



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 04:28 AM EDT

PDB ID : 3DTU / pdb_00003dtu
Title : Catalytic core subunits (I and II) of cytochrome c oxidase from Rhodobacter sphaeroides complexed with deoxycholic acid
Authors : Qin, L.; Mills, D.A.; Buhrow, L.; Hiser, C.; Ferguson-Miller, S.
Deposited on : 2008-07-15
Resolution : 2.15 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

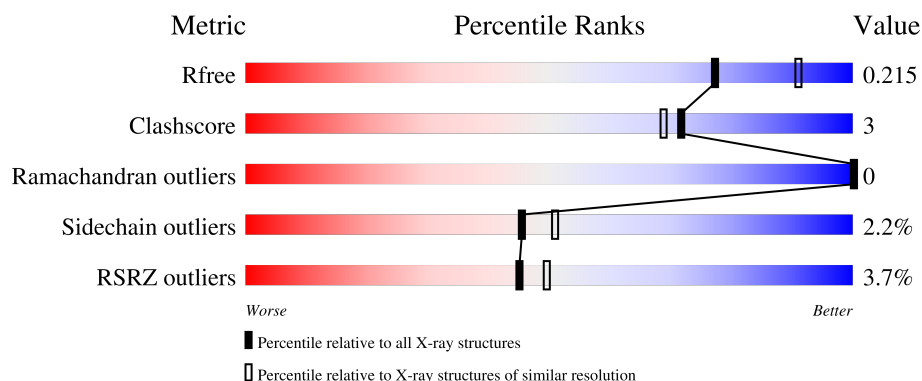
1 Overall quality at a glance

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))
R_{free}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (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.

Mol	Chain	Length	Quality of chain
1	A	566	4% 87% 8% 5%
1	C	566	3% 86% 8% 5%
2	B	262	7% 95% . .
2	D	262	2% 94% . .

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	TRD	C	581	-	-	-	X
10	TRD	C	584	-	-	X	-
12	HTO	B	1	X	-	-	-
3	DMU	A	1002	-	-	-	X
3	DMU	B	1003	-	-	-	X

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 13976 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	539	Total	C	N	O	S	33	0	0
			4249	2845	673	700	31			
1	C	536	Total	C	N	O	S	32	0	0
			4221	2827	664	699	31			

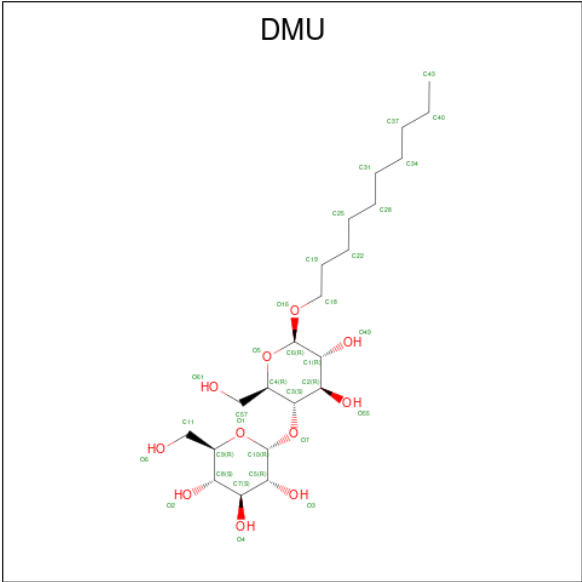
- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	259	Total	C	N	O	S	21	0	0
			2051	1336	340	369	6			
2	D	258	Total	C	N	O	S	15	0	0
			2040	1329	336	369	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 DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			33	22	11		
3	A	1	Total	C	O	0	0
			22	11	11		
3	A	1	Total	C	O	0	0
			22	16	6		
3	A	1	Total	C	O	0	0
			33	22	11		
3	B	1	Total	C	O	0	0
			23	17	6		
3	B	1	Total	C	O	0	0
			23	12	11		
3	C	1	Total	C	O	0	0
			33	22	11		
3	C	1	Total	C	O	0	0
			33	22	11		
3	D	1	Total	C	O	0	0
			33	22	11		

- Molecule 4 is COPPER (II) ION (CCD ID: CU) (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		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	2	Total Cu 2 2	0	0

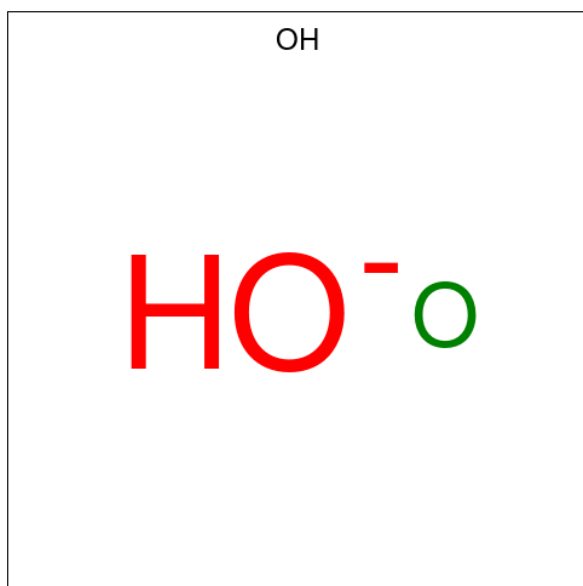
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

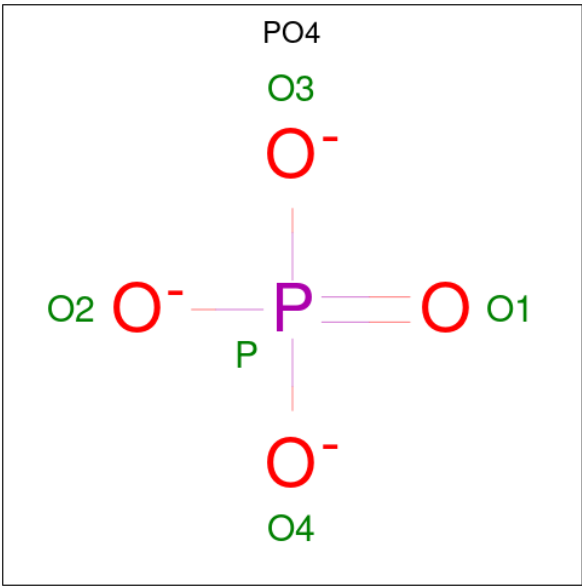
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ca 1 1	0	0
6	C	1	Total Ca 1 1	0	0

- Molecule 7 is HYDROXIDE ION (CCD ID: OH) (formula: HO).



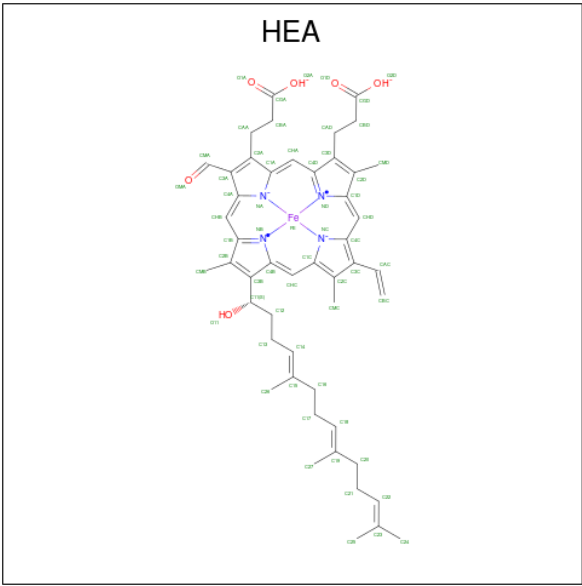
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O 1 1	0	0
7	C	1	Total O 1 1	0	0

- Molecule 8 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	O	P		0	0
			5	4	1			
8	C	1	Total	O	P		0	0
			5	4	1			

- Molecule 9 is HEME-A (CCD ID: HEA) (formula: C₄₉H₅₆FeN₄O₆).



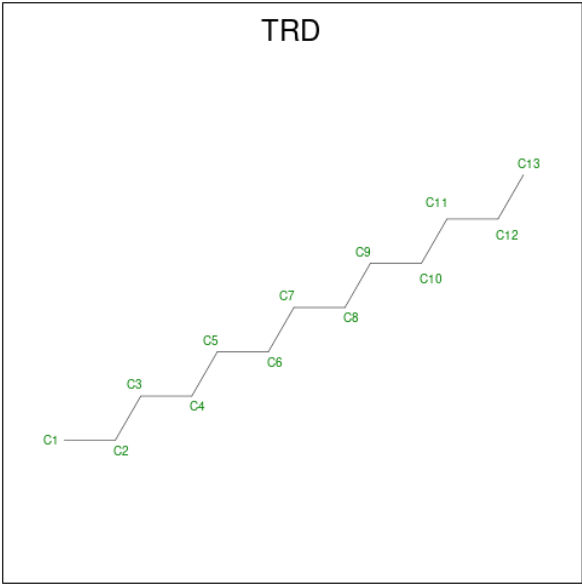
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	Fe	N	O	0
			60	49	1	4	6	

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

- Molecule 10 is TRIDECANE (CCD ID: TRD) (formula: C₁₃H₂₈).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	C	0	0
			13	13		
10	A	1	Total	C	0	0
			11	11		
10	A	1	Total	C	0	0
			13	13		
10	A	1	Total	C	0	0
			7	7		
10	A	1	Total	C	0	0
			11	11		
10	A	1	Total	C	0	0
			7	7		
10	A	1	Total	C	0	0
			7	7		
10	A	1	Total	C	0	0
			11	11		

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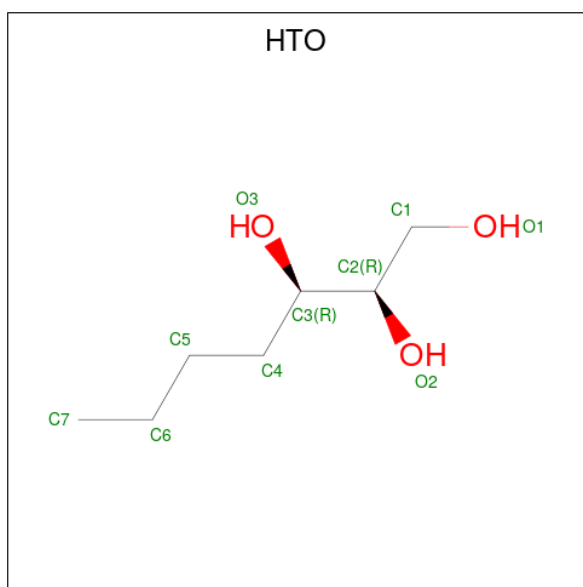
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total C 9 9	0	0
10	B	1	Total C 9 9	0	0
10	B	1	Total C 9 9	0	0
10	C	1	Total C 13 13	0	0
10	C	1	Total C 11 11	0	0
10	C	1	Total C 7 7	0	0
10	C	1	Total C 9 9	0	0
10	C	1	Total C 11 11	0	0
10	C	1	Total C 7 7	0	0
10	C	1	Total C 7 7	0	0
10	C	1	Total C 7 7	0	0
10	D	1	Total C 13 13	0	0
10	D	1	Total C 9 9	0	0
10	D	1	Total C 11 11	0	0
10	D	1	Total C 7 7	0	0

- Molecule 11 is CADMIUM ION (CCD ID: CD) (formula: Cd).

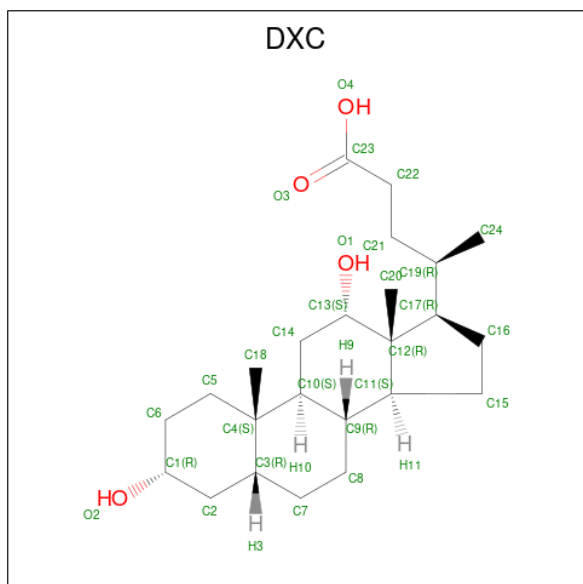
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	B	3	Total Cd 3 3	0	0
11	D	2	Total Cd 2 2	0	0

- Molecule 12 is HEPTANE-1,2,3-TRIOL (CCD ID: HTO) (formula: C₇H₁₆O₃).



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

- Molecule 13 is (3ALPHA,5BETA,12ALPHA)-3,12-DIHYDROXYCHOLAN-24-OIC ACID (CCD ID: DXC) (formula: $C_{24}H_{40}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O	0	0
			28	24	4		

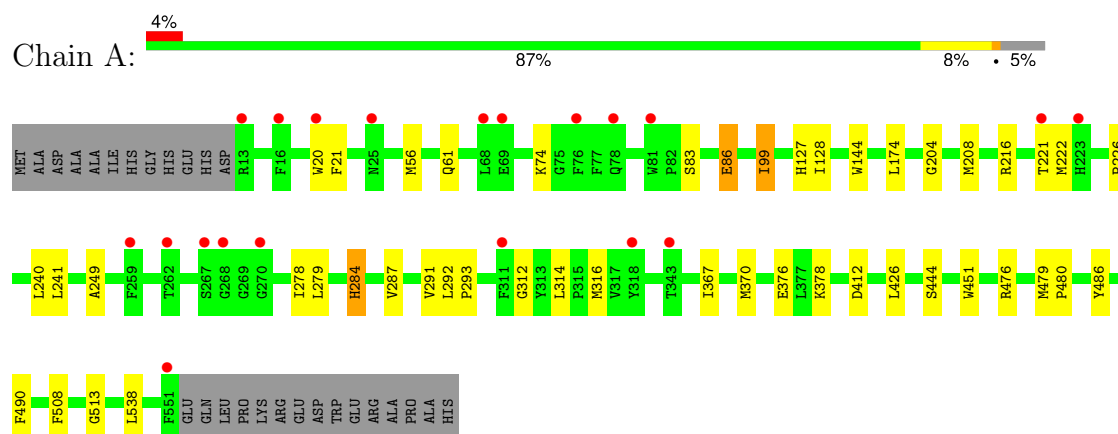
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	144	Total 144	O 144	0	0
14	B	160	Total 160	O 160	0	0
14	C	169	Total 169	O 169	0	0
14	D	163	Total 163	O 163	0	0

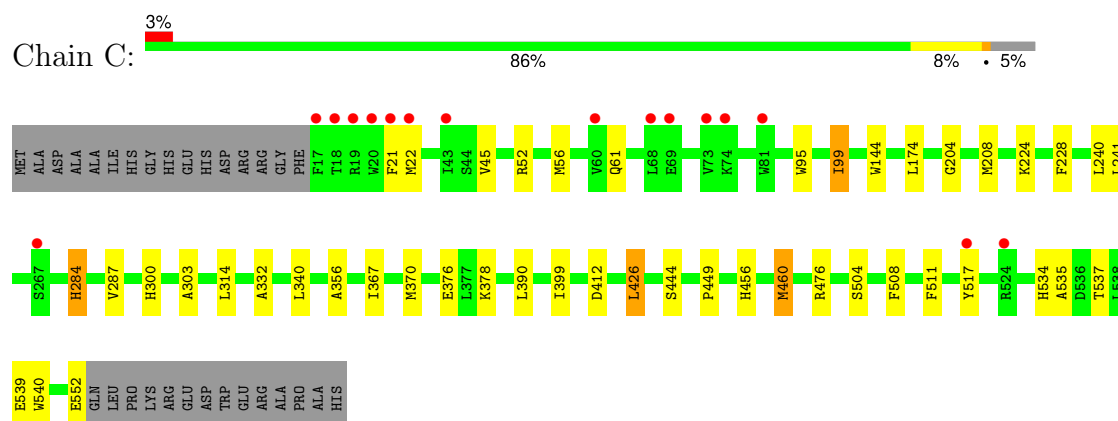
3 Residue-property plots [i](#)

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

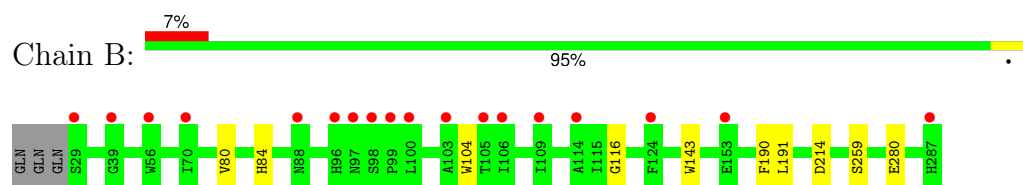
• Molecule 1: Cytochrome c oxidase subunit 1



• 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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	123.24Å 132.05Å 167.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.15 40.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	96.9 (40.00-2.15) 96.9 (40.00-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.184 , 0.212 0.184 , 0.215	Depositor DCC
R_{free} test set	3612 reflections (2.42%)	wwPDB-VP
Wilson B-factor (Å ²)	37.5	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.3	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	0.96	EDS
Total number of atoms	13976	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: HTO, CD, DMU, CA, OH, PO4, DXC, TRD, CU, HEA, MG

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	0.60	0/4406	0.87	2/6010 (0.0%)
1	C	0.64	0/4377	0.88	2/5973 (0.0%)
2	B	0.60	0/2115	0.79	0/2895
2	D	0.62	0/2102	0.79	0/2877
All	All	0.62	0/13000	0.85	4/17755 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	284	HIS	N-CA-CB	8.84	118.79	110.39
1	A	284	HIS	N-CA-CB	6.84	118.50	110.42
1	A	538	LEU	N-CA-C	5.49	118.02	111.71
1	C	284	HIS	CA-CB-CG	-5.18	108.62	113.80

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	4249	0	4172	32	0
1	C	4221	0	4140	39	0
2	B	2051	0	2001	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2040	0	1995	6	0
3	A	110	0	131	8	0
3	B	46	0	52	0	0
3	C	66	0	84	2	0
3	D	33	0	42	0	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
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	1	0
8	A	5	0	0	0	0
8	C	5	0	0	0	0
9	A	120	0	108	3	0
9	C	120	0	108	6	0
10	A	80	0	158	7	0
10	B	27	0	51	1	0
10	C	72	0	139	13	0
10	D	40	0	79	2	0
11	B	3	0	0	0	0
11	D	2	0	0	0	0
12	B	10	0	16	1	0
13	C	28	0	39	0	0
14	A	144	0	0	1	0
14	B	160	0	0	0	0
14	C	169	0	0	3	0
14	D	163	0	0	1	0
All	All	13976	0	13315	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.

All (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)
1:C:303:ALA:HB3	10:C:584:TRD:H21	1.38	1.05
1:C:460:MET:HE3	1:C:460:MET:HA	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:572:OH:O	14:C:589:HOH:O	1.89	0.90
7:A:1501:OH:O	14:A:1511:HOH:O	2.00	0.79
1:C:367:ILE:HA	1:C:370:MET:HE2	1.64	0.78
1:C:390:LEU:HD13	1:C:426:LEU:HD12	1.65	0.78
1:A:56:MET:HE1	3:A:1005:DMU:H7	1.67	0.77
1:C:540:TRP:HE1	10:C:584:TRD:H61	1.49	0.76
1:A:20:TRP:HH2	3:A:1004:DMU:H1	1.52	0.74
1:C:460:MET:HA	1:C:460:MET:CE	2.20	0.72
1:C:228:PHE:H	1:C:300:HIS:HE2	1.38	0.70
3:A:567:DMU:H35	3:A:567:DMU:H29	1.75	0.69
1:C:303:ALA:CB	10:C:584:TRD:H21	2.18	0.68
1:C:537:THR:OG1	10:C:584:TRD:H51	1.94	0.68
1:C:534:HIS:ND1	14:C:747:HOH:O	2.27	0.67
1:C:56:MET:HE1	3:C:567:DMU:H7	1.77	0.67
1:C:476:ARG:HH21	10:D:7:TRD:H12	1.61	0.66
1:A:451:TRP:HZ2	10:A:1504:TRD:H52	1.60	0.66
1:A:513:GLY:HA3	10:A:1504:TRD:H101	1.80	0.63
1:C:303:ALA:HB3	10:C:584:TRD:C2	2.22	0.63
1:C:300:HIS:ND1	10:C:584:TRD:C7	2.62	0.62
1:A:367:ILE:HA	1:A:370:MET:HE2	1.82	0.61
1:A:451:TRP:HE1	10:A:1504:TRD:H32	1.66	0.60
1:C:460:MET:HE1	1:C:504:SER:HB3	1.84	0.59
1:A:20:TRP:CH2	3:A:1004:DMU:H1	2.36	0.58
10:C:584:TRD:H11	14:C:686:HOH:O	2.02	0.58
1:A:204:GLY:O	1:A:208:MET:HG2	2.04	0.57
1:C:456:HIS:CE1	1:C:511:PHE:HB2	2.40	0.56
1:A:21:PHE:HB3	1:A:144:TRP:HZ2	1.70	0.56
1:C:21:PHE:HB3	1:C:144:TRP:HZ2	1.70	0.56
1:C:204:GLY:O	1:C:208:MET:HG2	2.06	0.56
1:C:332:ALA:HB1	1:C:340:LEU:HD11	1.88	0.55
1:C:287:VAL:HB	9:C:575:HEA:CAC	2.36	0.55
1:C:22:MET:HA	1:C:22:MET:HE2	1.89	0.54
1:A:476:ARG:HH21	10:A:1506:TRD:C2	2.20	0.54
1:C:540:TRP:HE1	10:C:584:TRD:C6	2.18	0.53
1:A:287:VAL:HB	9:A:1503:HEA:CAC	2.38	0.53
1:C:535:ALA:HA	10:C:584:TRD:H31	1.91	0.52
9:C:574:HEA:HBC1	9:C:574:HEA:HMC3	1.91	0.51
1:A:284:HIS:C	1:A:284:HIS:CD2	2.87	0.51
1:C:284:HIS:CD2	1:C:284:HIS:C	2.89	0.51
1:A:127:HIS:HB3	1:A:226:PRO:HG2	1.92	0.50
1:C:376:GLU:OE2	1:C:378:LYS:HE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ILE:HG13	9:A:1502:HEA:HBA1	1.94	0.50
1:C:539:GLU:OE2	10:C:584:TRD:C7	2.60	0.50
1:C:444:SER:HA	10:C:577:TRD:H42	1.94	0.49
9:C:574:HEA:HBC1	9:C:574:HEA:CMC	2.42	0.49
1:C:287:VAL:HB	9:C:575:HEA:C3C	2.44	0.48
1:A:249:ALA:HB2	1:A:278:ILE:HG22	1.95	0.47
1:C:300:HIS:HB3	10:C:584:TRD:H62	1.96	0.47
1:A:86:GLU:HG3	2:D:96:HIS:CG	2.49	0.47
1:A:476:ARG:HH21	10:A:1506:TRD:H21	1.79	0.46
1:C:95:TRP:CE2	1:C:99:ILE:HD13	2.50	0.46
1:C:508:PHE:HB2	9:C:574:HEA:H261	1.97	0.46
1:A:486:TYR:CD2	1:A:490:PHE:HB2	2.50	0.46
1:A:83:SER:HA	3:A:567:DMU:H41	1.98	0.45
1:C:45:VAL:HG21	9:C:574:HEA:H171	1.96	0.45
2:B:280:GLU:HB2	12:B:1:HTO:H73	1.98	0.45
1:A:451:TRP:CZ2	10:A:1504:TRD:H52	2.46	0.45
3:A:567:DMU:H18	2:D:75:LEU:HD13	1.97	0.45
2:D:228:GLN:NE2	14:D:387:HOH:O	2.47	0.45
1:A:279:LEU:O	1:A:279:LEU:HG	2.14	0.44
2:B:80:VAL:O	2:B:84:HIS:HB2	2.17	0.44
2:B:190:PHE:O	2:B:191:LEU:HB2	2.17	0.44
1:A:476:ARG:HH21	10:A:1506:TRD:H22	1.81	0.44
1:A:21:PHE:HB3	1:A:144:TRP:CZ2	2.50	0.44
1:A:376:GLU:HG2	1:A:378:LYS:HG2	2.00	0.44
1:A:444:SER:HA	3:A:1004:DMU:H5	1.99	0.44
1:A:284:HIS:CD2	1:A:284:HIS:O	2.71	0.43
1:A:128:ILE:HB	1:A:216:ARG:HG2	2.00	0.43
1:A:508:PHE:HB2	9:A:1502:HEA:H261	2.01	0.42
2:D:98:SER:HB3	2:D:99:PRO:HD3	2.01	0.42
1:C:537:THR:HG23	10:C:584:TRD:H42	2.01	0.42
2:B:116:GLY:HA3	10:B:1023:TRD:H42	2.02	0.42
2:B:143:TRP:CG	2:B:259:SER:HB2	2.55	0.41
1:C:460:MET:HE1	1:C:504:SER:CB	2.50	0.41
2:D:220:THR:O	2:D:250:GLY:HA3	2.20	0.41
1:A:479:MET:HA	1:A:480:PRO:HD3	1.89	0.41
1:C:449:PRO:HG3	1:C:517:TYR:CE2	2.56	0.41
1:C:460:MET:CE	1:C:460:MET:CA	2.95	0.41
1:A:292:LEU:HB2	1:A:293:PRO:HD3	2.03	0.41
1:C:356:ALA:HB2	1:C:399:ILE:HD11	2.03	0.41
1:C:476:ARG:NH2	10:D:7:TRD:H12	2.33	0.41
1:C:56:MET:HE1	3:C:567:DMU:C18	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLY:O	1:A:316:MET:HG2	2.21	0.40
1:A:56:MET:HE1	3:A:1005:DMU:H10	2.04	0.40
2:D:138:VAL:HG11	2:D:219:TRP:CD1	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	537/566 (95%)	525 (98%)	12 (2%)	0	100	100
1	C	534/566 (94%)	526 (98%)	8 (2%)	0	100	100
2	B	257/262 (98%)	250 (97%)	7 (3%)	0	100	100
2	D	256/262 (98%)	251 (98%)	5 (2%)	0	100	100
All	All	1584/1656 (96%)	1552 (98%)	32 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	438/459 (95%)	425 (97%)	13 (3%)	36	38
1	C	436/459 (95%)	424 (97%)	12 (3%)	38	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	218/221 (99%)	216 (99%)	2 (1%)	70	77
2	D	217/221 (98%)	215 (99%)	2 (1%)	70	77
All	All	1309/1360 (96%)	1280 (98%)	29 (2%)	45	51

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	74	LYS
1	A	86	GLU
1	A	99	ILE
1	A	174	LEU
1	A	221	THR
1	A	222	MET
1	A	240	LEU
1	A	241	LEU
1	A	291	VAL
1	A	314	LEU
1	A	412	ASP
1	A	426	LEU
2	B	104	TRP
2	B	214	ASP
1	C	52	ARG
1	C	61	GLN
1	C	99	ILE
1	C	174	LEU
1	C	224	LYS
1	C	240	LEU
1	C	241	LEU
1	C	314	LEU
1	C	412	ASP
1	C	426	LEU
1	C	460	MET
1	C	552	GLU
2	D	30	LEU
2	D	104	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	ASN
1	A	163	ASN
1	A	165	GLN
1	A	223	HIS
1	A	465	ASN
2	B	96	HIS
2	B	125	ASN
2	B	170	ASN
1	C	140	ASN
1	C	163	ASN
2	D	125	ASN
2	D	170	ASN
2	D	178	GLN
2	D	179	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 57 ligands modelled in this entry, 15 are monoatomic and 2 are modelled with single atom - leaving 40 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
3	DMU	C	567	-	34,34,34	0.65	1 (2%)	45,45,45	0.74	1 (2%)
13	DXC	C	576	11	31,31,31	0.60	0	49,49,49	1.31	7 (14%)
3	DMU	A	1005	-	34,34,34	0.60	0	45,45,45	0.67	0
10	TRD	C	580	-	8,8,12	0.25	0	7,7,11	0.45	0
10	TRD	A	1013	-	6,6,12	0.28	0	5,5,11	0.31	0
10	TRD	D	12	-	10,10,12	0.27	0	9,9,11	0.41	0
9	HEA	A	1503	14,1	67,67,67	1.55	8 (11%)	81,103,103	1.44	14 (17%)
10	TRD	A	1506	-	12,12,12	0.24	0	11,11,11	0.52	0
3	DMU	A	567	-	34,34,34	0.55	0	45,45,45	0.76	1 (2%)
3	DMU	C	568	-	34,34,34	0.58	1 (2%)	45,45,45	0.80	1 (2%)
9	HEA	C	574	1	67,67,67	1.09	5 (7%)	81,103,103	0.93	3 (3%)
10	TRD	C	579	-	6,6,12	0.26	0	5,5,11	0.31	0
10	TRD	D	23	-	6,6,12	0.22	0	5,5,11	0.44	0
8	PO4	C	573	-	4,4,4	0.92	0	6,6,6	0.37	0
10	TRD	D	7	-	12,12,12	0.24	0	11,11,11	0.58	0
10	TRD	B	1023	-	8,8,12	0.25	0	7,7,11	0.45	0
10	TRD	A	1504	-	12,12,12	0.28	0	11,11,11	0.45	0
3	DMU	B	1003	-	23,23,34	0.56	0	28,28,45	0.64	0
10	TRD	C	584	-	6,6,12	0.10	0	5,5,11	0.58	0
10	TRD	B	1031	-	8,8,12	0.28	0	7,7,11	0.37	0
10	TRD	A	1505	-	10,10,12	0.26	0	9,9,11	0.47	0
10	TRD	B	1012	-	8,8,12	0.26	0	7,7,11	0.43	0
10	TRD	C	577	-	12,12,12	0.29	0	11,11,11	0.42	0
10	TRD	A	1009	-	6,6,12	0.23	0	5,5,11	0.41	0
12	HTO	B	1	-	9,9,9	0.21	0	10,10,10	0.82	0
9	HEA	C	575	14,1	67,67,67	1.50	8 (11%)	81,103,103	1.42	11 (13%)
10	TRD	C	582	-	6,6,12	0.25	0	5,5,11	0.39	0
8	PO4	A	1001	-	4,4,4	0.94	0	6,6,6	0.46	0
10	TRD	D	288	-	8,8,12	0.24	0	7,7,11	0.44	0
3	DMU	A	1002	-	21,21,34	0.56	0	26,28,45	0.82	0
9	HEA	A	1502	1	67,67,67	1.10	6 (8%)	81,103,103	1.01	5 (6%)
10	TRD	C	581	-	10,10,12	0.27	0	9,9,11	0.50	0
10	TRD	C	578	-	10,10,12	0.30	0	9,9,11	0.39	0
10	TRD	A	1015	-	10,10,12	0.27	0	9,9,11	0.50	0
3	DMU	B	1011	-	24,24,34	0.50	0	35,35,45	0.75	0
3	DMU	A	1004	-	22,22,34	0.62	1 (4%)	27,27,45	0.89	1 (3%)
10	TRD	C	583	-	6,6,12	0.22	0	5,5,11	0.45	0
10	TRD	A	1014	-	6,6,12	0.22	0	5,5,11	0.43	0
3	DMU	D	11	-	34,34,34	0.57	0	45,45,45	0.79	1 (2%)
10	TRD	A	1010	-	10,10,12	0.25	0	9,9,11	0.51	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
3	DMU	C	567	-	-	7/19/59/59	0/2/2/2
13	DXC	C	576	11	-	5/9/71/71	0/4/4/4
3	DMU	A	1005	-	-	11/19/59/59	0/2/2/2
10	TRD	C	580	-	-	3/6/6/10	-
10	TRD	A	1013	-	-	2/4/4/10	-
10	TRD	D	12	-	-	4/8/8/10	-
9	HEA	A	1503	14,1	-	7/36/76/76	-
10	TRD	A	1506	-	-	7/10/10/10	-
3	DMU	A	567	-	-	9/19/59/59	0/2/2/2
3	DMU	C	568	-	-	9/19/59/59	0/2/2/2
9	HEA	C	574	1	-	5/36/76/76	-
10	TRD	C	579	-	-	1/4/4/10	-
10	TRD	D	23	-	-	2/4/4/10	-
10	TRD	D	7	-	-	6/10/10/10	-
10	TRD	B	1023	-	-	1/6/6/10	-
10	TRD	A	1504	-	-	4/10/10/10	-
3	DMU	B	1003	-	-	9/15/35/59	0/1/1/2
10	TRD	C	584	-	-	2/4/4/10	-
10	TRD	B	1031	-	-	3/6/6/10	-
10	TRD	A	1505	-	-	6/8/8/10	-
10	TRD	B	1012	-	-	4/6/6/10	-
10	TRD	C	577	-	-	4/10/10/10	-
10	TRD	A	1009	-	-	3/4/4/10	-
12	HTO	B	1	-	1/1/2/2	5/10/10/10	-
9	HEA	C	575	14,1	-	5/36/76/76	-
10	TRD	C	582	-	-	4/4/4/10	-
10	TRD	D	288	-	-	3/6/6/10	-
3	DMU	A	1002	-	-	2/16/37/59	0/1/1/2
9	HEA	A	1502	1	-	6/36/76/76	-
10	TRD	C	581	-	-	3/8/8/10	-
10	TRD	C	578	-	-	4/8/8/10	-
10	TRD	A	1015	-	-	4/8/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMU	B	1011	-	-	4/8/48/59	0/2/2/2
3	DMU	A	1004	-	-	8/13/33/59	0/1/1/2
10	TRD	C	583	-	-	3/4/4/10	-
10	TRD	A	1014	-	-	3/4/4/10	-
3	DMU	D	11	-	-	4/19/59/59	0/2/2/2
10	TRD	A	1010	-	-	4/8/8/10	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1503	HEA	FE-NA	5.08	2.11	1.95
9	A	1503	HEA	FE-NC	4.87	2.11	1.95
9	C	575	HEA	FE-NB	4.76	2.09	1.94
9	C	575	HEA	FE-NC	4.64	2.10	1.95
9	A	1503	HEA	FE-ND	4.47	2.08	1.94
9	C	575	HEA	FE-ND	4.45	2.08	1.94
9	A	1503	HEA	C11-C3B	4.28	1.56	1.51
9	C	575	HEA	FE-NA	4.18	2.09	1.95
9	A	1503	HEA	FE-NB	4.07	2.07	1.94
9	C	575	HEA	C11-C3B	3.69	1.55	1.51
9	C	574	HEA	C11-C3B	3.44	1.55	1.51
9	A	1502	HEA	C11-C3B	3.07	1.55	1.51
9	A	1502	HEA	CMA-C3A	3.01	1.52	1.45
9	A	1502	HEA	CAC-C3C	2.69	1.54	1.47
9	C	574	HEA	CMA-C3A	2.62	1.51	1.45
9	C	575	HEA	CMA-C3A	2.61	1.51	1.45
9	A	1503	HEA	CAC-C3C	2.61	1.54	1.47
9	A	1503	HEA	CMA-C3A	2.55	1.51	1.45
9	C	575	HEA	CAC-C3C	2.51	1.54	1.47
9	A	1503	HEA	CMD-C2D	2.50	1.55	1.50
9	C	575	HEA	CMD-C2D	2.47	1.55	1.50
9	A	1502	HEA	CMB-C2B	2.45	1.55	1.50
9	C	574	HEA	CAC-C3C	2.38	1.53	1.47
3	A	1004	DMU	O16-C6	2.16	1.43	1.40
9	A	1502	HEA	CMD-C2D	2.13	1.55	1.50
9	C	574	HEA	C3C-C2C	-2.12	1.34	1.41
3	C	567	DMU	O16-C6	2.07	1.43	1.40
9	A	1502	HEA	C3C-C2C	-2.06	1.34	1.41
9	C	574	HEA	CMB-C2B	2.03	1.54	1.50
3	C	568	DMU	O16-C6	2.01	1.43	1.40

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	575	HEA	CAD-CBD-CGD	-4.76	101.03	113.67
9	A	1503	HEA	C2A-C1A-NA	-3.79	106.67	110.32
13	C	576	DXC	C21-C19-C17	3.49	117.57	110.33
9	C	575	HEA	C3C-C4C-NC	-3.27	107.04	109.80
9	C	575	HEA	C2A-C1A-NA	-3.26	107.17	110.32
13	C	576	DXC	C16-C17-C19	3.08	116.85	112.18
3	A	1004	DMU	O16-C6-C1	2.88	112.65	108.27
9	A	1503	HEA	C4B-NB-C1B	2.88	108.62	105.21
9	A	1503	HEA	CAD-CBD-CGD	-2.88	106.02	113.67
9	A	1503	HEA	C4A-NA-C1A	2.82	110.42	105.82
9	A	1503	HEA	C27-C19-C20	2.79	120.08	115.23
9	C	575	HEA	C1D-ND-C4D	2.74	108.45	105.21
9	A	1502	HEA	CAD-CBD-CGD	-2.72	106.45	113.67
9	C	574	HEA	C27-C19-C20	2.68	119.88	115.23
9	A	1503	HEA	C2B-C1B-NB	-2.60	106.89	109.90
9	A	1502	HEA	C17-C18-C19	-2.58	121.73	127.62
9	A	1503	HEA	CMB-C2B-C3B	-2.55	125.35	130.28
13	C	576	DXC	C2-C1-C6	2.49	113.65	110.62
13	C	576	DXC	C12-C17-C19	-2.45	116.52	119.48
9	C	574	HEA	CAD-CBD-CGD	-2.43	107.21	113.67
13	C	576	DXC	C18-C4-C5	-2.43	104.44	108.31
9	C	575	HEA	C4B-NB-C1B	2.43	108.08	105.21
9	A	1503	HEA	C4A-C3A-C2A	2.42	108.91	106.81
13	C	576	DXC	C5-C6-C1	2.40	113.66	110.48
9	C	575	HEA	C3D-C4D-ND	-2.37	108.06	110.35
9	A	1503	HEA	CBA-CAA-C2A	-2.32	106.12	112.53
9	C	575	HEA	OMA-CMA-C3A	-2.25	120.53	125.62
9	C	574	HEA	C17-C18-C19	-2.23	122.52	127.62
9	A	1503	HEA	C3C-C4C-NC	-2.18	107.97	109.80
9	A	1502	HEA	C13-C12-C11	-2.17	110.93	114.39
3	C	568	DMU	C10-O1-C9	2.16	117.94	113.72
13	C	576	DXC	C14-C10-C4	2.14	115.88	113.70
9	C	575	HEA	CMB-C2B-C3B	-2.13	126.15	130.28
3	C	567	DMU	O7-C3-C2	2.13	112.63	107.23
9	C	575	HEA	C27-C19-C20	2.12	118.91	115.23
9	A	1502	HEA	C25-C23-C24	2.11	119.45	114.59
9	C	575	HEA	C4C-NC-C1C	2.11	109.26	105.82
9	A	1502	HEA	C13-C14-C15	-2.08	122.85	127.62
3	A	567	DMU	O1-C9-C11	2.05	111.53	106.44
3	D	11	DMU	C10-O7-C3	-2.05	113.11	117.98
9	A	1503	HEA	CHB-C4A-C3A	2.05	128.67	125.21
9	A	1503	HEA	C1D-ND-C4D	2.04	107.63	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1503	HEA	OMA-CMA-C3A	-2.03	121.03	125.62
9	C	575	HEA	C2D-C1D-ND	-2.03	107.51	109.84
9	A	1503	HEA	C3D-C4D-ND	-2.03	108.39	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
12	B	1	HTO	C2

All (176) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	567	DMU	C19-C18-O16-C6
3	A	1002	DMU	C3-C4-O5-C6
3	A	1002	DMU	C57-C4-O5-C6
3	A	1004	DMU	C1-C6-O16-C18
3	A	1004	DMU	O5-C6-O16-C18
12	B	1	HTO	O1-C1-C2-C3
12	B	1	HTO	C2-C3-C4-C5
12	B	1	HTO	O1-C1-C2-O2
3	A	567	DMU	O6-C11-C9-O1
3	C	568	DMU	O6-C11-C9-O1
3	D	11	DMU	O6-C11-C9-O1
3	B	1011	DMU	O5-C4-C57-O61
3	D	11	DMU	O6-C11-C9-C8
3	B	1011	DMU	C3-C4-C57-O61
3	C	568	DMU	O6-C11-C9-C8
3	B	1011	DMU	O6-C11-C9-O1
3	B	1003	DMU	O5-C4-C57-O61
3	A	567	DMU	O5-C6-O16-C18
3	B	1003	DMU	C3-C4-C57-O61
13	C	576	DXC	C12-C17-C19-C21
3	A	1005	DMU	O1-C10-O7-C3
3	C	567	DMU	O1-C10-O7-C3
3	A	567	DMU	O6-C11-C9-C8
3	A	567	DMU	C1-C6-O16-C18
3	B	1003	DMU	C1-C6-O16-C18
12	B	1	HTO	O3-C3-C4-C5
3	B	1003	DMU	O5-C6-O16-C18
10	D	12	TRD	C3-C4-C5-C6
13	C	576	DXC	C16-C17-C19-C21
10	C	578	TRD	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
3	A	1005	DMU	C18-C19-C22-C25
3	C	567	DMU	C28-C31-C34-C37
10	A	1010	TRD	C5-C6-C7-C8
10	A	1015	TRD	C5-C6-C7-C8
10	B	1031	TRD	C2-C3-C4-C5
10	C	580	TRD	C2-C3-C4-C5
10	D	23	TRD	C2-C3-C4-C5
10	C	580	TRD	C3-C4-C5-C6
10	C	581	TRD	C4-C5-C6-C7
3	C	568	DMU	C28-C31-C34-C37
10	D	12	TRD	C6-C7-C8-C9
10	A	1504	TRD	C5-C6-C7-C8
3	C	568	DMU	C22-C25-C28-C31
10	C	577	TRD	C5-C6-C7-C8
3	C	568	DMU	C18-C19-C22-C25
10	C	577	TRD	C3-C4-C5-C6
10	C	577	TRD	C4-C5-C6-C7
10	A	1506	TRD	C4-C5-C6-C7
3	C	567	DMU	C18-C19-C22-C25
3	B	1003	DMU	C31-C34-C37-C40
10	C	578	TRD	C7-C8-C9-C10
10	A	1505	TRD	C6-C7-C8-C9
3	D	11	DMU	C19-C22-C25-C28
10	C	582	TRD	C2-C3-C4-C5
3	B	1003	DMU	C25-C28-C31-C34
10	C	582	TRD	C3-C4-C5-C6
10	A	1506	TRD	C2-C3-C4-C5
10	C	584	TRD	C3-C4-C5-C6
10	A	1505	TRD	C4-C5-C6-C7
10	B	1012	TRD	C3-C4-C5-C6
3	A	1005	DMU	C28-C31-C34-C37
10	A	1010	TRD	C4-C5-C6-C7
10	A	1504	TRD	C3-C4-C5-C6
10	A	1014	TRD	C2-C3-C4-C5
10	A	1015	TRD	C7-C8-C9-C10
3	A	567	DMU	C22-C25-C28-C31
10	A	1505	TRD	C5-C6-C7-C8
10	C	581	TRD	C3-C4-C5-C6
3	D	11	DMU	C28-C31-C34-C37
10	D	7	TRD	C6-C7-C8-C9
10	D	12	TRD	C4-C5-C6-C7
10	A	1010	TRD	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
13	C	576	DXC	C16-C17-C19-C24
3	C	568	DMU	C25-C28-C31-C34
10	A	1505	TRD	C7-C8-C9-C10
10	A	1506	TRD	C9-C10-C11-C12
10	A	1506	TRD	C11-C10-C9-C8
3	A	1005	DMU	C2-C3-O7-C10
10	C	580	TRD	C1-C2-C3-C4
10	D	7	TRD	C1-C2-C3-C4
10	B	1012	TRD	C5-C6-C7-C8
10	A	1013	TRD	C1-C2-C3-C4
10	A	1015	TRD	C1-C2-C3-C4
10	A	1506	TRD	C5-C6-C7-C8
10	A	1014	TRD	C1-C2-C3-C4
10	C	583	TRD	C1-C2-C3-C4
10	A	1009	TRD	C4-C5-C6-C7
10	A	1010	TRD	C11-C10-C9-C8
3	A	1004	DMU	C19-C18-O16-C6
3	A	1005	DMU	C19-C18-O16-C6
3	B	1003	DMU	C19-C18-O16-C6
10	B	1023	TRD	C5-C6-C7-C8
10	C	578	TRD	C11-C10-C9-C8
10	A	1506	TRD	C6-C7-C8-C9
3	A	1005	DMU	C4-C3-O7-C10
3	C	568	DMU	C34-C37-C40-C43
3	B	1003	DMU	C28-C31-C34-C37
10	A	1505	TRD	C11-C10-C9-C8
10	C	582	TRD	C1-C2-C3-C4
10	A	1505	TRD	C2-C3-C4-C5
10	B	1031	TRD	C5-C6-C7-C8
13	C	576	DXC	C12-C17-C19-C24
10	C	584	TRD	C4-C5-C6-C7
3	A	1004	DMU	C25-C28-C31-C34
10	B	1031	TRD	C6-C7-C8-C9
3	C	567	DMU	C2-C3-O7-C10
10	C	579	TRD	C2-C3-C4-C5
10	D	7	TRD	C4-C5-C6-C7
10	C	582	TRD	C4-C5-C6-C7
3	A	1004	DMU	C19-C22-C25-C28
10	D	23	TRD	C4-C5-C6-C7
3	B	1003	DMU	C22-C25-C28-C31
10	A	1014	TRD	C3-C4-C5-C6
3	C	567	DMU	C4-C3-O7-C10

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Mol	Chain	Res	Type	Atoms
3	A	1004	DMU	O16-C18-C19-C22
10	D	7	TRD	C11-C10-C9-C8
3	A	567	DMU	C18-C19-C22-C25
10	D	288	TRD	C6-C7-C8-C9
10	B	1012	TRD	C4-C5-C6-C7
10	C	583	TRD	C4-C5-C6-C7
3	C	568	DMU	O16-C18-C19-C22
3	A	1005	DMU	C19-C22-C25-C28
13	C	576	DXC	C19-C21-C22-C23
10	C	583	TRD	C2-C3-C4-C5
10	D	7	TRD	C5-C6-C7-C8
10	A	1504	TRD	C1-C2-C3-C4
3	A	1005	DMU	C31-C34-C37-C40
10	D	7	TRD	C9-C10-C11-C12
10	A	1506	TRD	C1-C2-C3-C4
10	B	1012	TRD	C1-C2-C3-C4
3	A	1005	DMU	C3-C4-C57-O61
10	C	581	TRD	C1-C2-C3-C4
10	A	1013	TRD	C3-C4-C5-C6
9	C	575	HEA	C3B-C11-C12-C13
3	A	1004	DMU	O5-C4-C57-O61
10	C	577	TRD	C7-C8-C9-C10
10	A	1504	TRD	C6-C7-C8-C9
9	A	1502	HEA	C26-C15-C16-C17
3	B	1011	DMU	O6-C11-C9-C8
10	D	12	TRD	C11-C10-C9-C8
9	C	575	HEA	CAA-CBA-CGA-O1A
10	A	1009	TRD	C2-C3-C4-C5
12	B	1	HTO	C4-C5-C6-C7
10	D	288	TRD	C3-C4-C5-C6
9	C	574	HEA	C26-C15-C16-C17
9	A	1503	HEA	CAA-CBA-CGA-O1A
9	A	1503	HEA	CAA-CBA-CGA-O2A
10	A	1009	TRD	C1-C2-C3-C4
3	C	567	DMU	C19-C22-C25-C28
9	C	575	HEA	CAA-CBA-CGA-O2A
9	A	1502	HEA	CAD-CBD-CGD-O2D
9	C	575	HEA	CAD-CBD-CGD-O1D
9	A	1502	HEA	C14-C15-C16-C17
9	C	574	HEA	CAD-CBD-CGD-O2D
3	A	567	DMU	C25-C28-C31-C34
9	A	1503	HEA	CAD-CBD-CGD-O1D

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Mol	Chain	Res	Type	Atoms
3	A	1004	DMU	C34-C37-C40-C43
9	A	1503	HEA	CAD-CBD-CGD-O2D
9	C	574	HEA	CAD-CBD-CGD-O1D
3	C	567	DMU	C5-C10-O7-C3
3	A	1005	DMU	C5-C10-O7-C3
9	A	1502	HEA	CAD-CBD-CGD-O1D
9	C	574	HEA	CAA-CBA-CGA-O1A
9	C	575	HEA	CAD-CBD-CGD-O2D
9	A	1503	HEA	O11-C11-C12-C13
9	A	1503	HEA	C3B-C11-C12-C13
3	A	1005	DMU	O6-C11-C9-C8
10	D	288	TRD	C1-C2-C3-C4
10	A	1015	TRD	C11-C10-C9-C8
9	A	1503	HEA	C26-C15-C16-C17
3	C	568	DMU	C31-C34-C37-C40
9	C	574	HEA	CAA-CBA-CGA-O2A
3	A	567	DMU	C31-C34-C37-C40
9	A	1502	HEA	CAA-CBA-CGA-O1A
9	A	1502	HEA	CAA-CBA-CGA-O2A
10	C	578	TRD	C5-C6-C7-C8

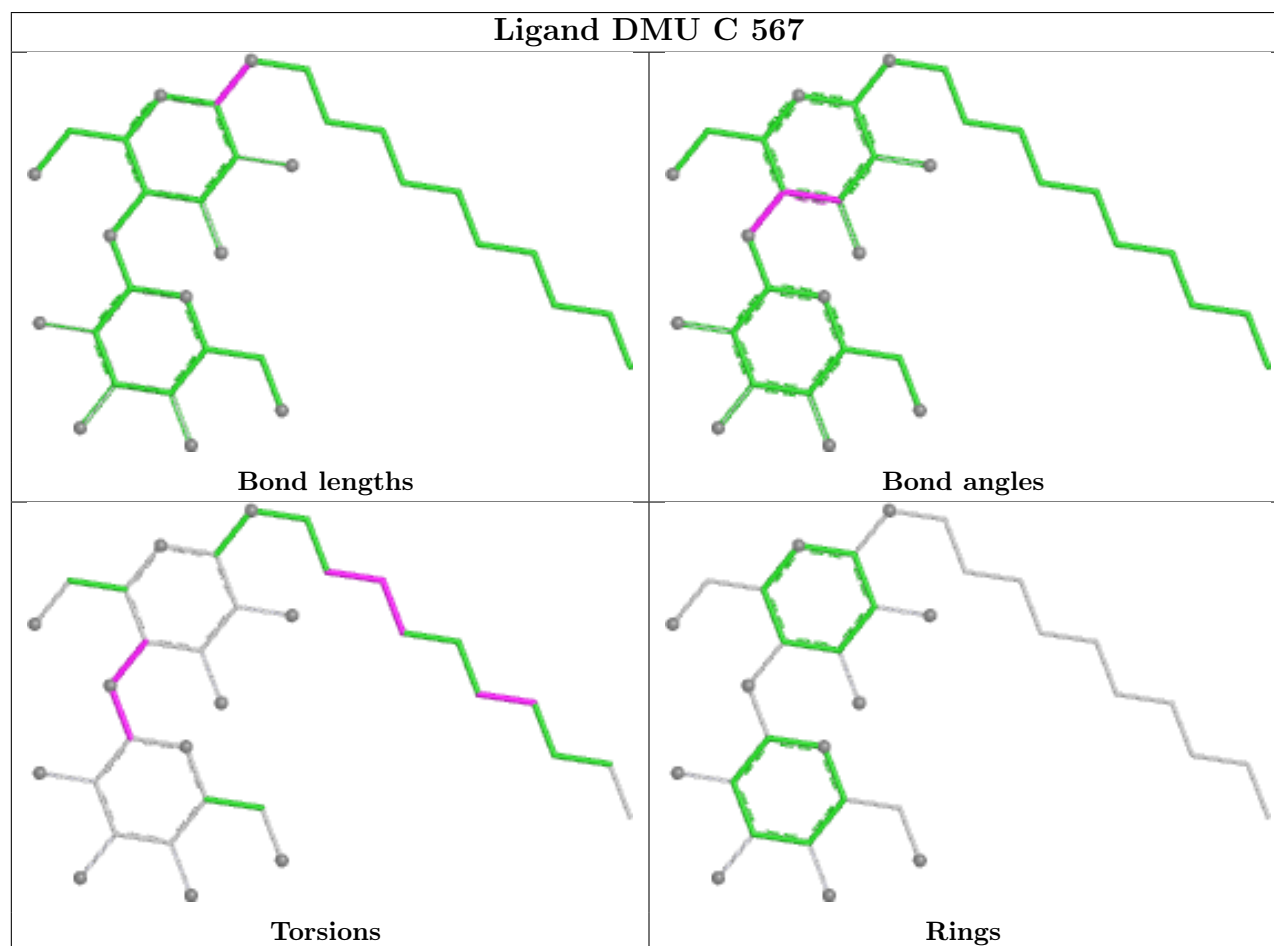
There are no ring outliers.

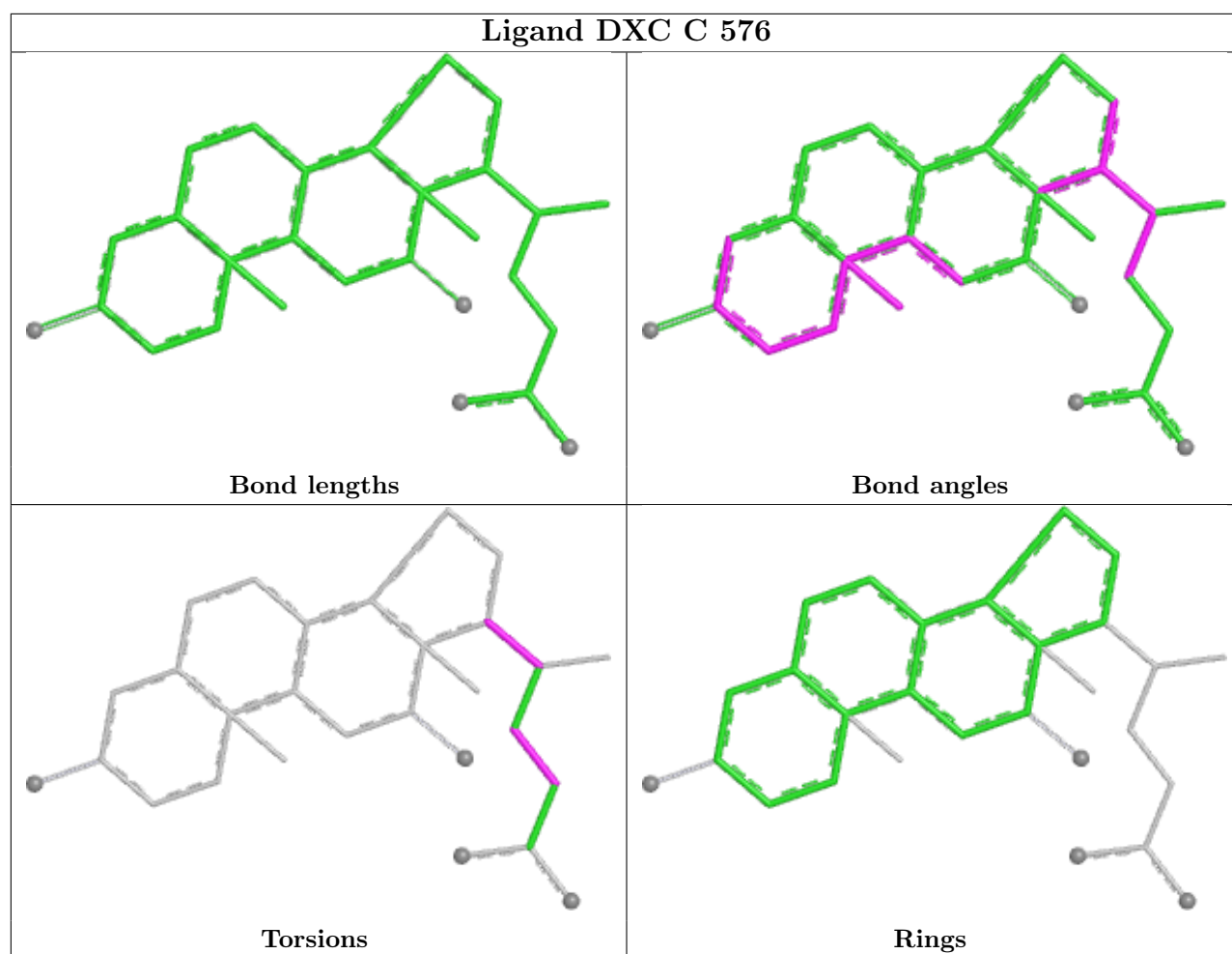
15 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	567	DMU	2	0
3	A	1005	DMU	2	0
9	A	1503	HEA	1	0
10	A	1506	TRD	3	0
3	A	567	DMU	3	0
9	C	574	HEA	4	0
10	D	7	TRD	2	0
10	B	1023	TRD	1	0
10	A	1504	TRD	4	0
10	C	584	TRD	12	0
10	C	577	TRD	1	0
12	B	1	HTO	1	0
9	C	575	HEA	2	0
9	A	1502	HEA	2	0
3	A	1004	DMU	3	0

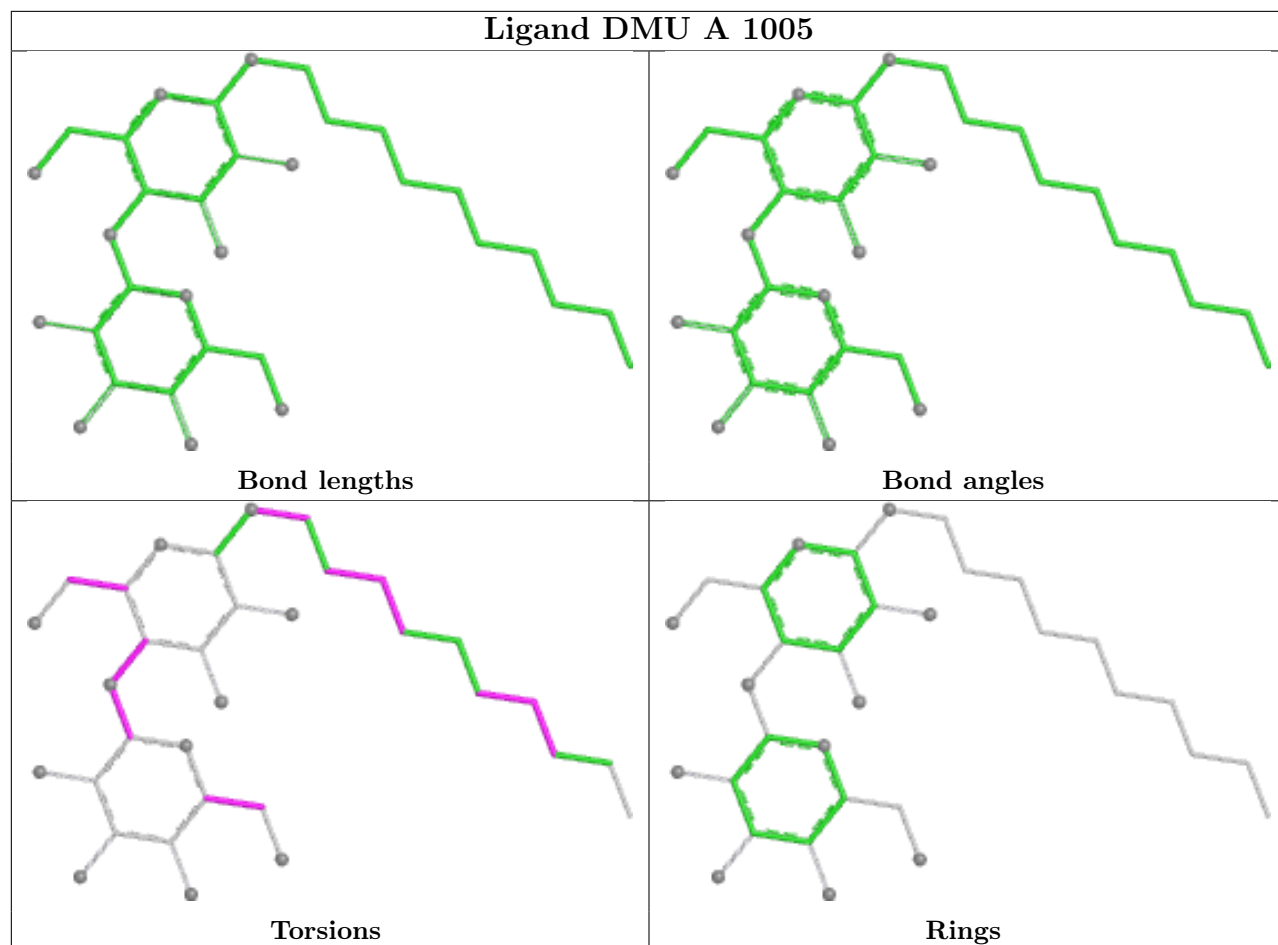
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

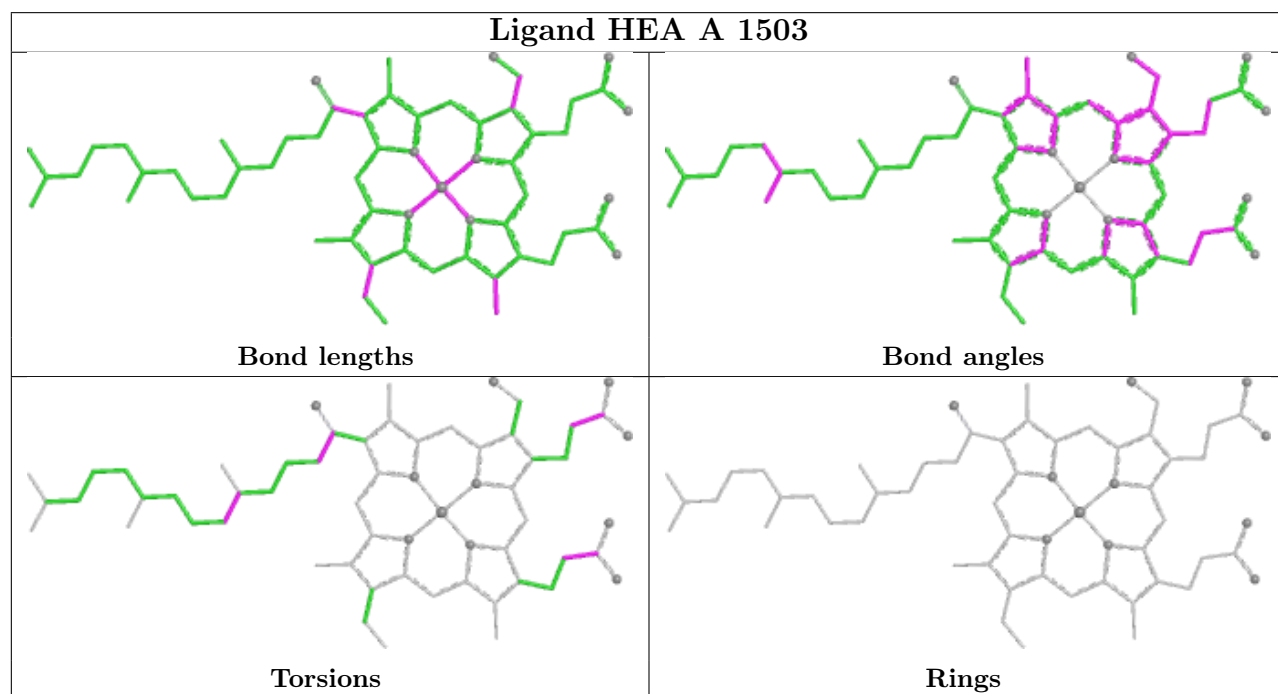


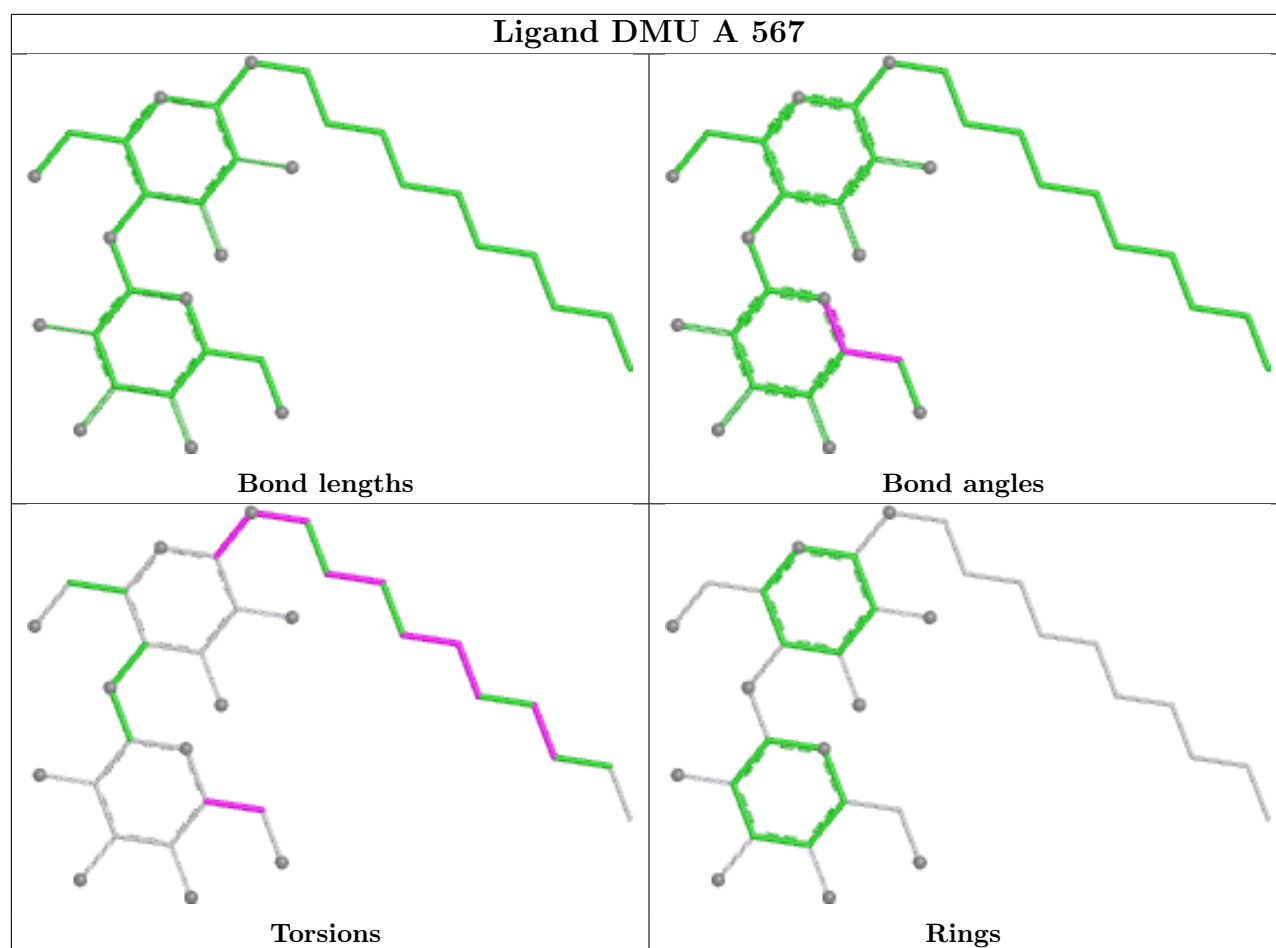


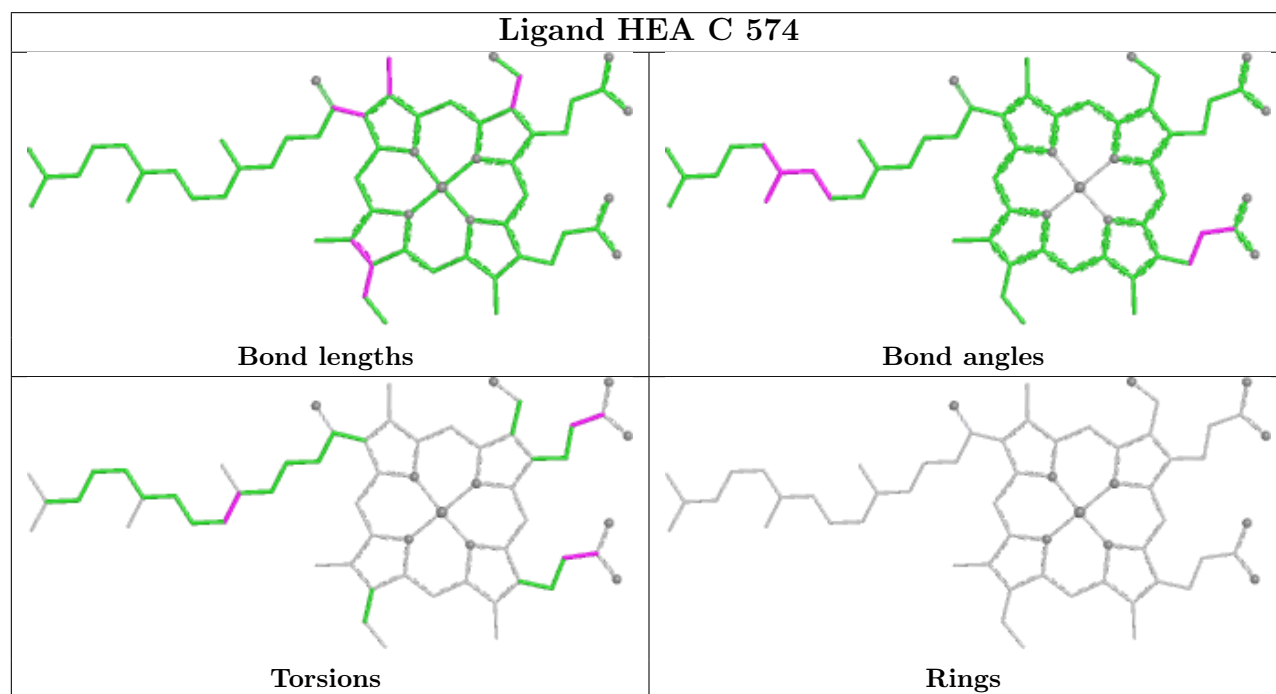
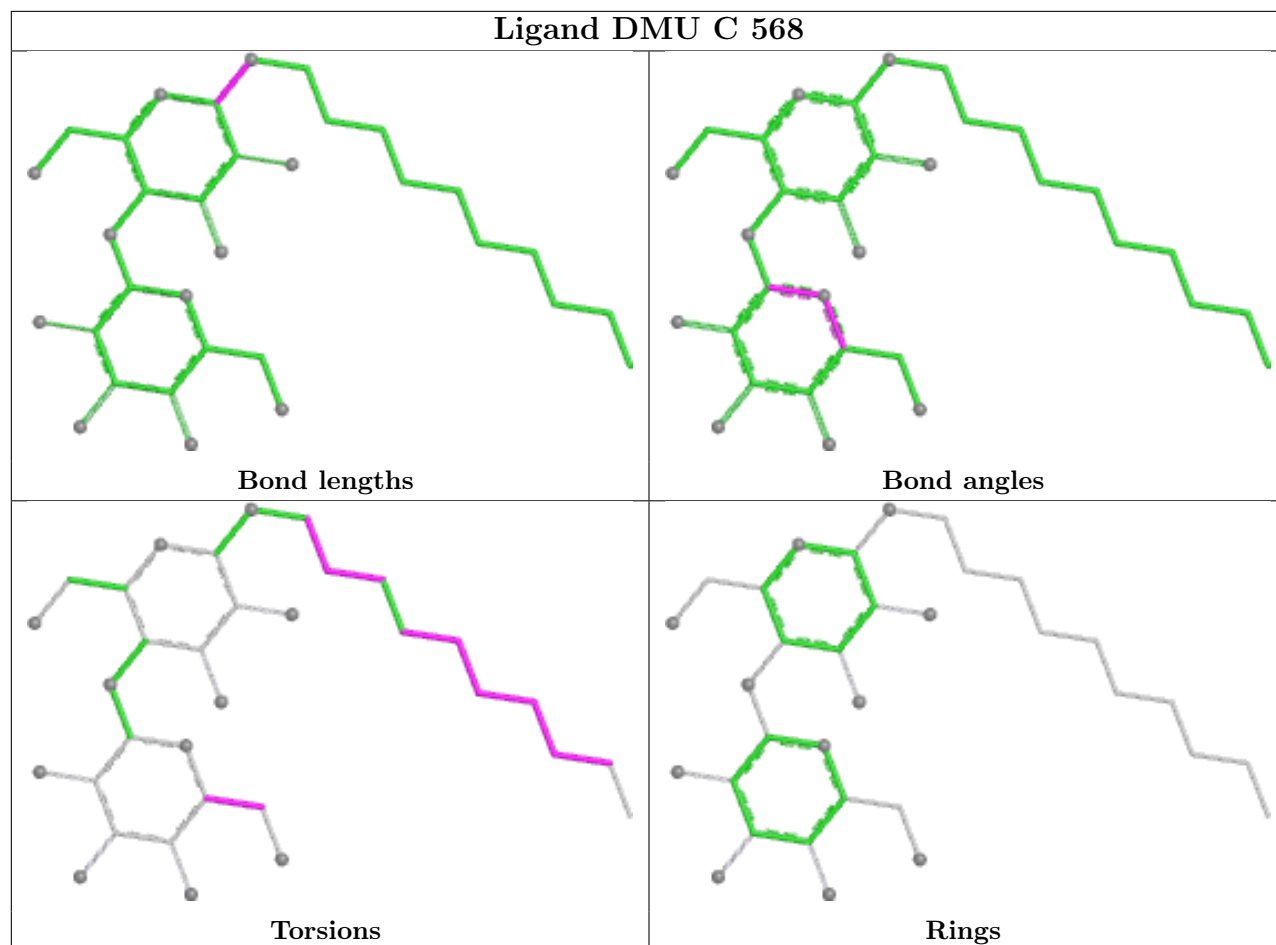
Ligand DMU A 1005

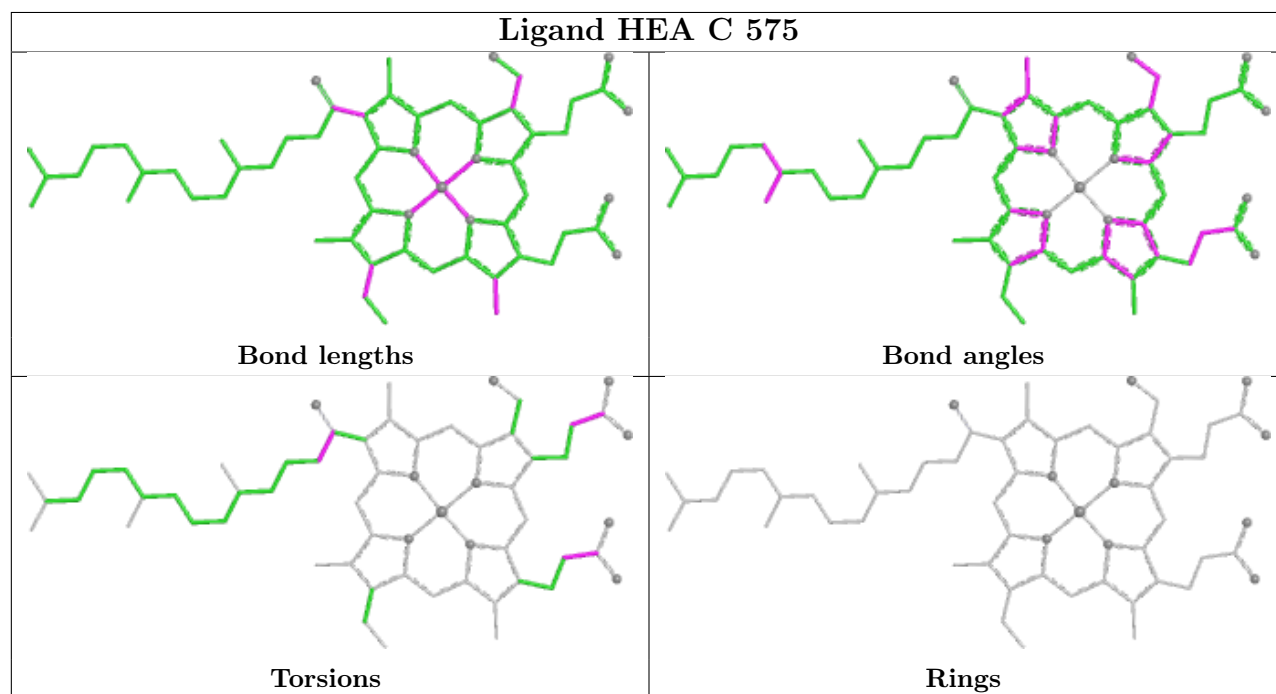
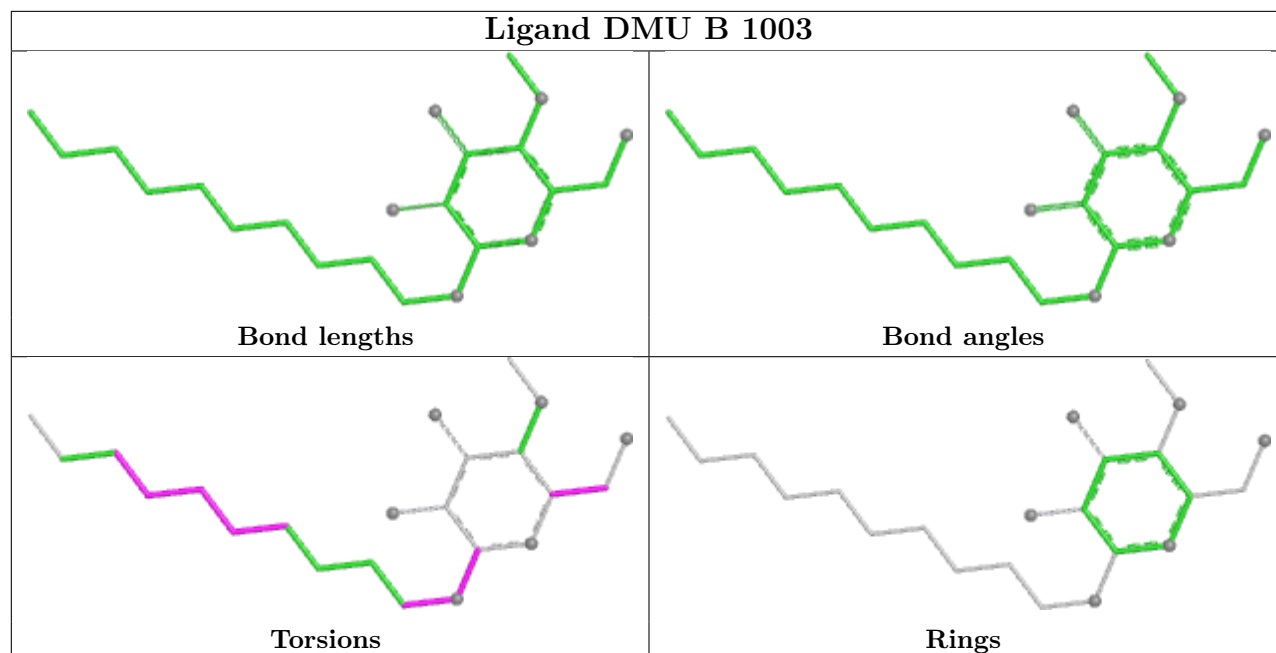


Ligand HEA A 1503

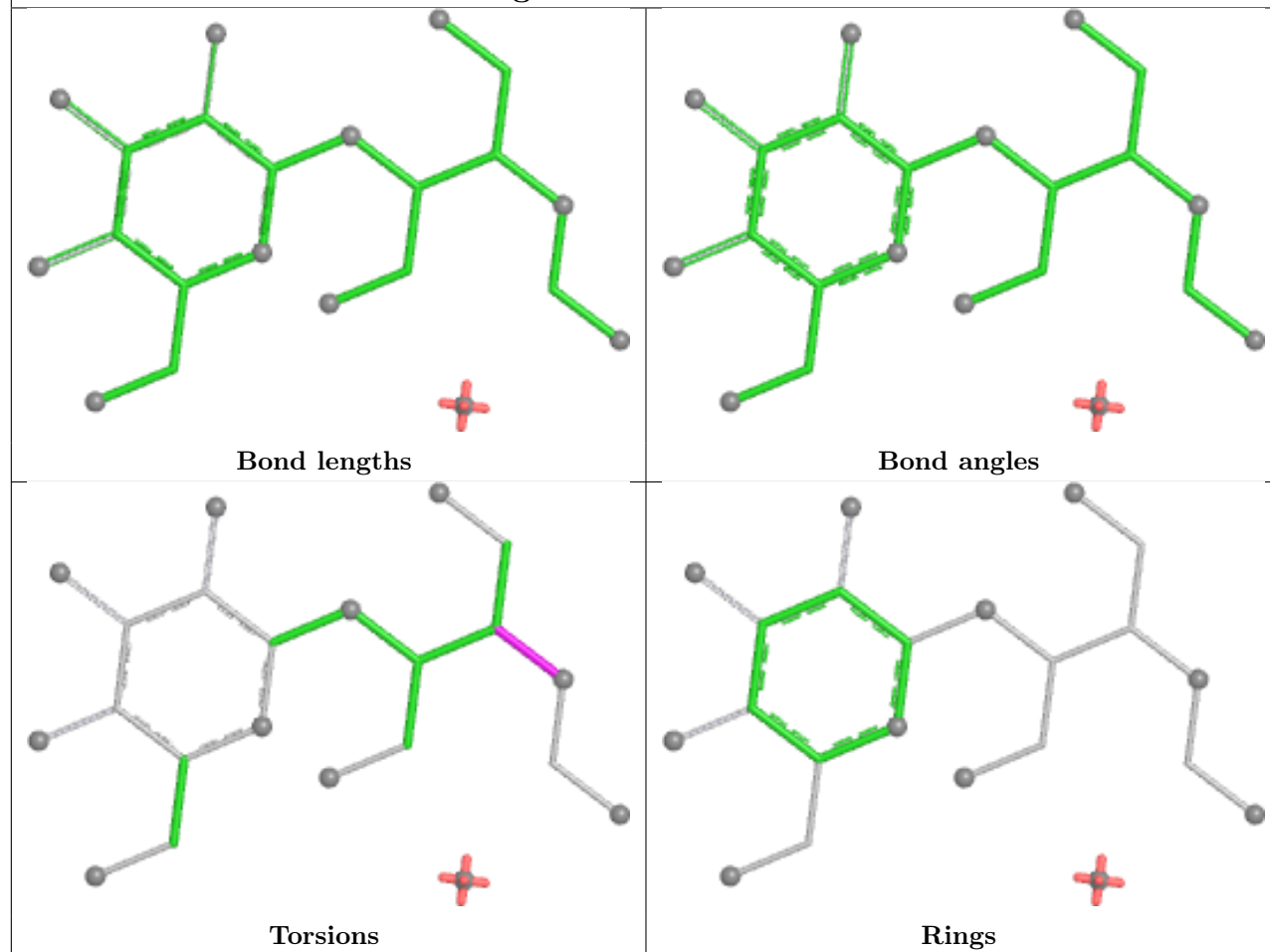




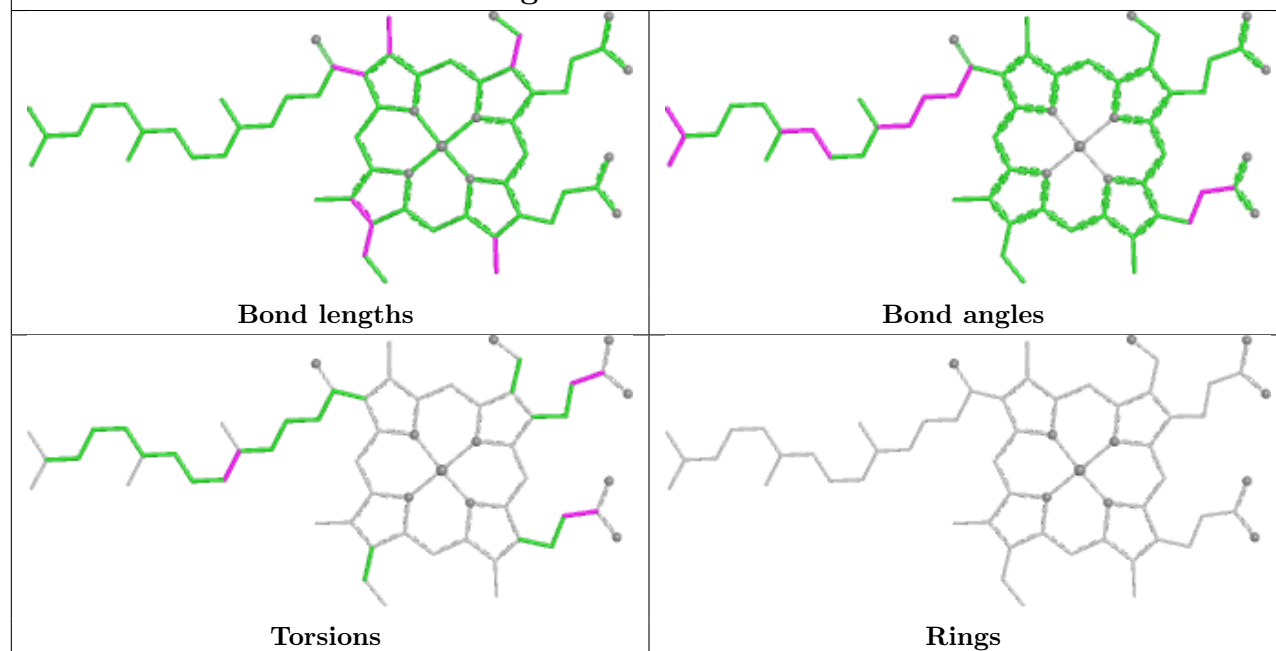




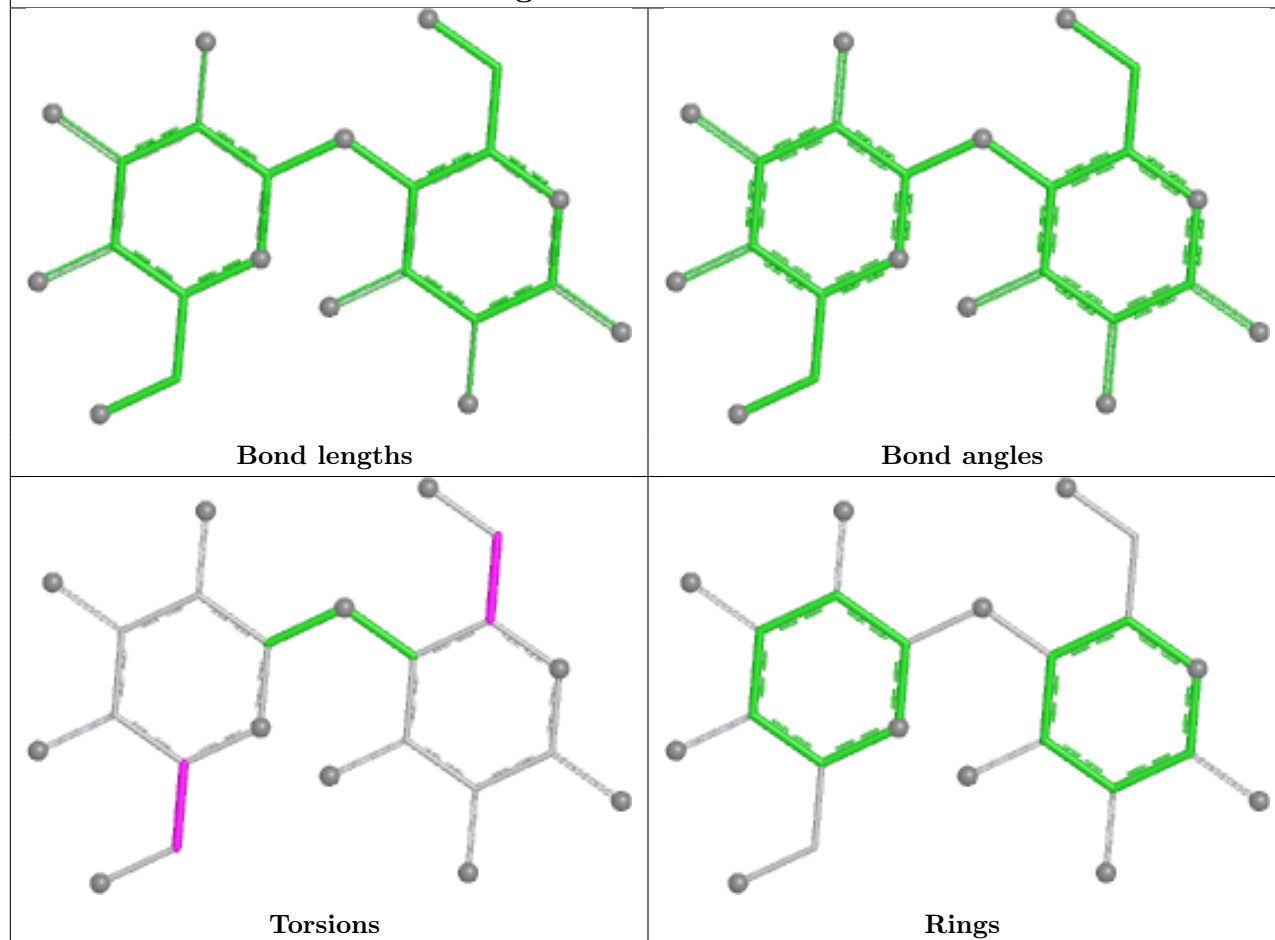
Ligand DMU A 1002



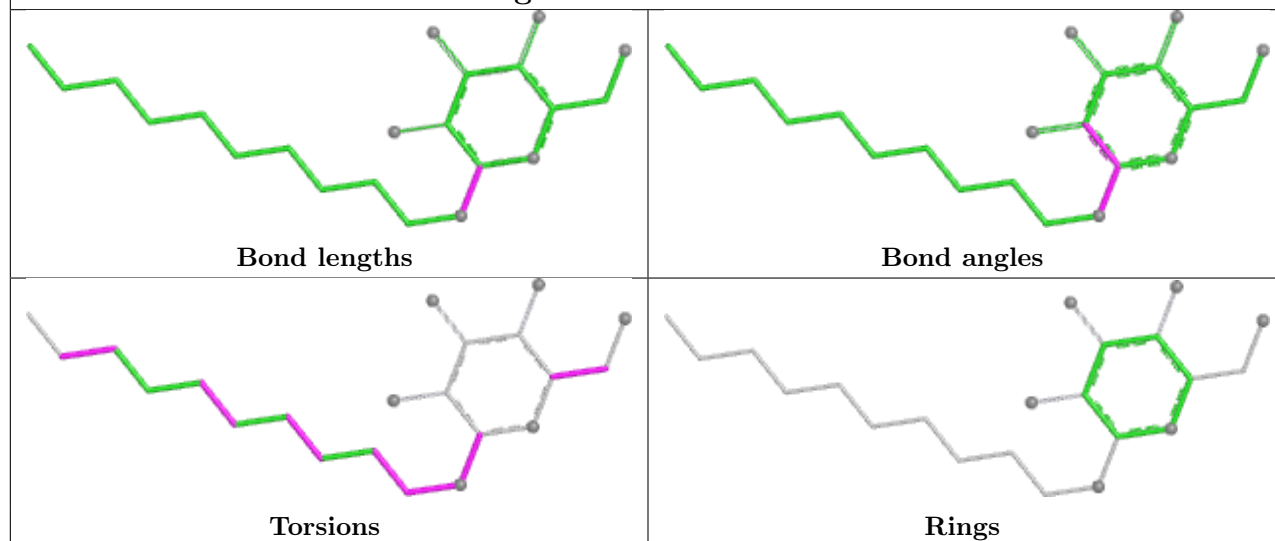
Ligand HEA A 1502

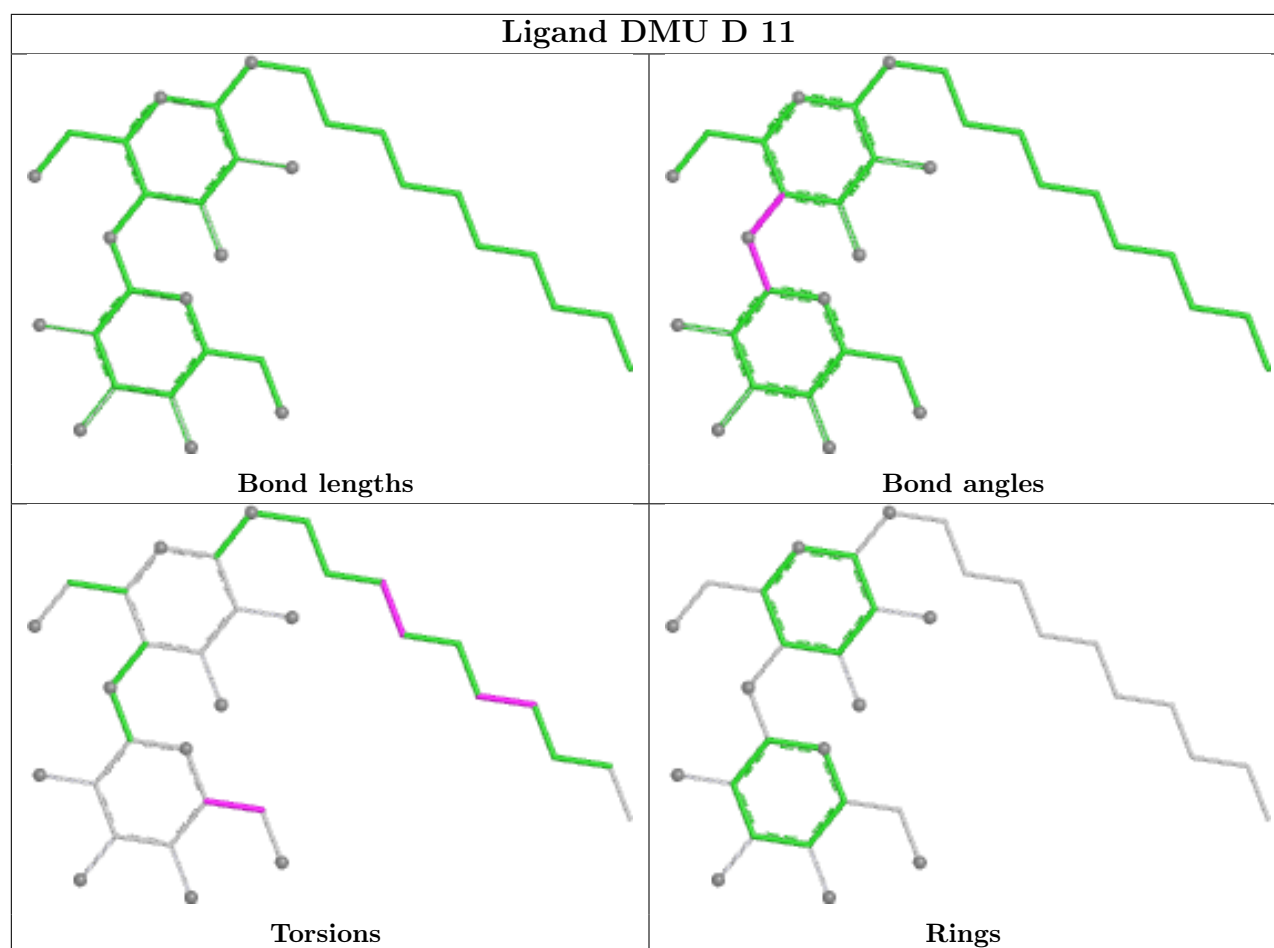


Ligand DMU B 1011



Ligand DMU A 1004





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	539/566 (95%)	0.31	20 (3%)	45 49	22, 37, 58, 76	7 (1%)
1	C	536/566 (94%)	0.19	16 (2%)	52 56	20, 33, 48, 67	7 (1%)
2	B	259/262 (98%)	0.35	18 (6%)	23 26	23, 37, 52, 65	5 (1%)
2	D	258/262 (98%)	0.20	5 (1%)	66 70	20, 35, 45, 57	4 (1%)
All	All	1592/1656 (96%)	0.26	59 (3%)	45 49	20, 35, 51, 76	23 (1%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	20	TRP	5.0
1	A	81	TRP	4.8
2	D	56	TRP	4.3
2	B	99	PRO	4.0
1	A	268	GLY	4.0
1	A	267	SER	3.8
1	A	69	GLU	3.7
1	C	18	THR	3.6
1	C	81	TRP	3.4
1	C	21	PHE	3.1
1	A	13	ARG	3.1
2	B	105	THR	3.1
2	D	81	TRP	3.0
1	A	262	THR	2.8
1	C	17	PHE	2.8
2	D	87	ARG	2.7
2	B	70	ILE	2.7
1	C	22	MET	2.7
2	D	28	GLN	2.7
2	B	88	ASN	2.7
1	A	68	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	318	TYR	2.6
1	C	73	VAL	2.6
2	B	56	TRP	2.6
1	A	16	PHE	2.5
1	A	20	TRP	2.5
1	A	270	GLY	2.5
1	C	68	LEU	2.5
2	B	109	ILE	2.5
2	B	287	HIS	2.4
2	B	124	PHE	2.4
2	B	29	SER	2.4
1	A	221	THR	2.4
1	A	76	PHE	2.4
1	C	43	ILE	2.4
2	B	97	ASN	2.4
2	B	153	GLU	2.3
1	A	259	PHE	2.3
1	C	60	VAL	2.3
1	C	19	ARG	2.3
2	B	100	LEU	2.3
2	B	106	ILE	2.3
2	B	114	ALA	2.3
1	A	551	PHE	2.2
1	C	74	LYS	2.2
1	A	25	ASN	2.2
1	A	78	GLN	2.1
1	A	223	HIS	2.1
2	B	103	ALA	2.1
2	D	99	PRO	2.1
2	B	98	SER	2.1
2	B	96	HIS	2.1
1	C	267	SER	2.1
1	C	69	GLU	2.1
1	C	517	TYR	2.1
1	C	524	ARG	2.1
1	A	343	THR	2.0
1	A	311	PHE	2.0
2	B	39	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

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
10	TRD	A	1015	11/13	0.70	0.39	63,65,70,70	11
10	TRD	A	1013	7/13	0.71	0.30	53,54,55,55	0
3	DMU	B	1003	23/33	0.71	0.42	49,54,56,56	23
3	DMU	B	1011	23/33	0.72	0.36	57,58,58,58	23
3	DMU	C	567	33/33	0.73	0.22	77,81,82,83	0
10	TRD	A	1505	11/13	0.73	0.39	64,65,66,66	11
10	TRD	C	581	11/13	0.73	0.42	74,75,77,77	11
3	DMU	A	1002	22/33	0.74	0.45	66,66,67,67	22
10	TRD	C	582	7/13	0.74	0.35	67,67,67,67	7
8	PO4	C	573	5/5	0.77	0.23	53,53,54,55	5
10	TRD	C	579	7/13	0.78	0.31	68,68,69,69	0
10	TRD	C	580	9/13	0.80	0.36	62,64,64,64	9
10	TRD	C	578	11/13	0.80	0.22	61,62,63,63	0
3	DMU	D	11	33/33	0.80	0.23	70,73,74,75	33
10	TRD	C	577	13/13	0.81	0.18	45,50,53,54	0
8	PO4	A	1001	5/5	0.81	0.23	69,69,70,70	5
10	TRD	D	23	7/13	0.82	0.29	61,61,62,62	7
10	TRD	B	1031	9/13	0.83	0.23	53,55,58,58	0
10	TRD	A	1009	7/13	0.83	0.23	60,60,62,62	0
10	TRD	B	1012	9/13	0.84	0.26	74,75,77,77	0
3	DMU	A	1004	22/33	0.84	0.20	44,61,65,66	22
10	TRD	C	583	7/13	0.84	0.26	57,57,59,59	0
3	DMU	A	1005	33/33	0.84	0.17	50,57,61,61	33
3	DMU	C	568	33/33	0.85	0.15	65,68,69,70	0
10	TRD	C	584	7/13	0.85	0.21	46,50,54,55	0
10	TRD	B	1023	9/13	0.85	0.18	58,59,60,61	0
10	TRD	A	1504	13/13	0.86	0.23	56,58,61,62	0
10	TRD	D	12	11/13	0.86	0.29	58,58,58,59	11
10	TRD	A	1010	11/13	0.86	0.31	58,59,59,60	11
3	DMU	A	567	33/33	0.87	0.15	48,63,67,68	0
10	TRD	A	1014	7/13	0.89	0.39	73,73,74,74	7
10	TRD	D	7	13/13	0.89	0.15	41,43,50,50	0

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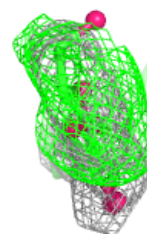
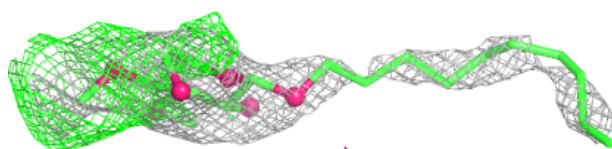
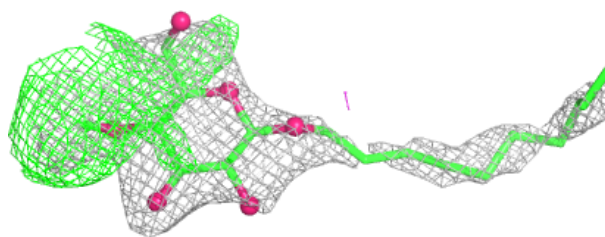
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	TRD	D	288	9/13	0.89	0.19	52,53,56,56	0
10	TRD	A	1506	13/13	0.89	0.18	45,46,51,53	0
7	OH	A	1501	1/1	0.89	0.16	35,35,35,35	0
13	DXC	C	576	28/28	0.91	0.12	46,50,52,52	0
12	HTO	B	1	10/10	0.93	0.15	51,54,55,56	0
7	OH	C	572	1/1	0.95	0.08	28,28,28,28	0
9	HEA	A	1503	60/60	0.97	0.08	26,29,41,42	0
11	CD	B	1009	1/1	0.97	0.04	45,45,45,45	1
9	HEA	C	574	60/60	0.98	0.07	23,26,32,33	0
9	HEA	A	1502	60/60	0.98	0.06	23,26,33,34	0
6	CA	C	571	1/1	0.98	0.03	32,32,32,32	0
11	CD	B	1008	1/1	0.99	0.02	35,35,35,35	0
9	HEA	C	575	60/60	0.99	0.05	21,24,32,33	0
11	CD	B	1010	1/1	0.99	0.09	53,53,53,53	1
11	CD	D	8	1/1	0.99	0.02	36,36,36,36	0
11	CD	D	9	1/1	0.99	0.02	46,46,46,46	0
4	CU	A	1023	1/1	0.99	0.02	32,32,32,32	0
4	CU	B	1022	1/1	0.99	0.01	28,28,28,28	0
5	MG	A	1006	1/1	1.00	0.05	16,16,16,16	0
5	MG	C	570	1/1	1.00	0.05	15,15,15,15	0
6	CA	A	1007	1/1	1.00	0.02	27,27,27,27	0
4	CU	B	1004	1/1	1.00	0.01	29,29,29,29	0
4	CU	C	569	1/1	1.00	0.02	26,26,26,26	0
4	CU	D	3	1/1	1.00	0.02	28,28,28,28	0
4	CU	D	4	1/1	1.00	0.01	28,28,28,28	0

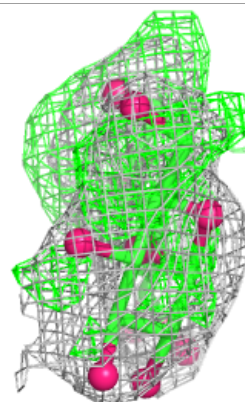
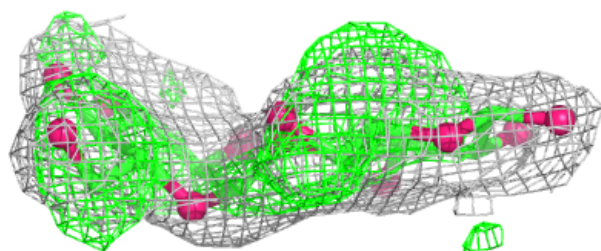
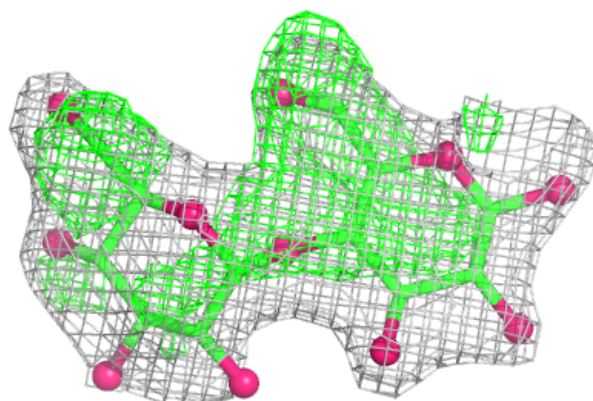
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around DMU B 1003:

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

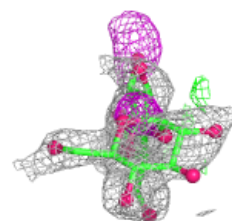
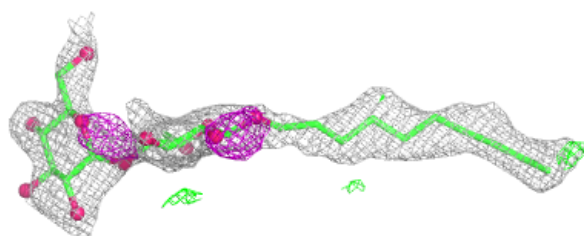
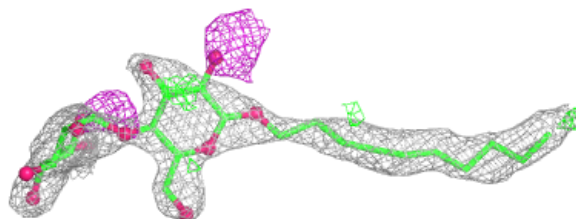
**Electron density around DMU B 1011:**

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



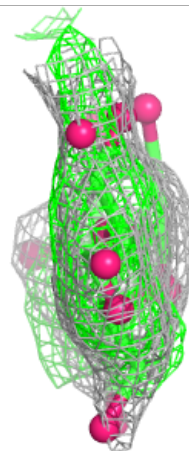
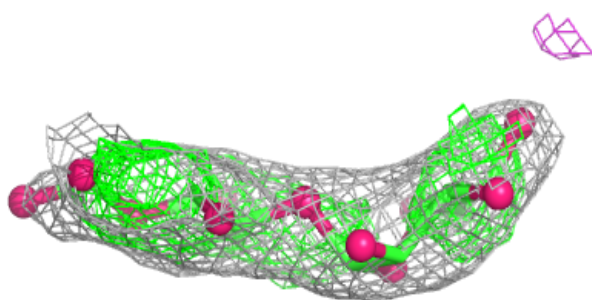
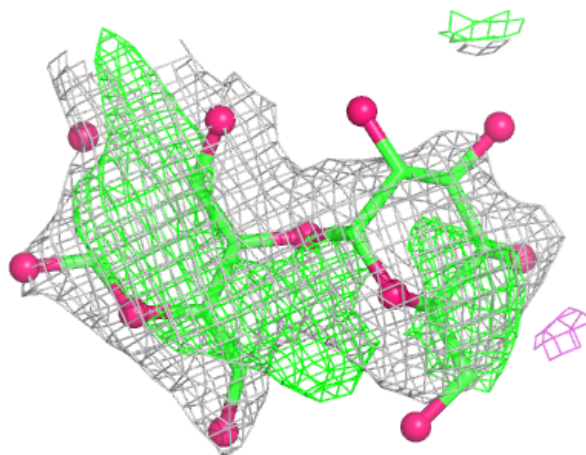
Electron density around DMU C 567:

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



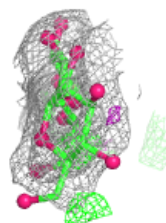
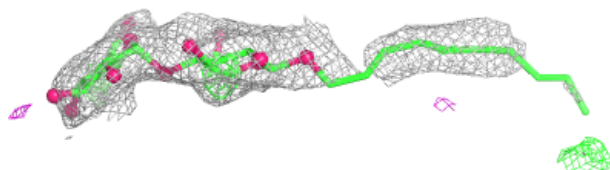
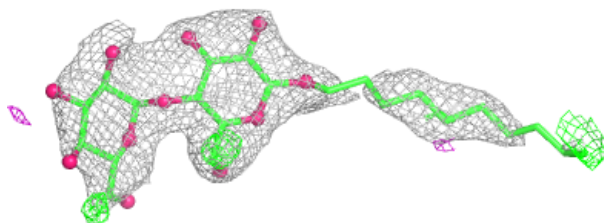
Electron density around DMU A 1002:

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

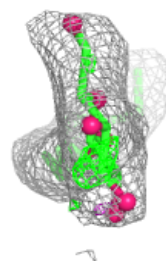
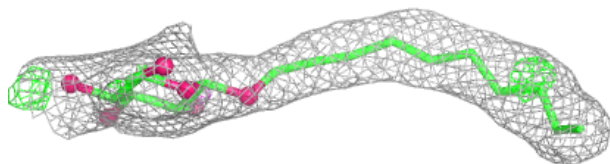
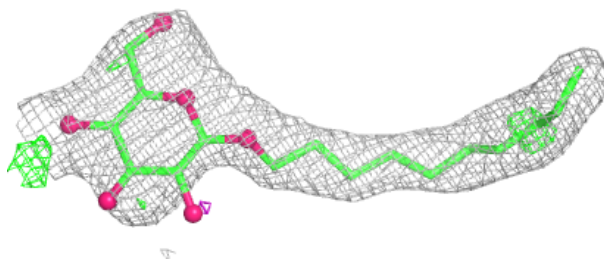


Electron density around DMU D 11:

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

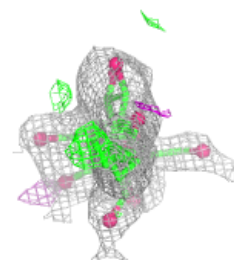
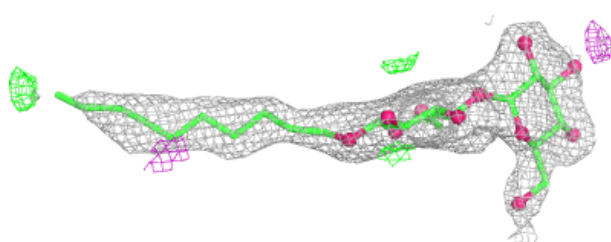
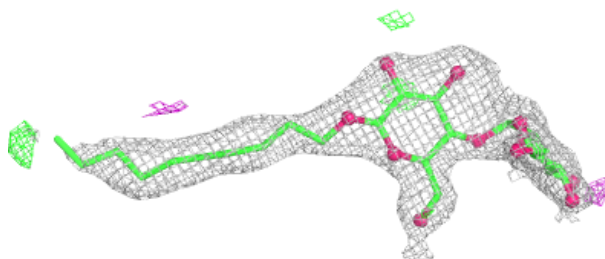
**Electron density around DMU A 1004:**

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

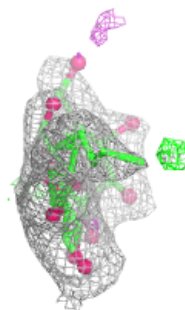
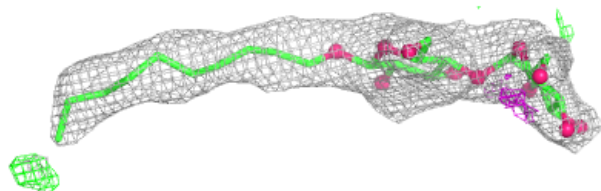
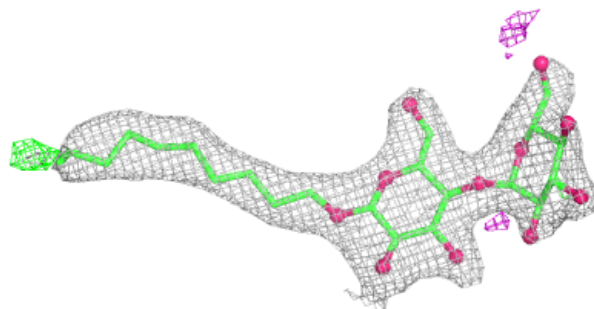


Electron density around DMU A 1005:

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

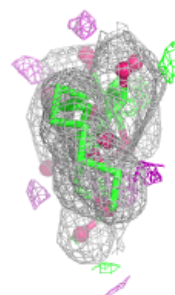
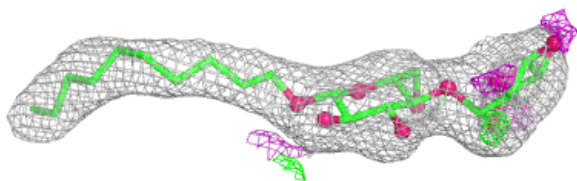
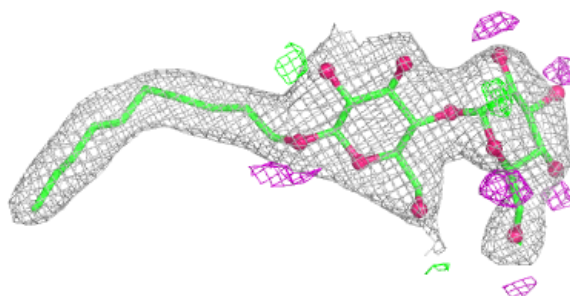
**Electron density around DMU C 568:**

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

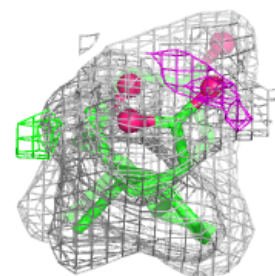
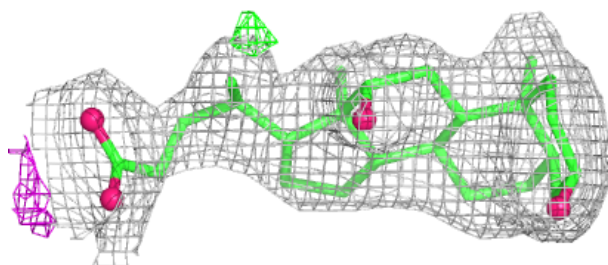
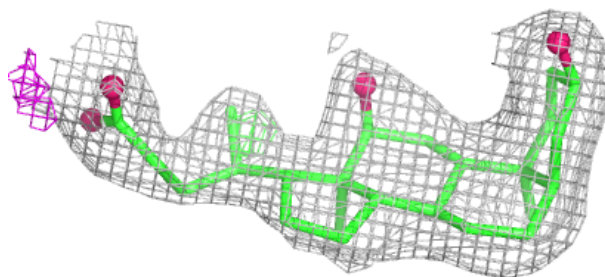


Electron density around DMU A 567:

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

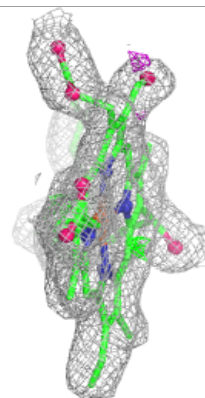
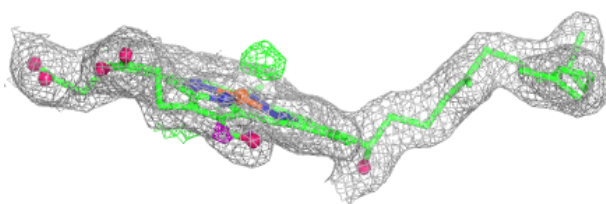
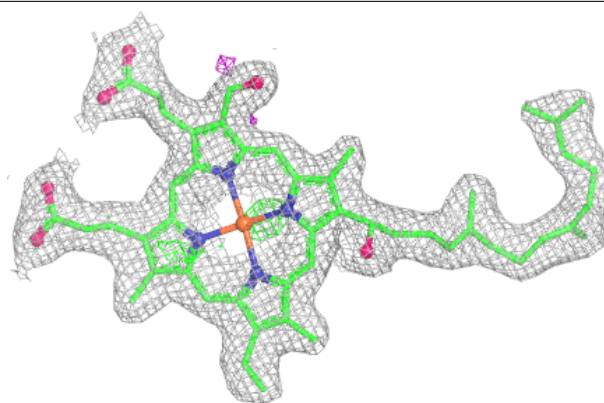
**Electron density around DXC C 576:**

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

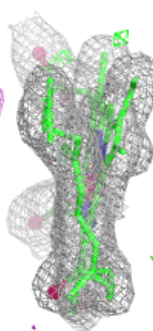
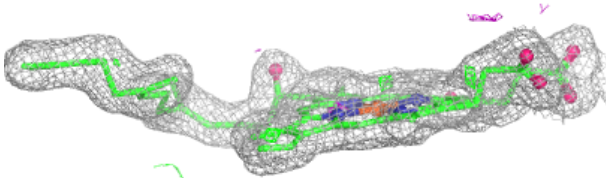
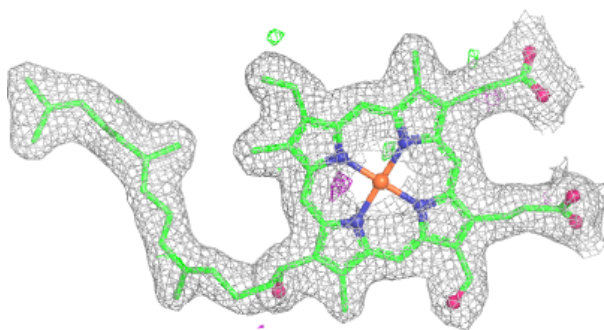


Electron density around HEA A 1503:

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

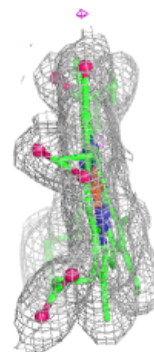
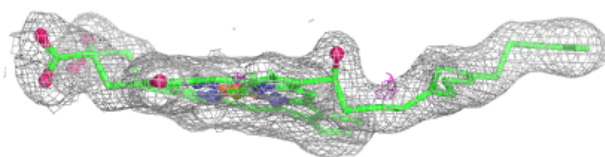
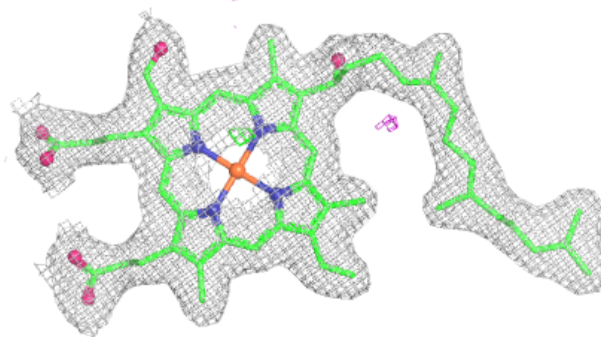
**Electron density around HEA C 574:**

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

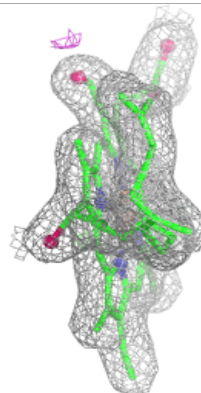
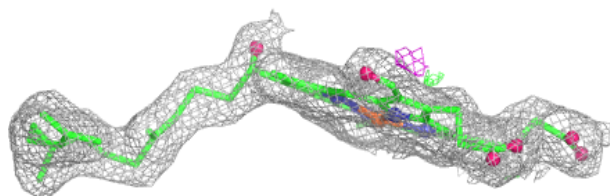
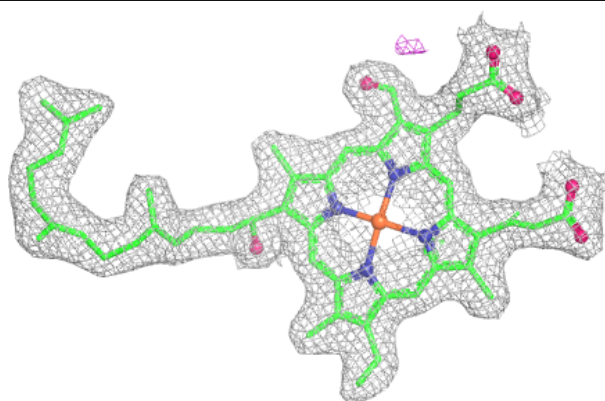


Electron density around HEA A 1502:

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

**Electron density around HEA C 575:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.