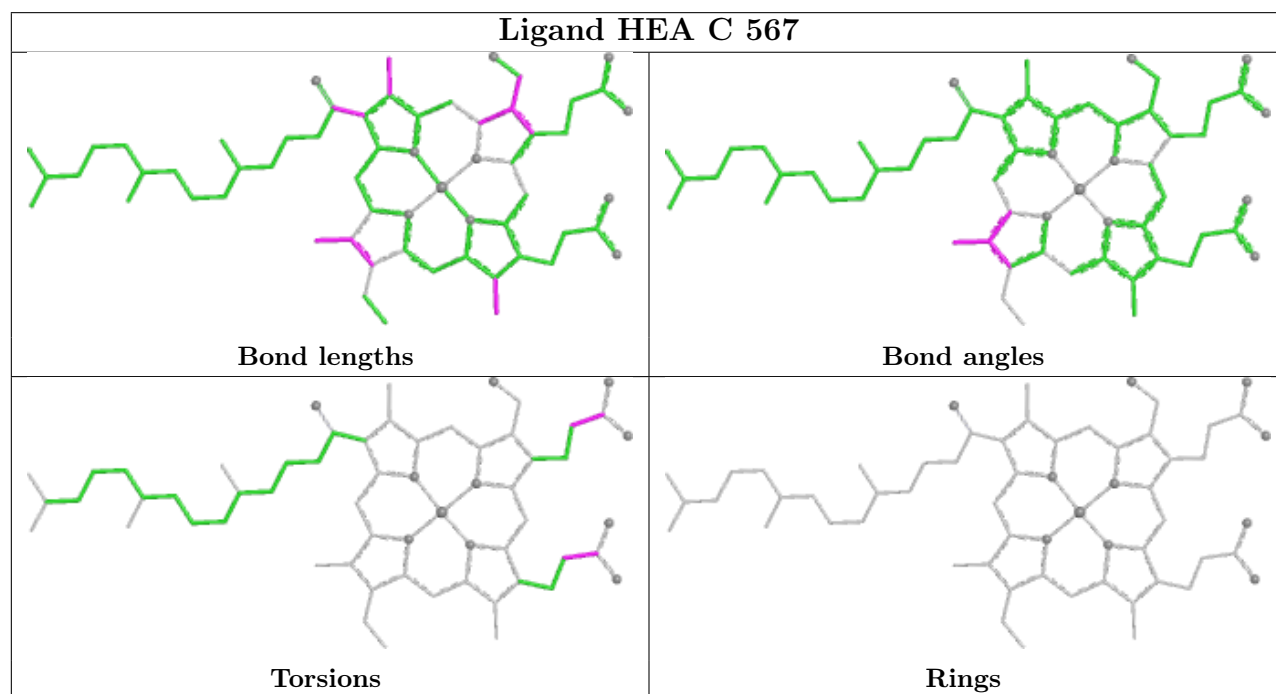
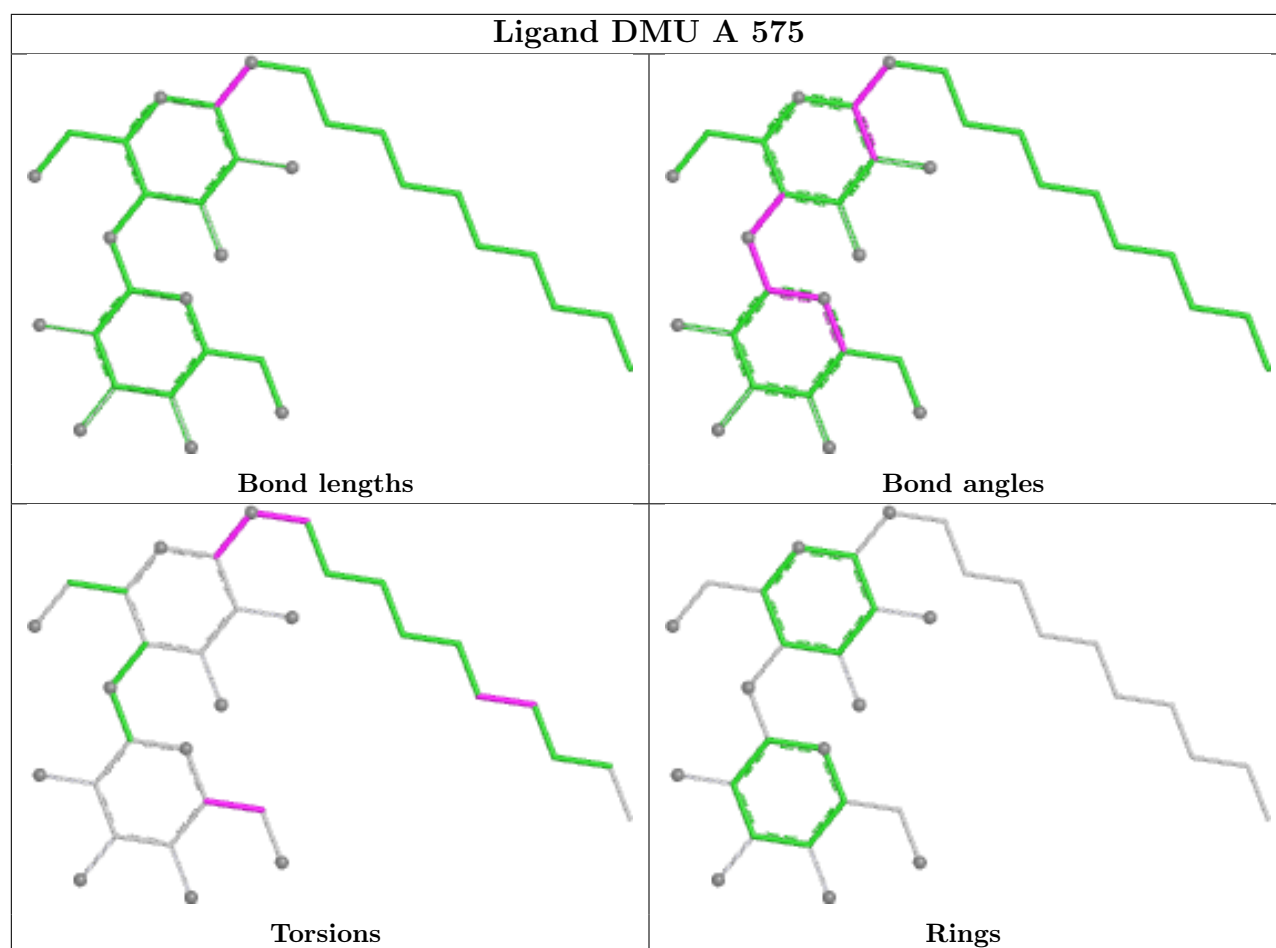
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	577	DMU	2	0
3	C	568	HEA	7	0
3	C	567	HEA	1	0
9	C	1010	TRD	1	0
8	C	1005	DMU	1	0
3	A	567	HEA	2	0
9	B	289	TRD	2	0
3	A	568	HEA	6	0
9	A	578	TRD	1	0
9	D	1007	TRD	1	0
8	D	1003	DMU	1	0

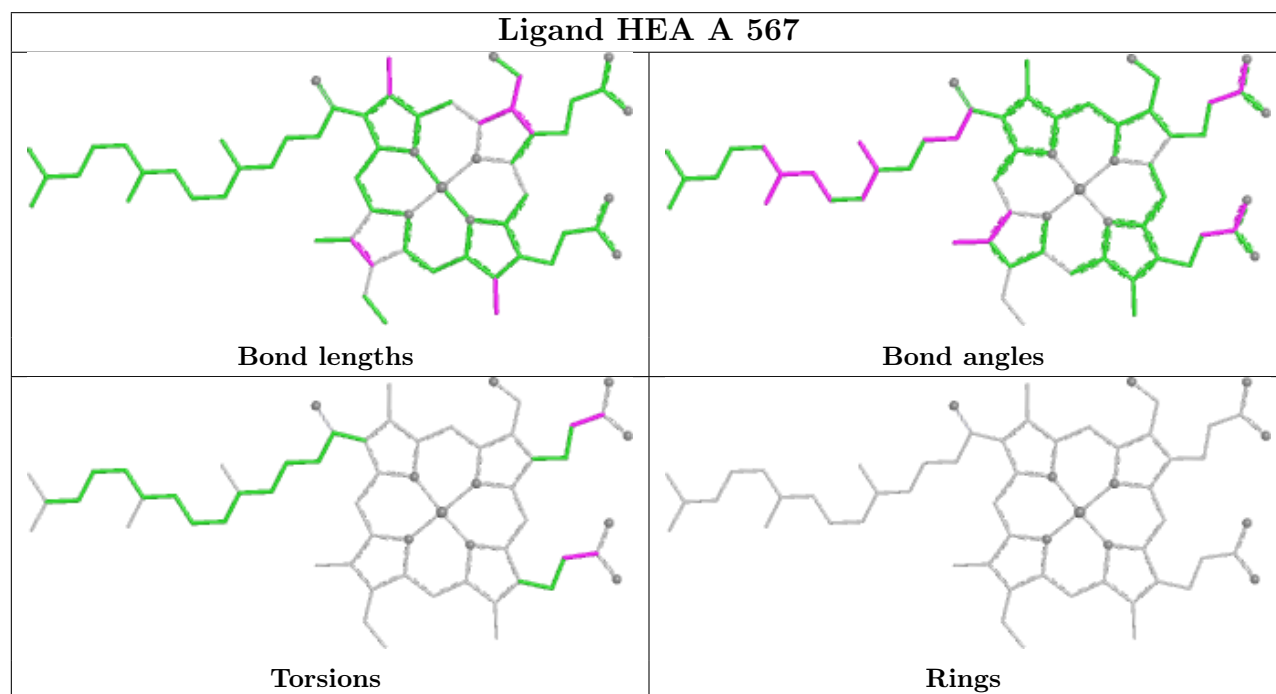
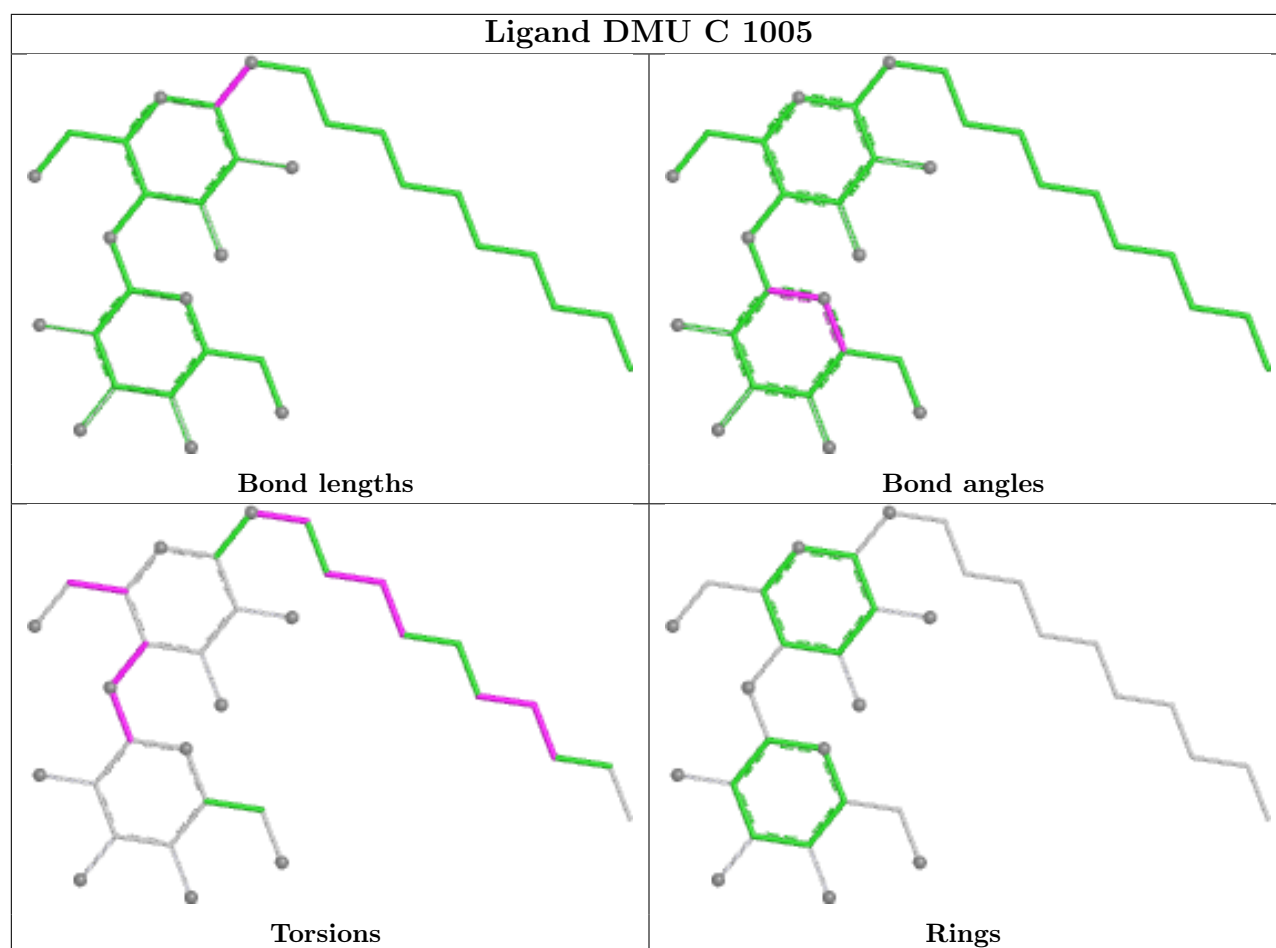
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

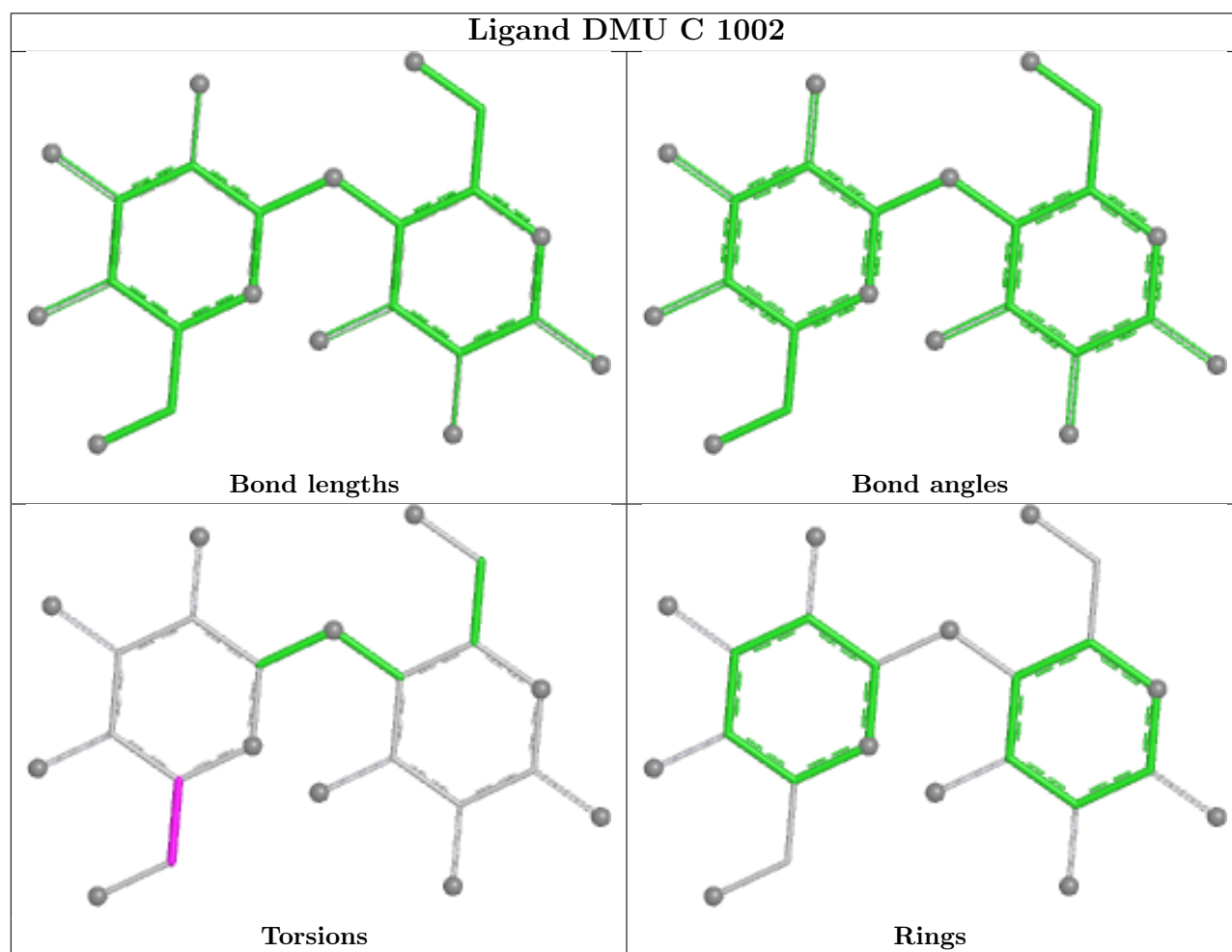
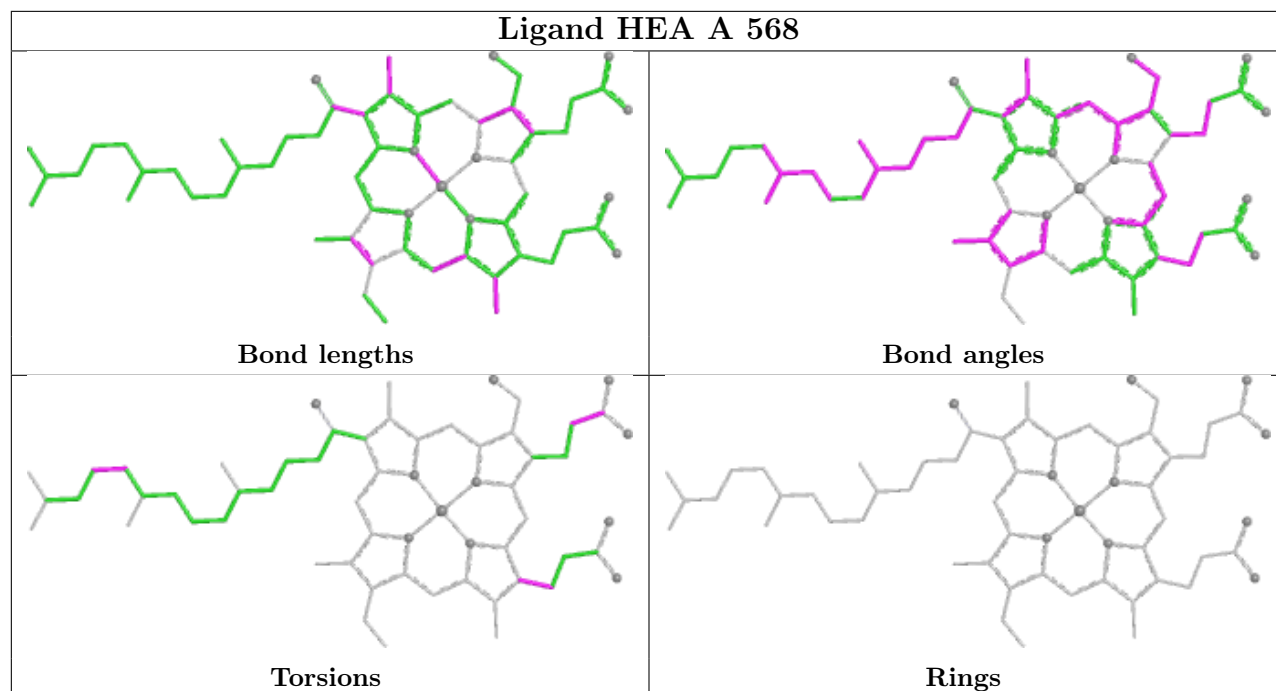
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



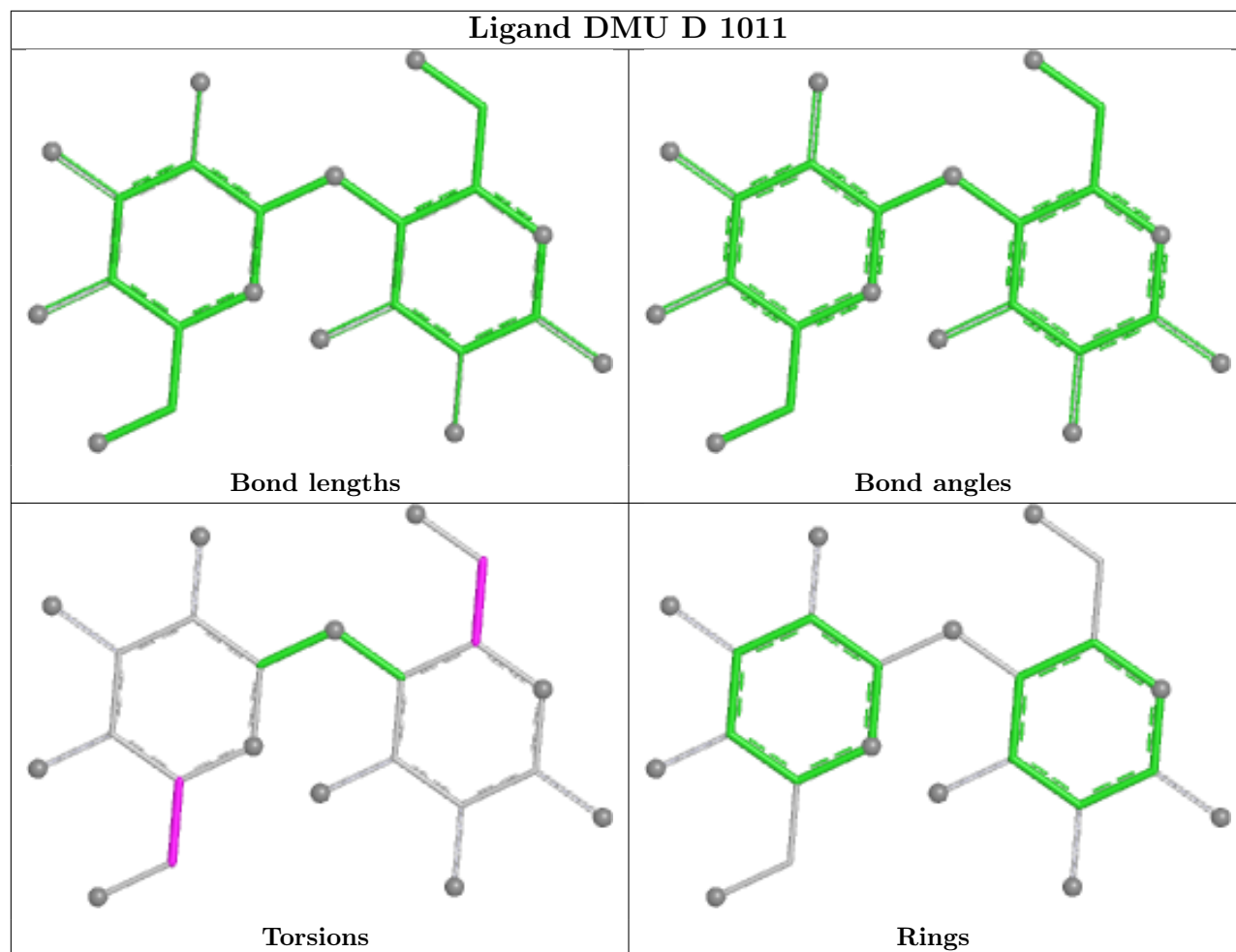


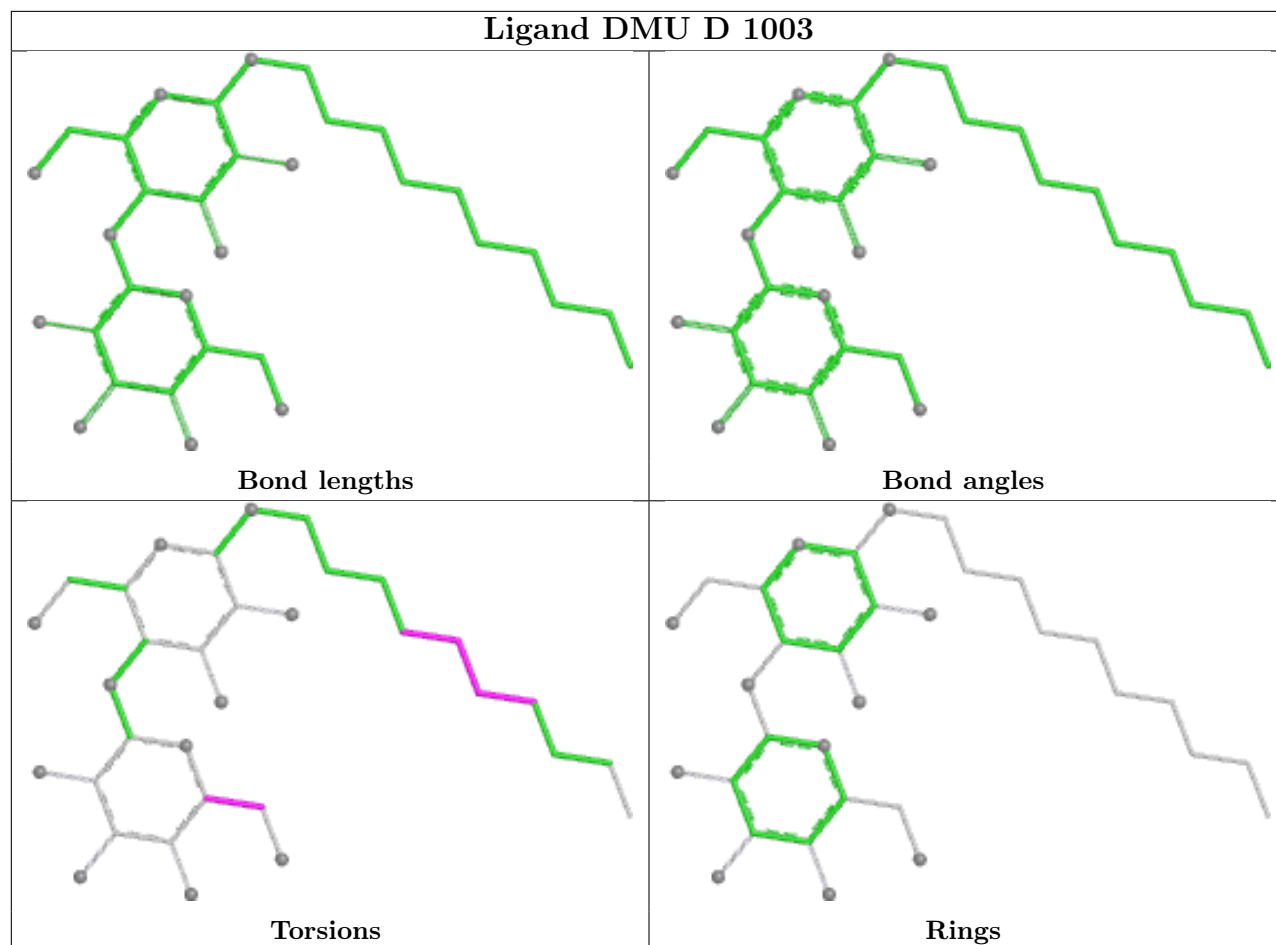




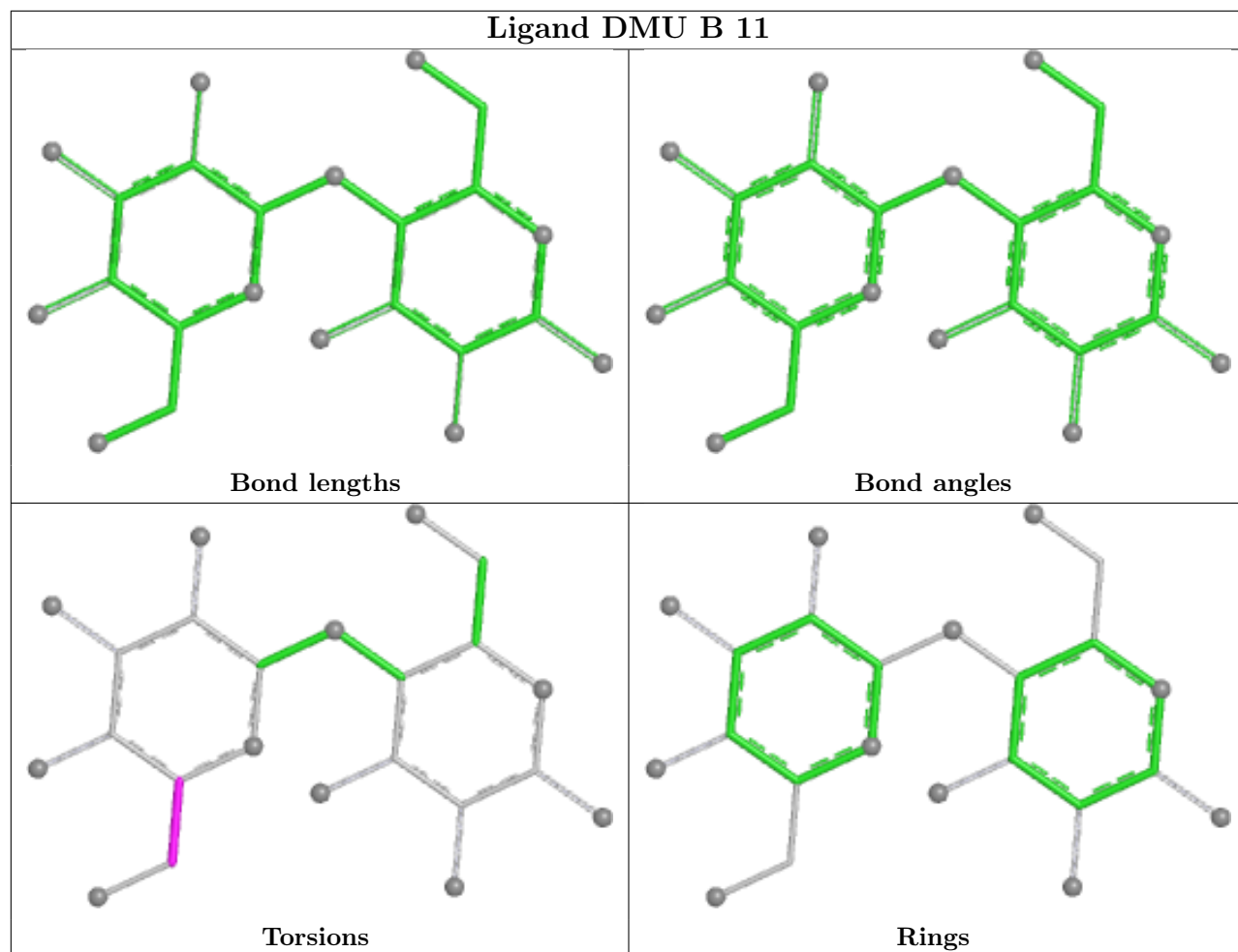


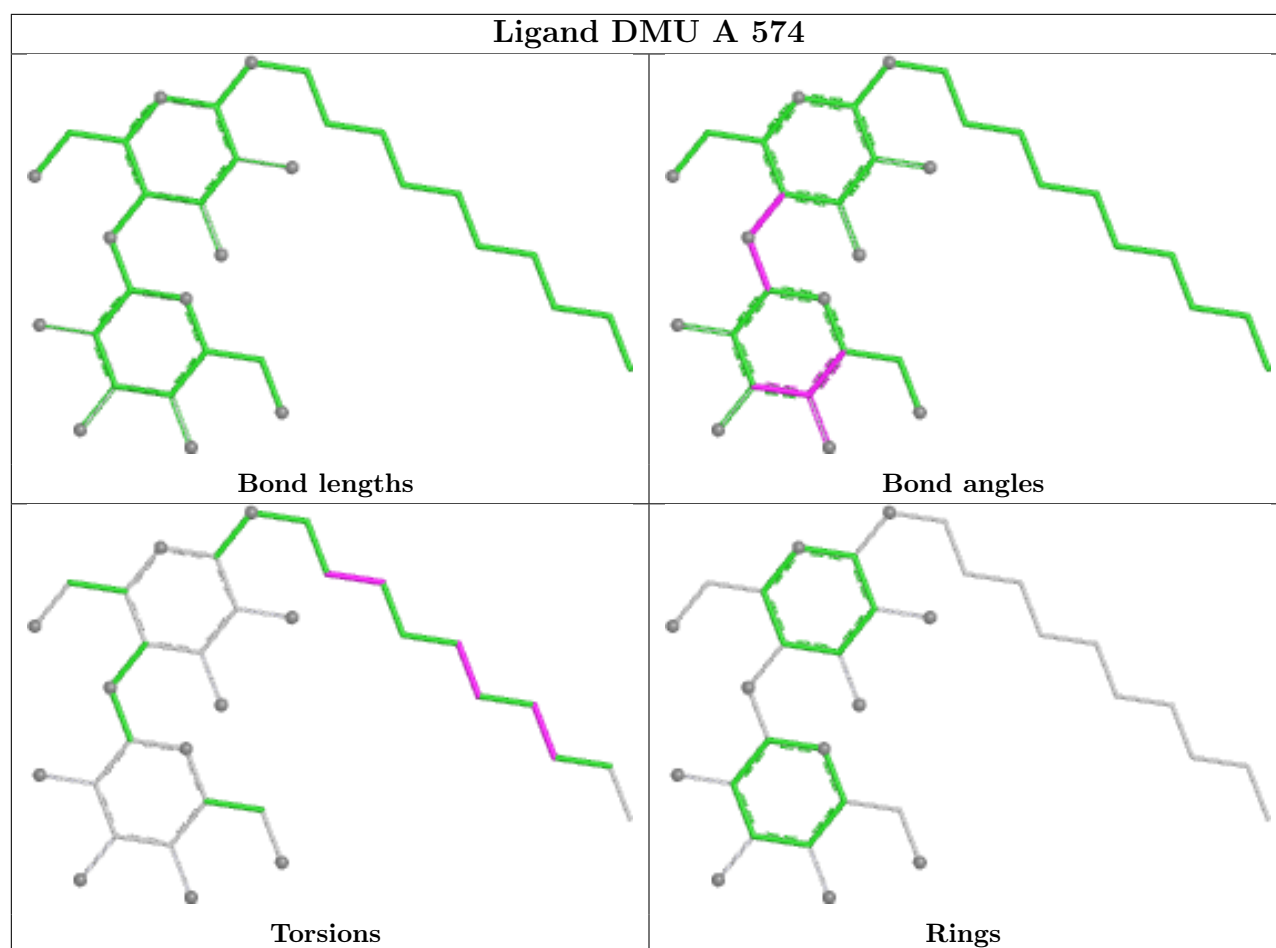
Ligand DMU D 1011





Ligand DMU B 11





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 ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

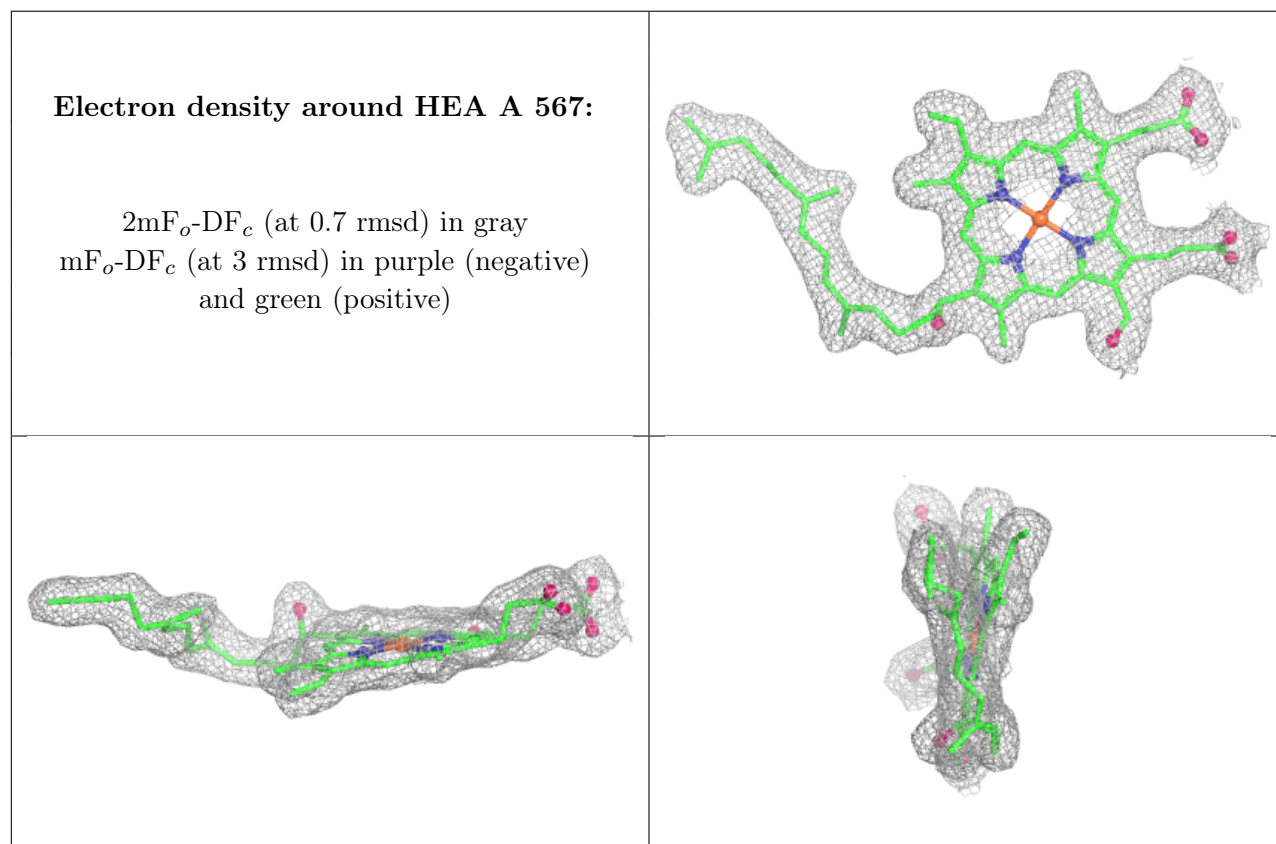
6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

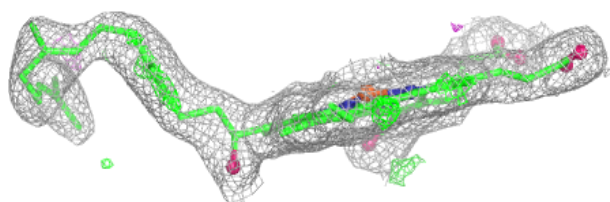
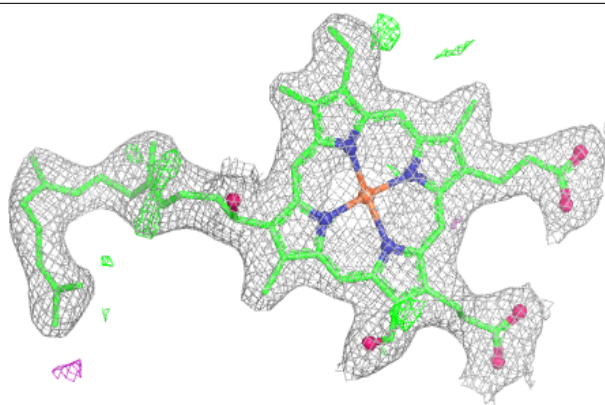
EDS failed to run properly - this section is therefore empty.

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.

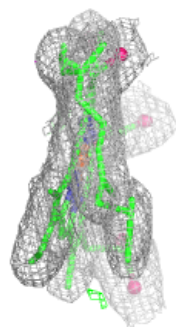
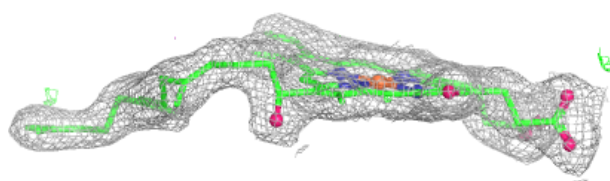
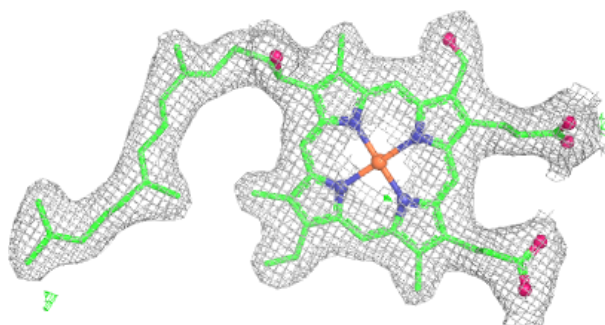


Electron density around HEA A 568:

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

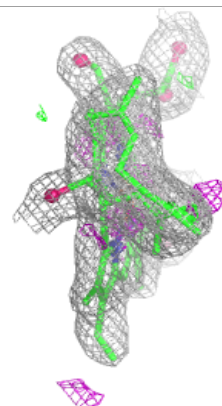
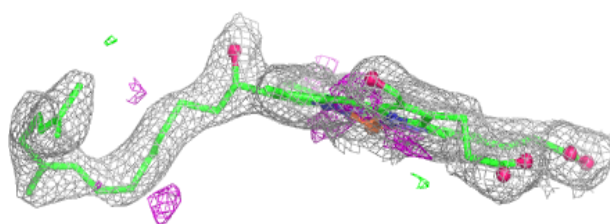
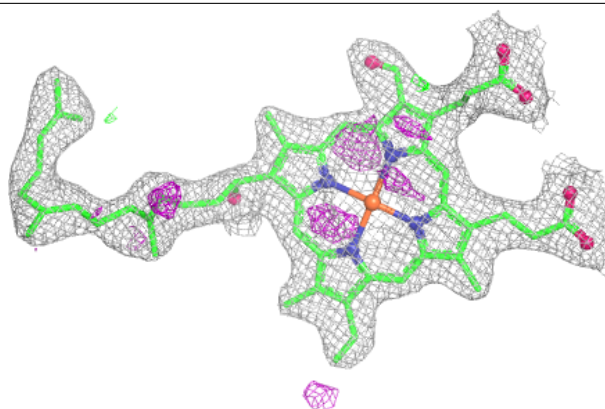
**Electron density around HEA C 567:**

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

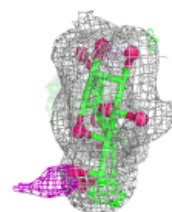
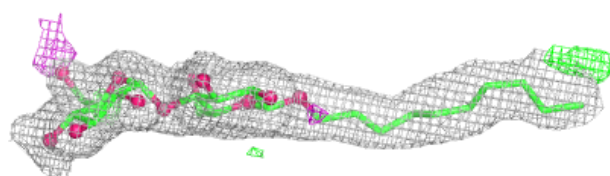
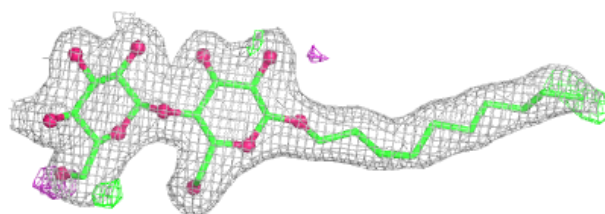


Electron density around HEA C 568:

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

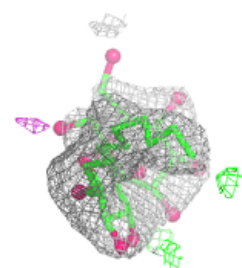
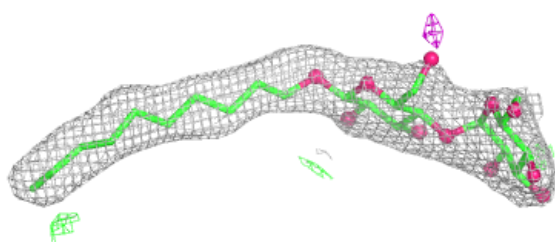
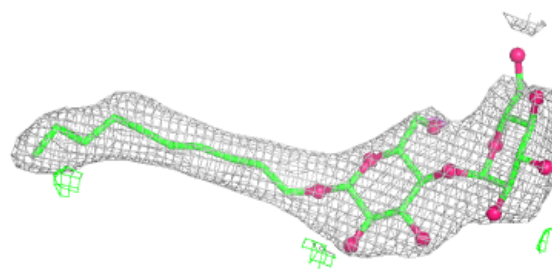
**Electron density around DMU A 574:**

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

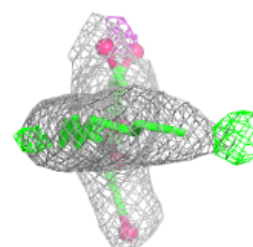
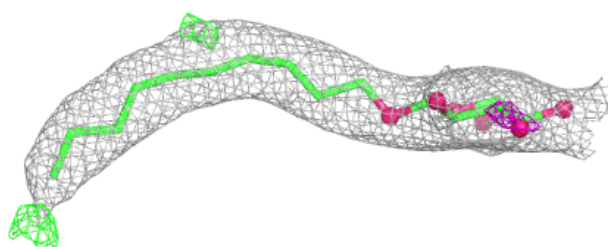
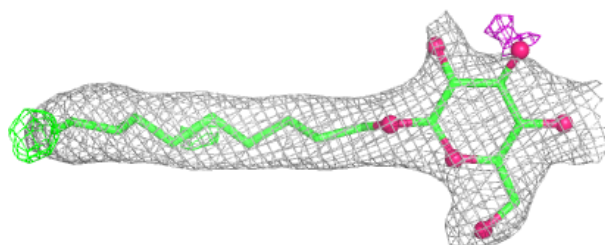


Electron density around DMU A 575:

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

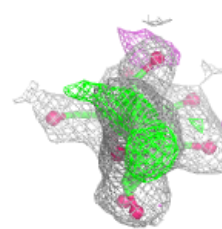
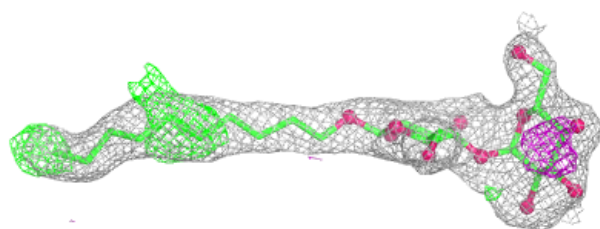
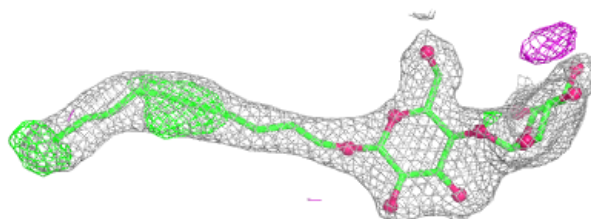
**Electron density around DMU A 576:**

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

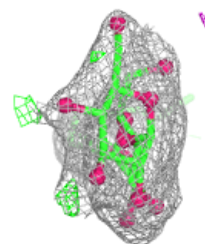
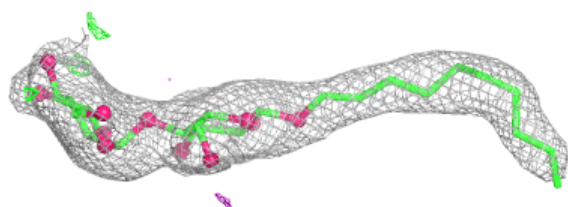
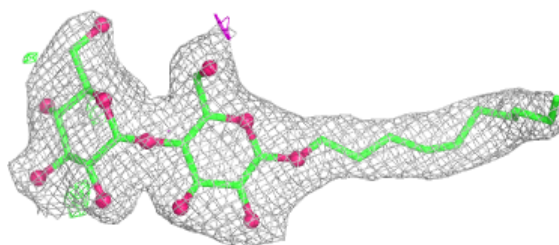


Electron density around DMU A 577:

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

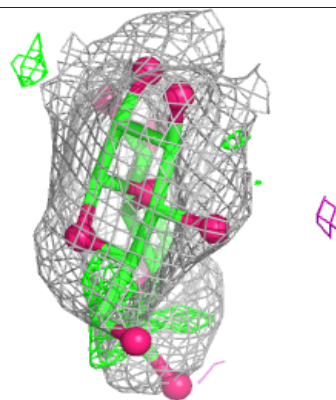
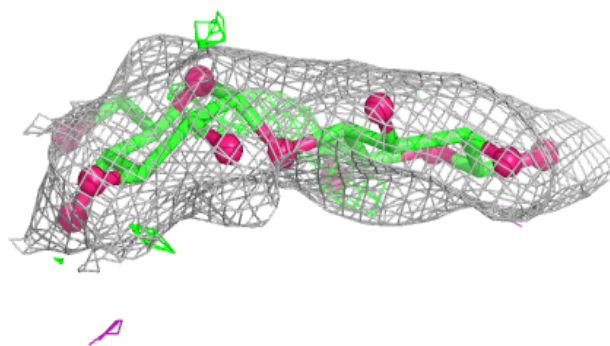
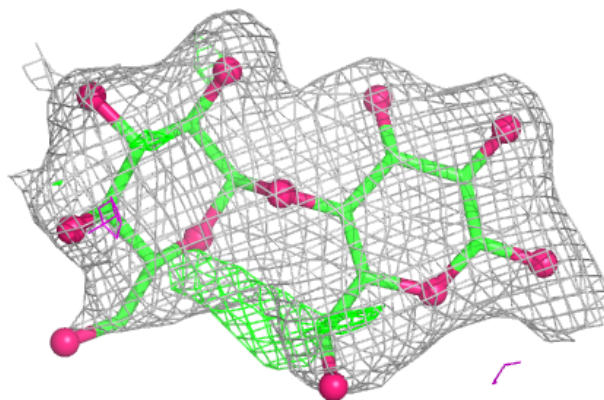
**Electron density around DMU B 288:**

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



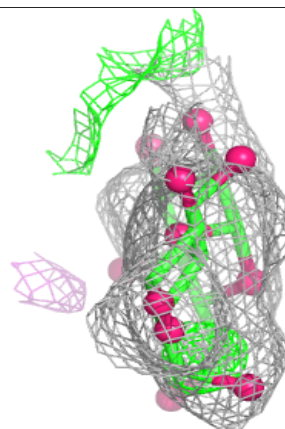
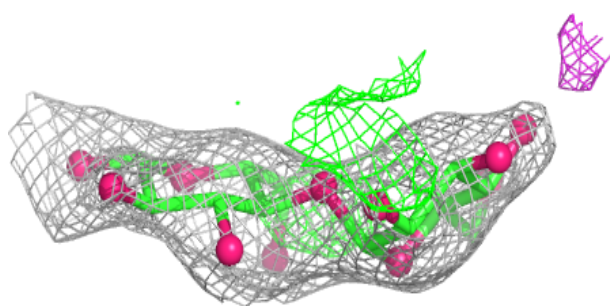
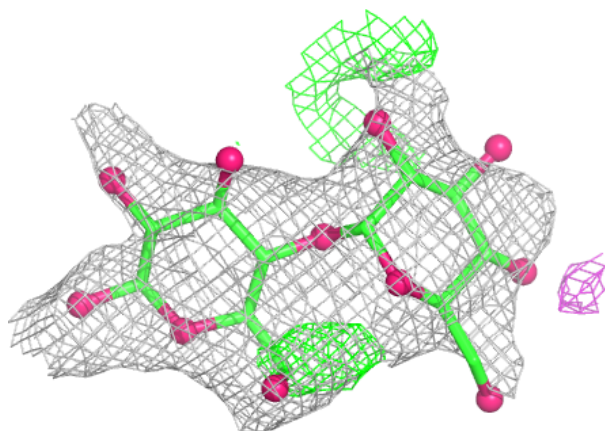
Electron density around DMU B 11:

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

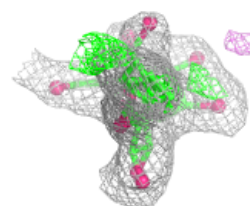
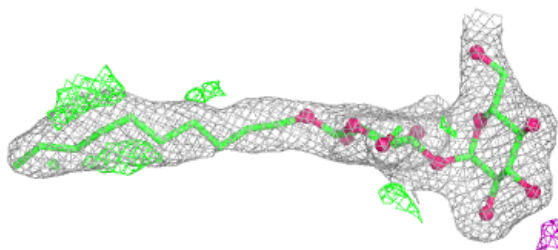
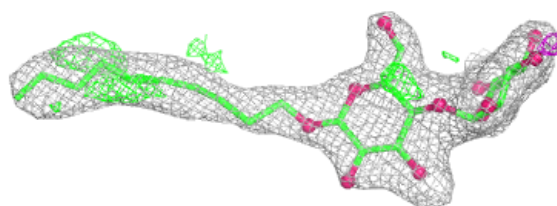


Electron density around DMU C 1002:

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

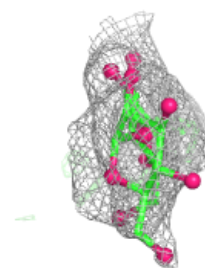
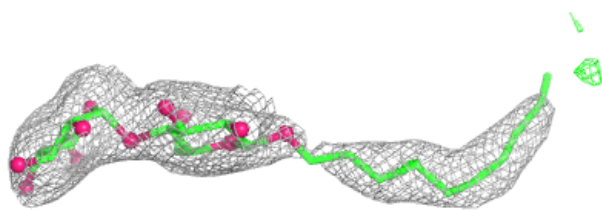
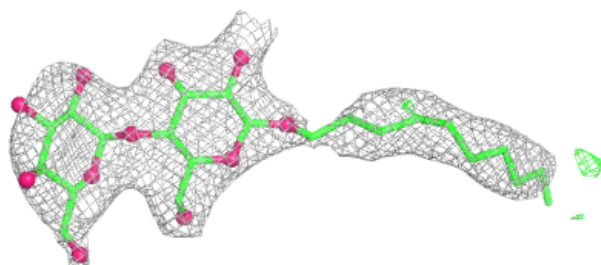
**Electron density around DMU C 1005:**

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

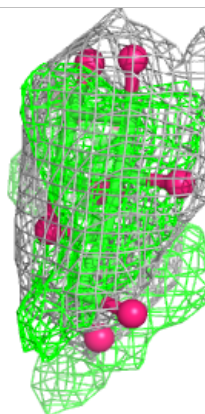
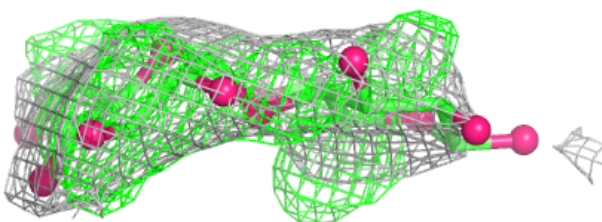
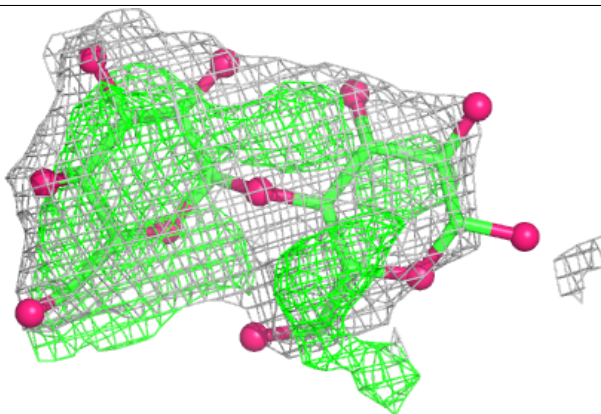


Electron density around DMU D 1003:

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

**Electron density around DMU D 1011:**

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



6.5 Other polymers

EDS failed to run properly - this section is therefore empty.