



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:19 PM UTC

PDB ID : 3FYE / pdb_00003fye
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 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

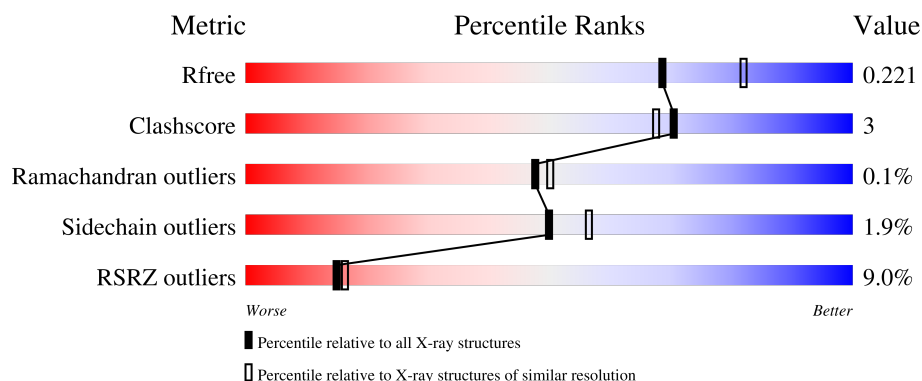
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	5% 85% 9% 5%
1	C	566	14% 86% 7% 6%
2	B	262	4% 94% ...
2	D	262	9% 92% ...

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	-	-	-
8	DMU	D	1011	-	-	-	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			

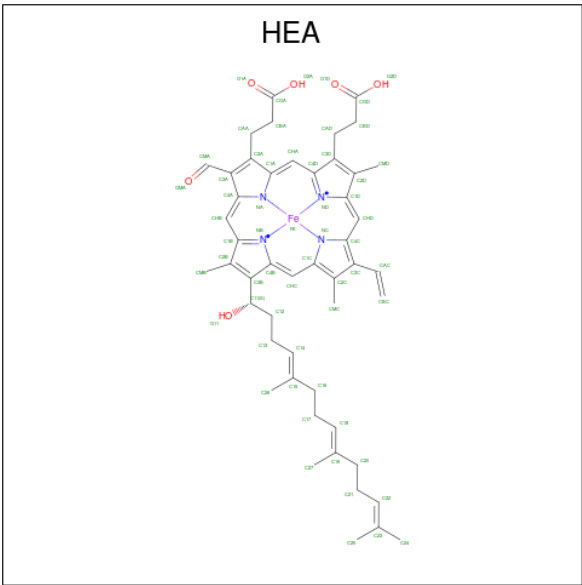
- Molecule 2 is a protein called Cytochrome C oxidase subunit 2.

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 (CCD ID: 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 (CCD ID: 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 (CCD ID: 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		

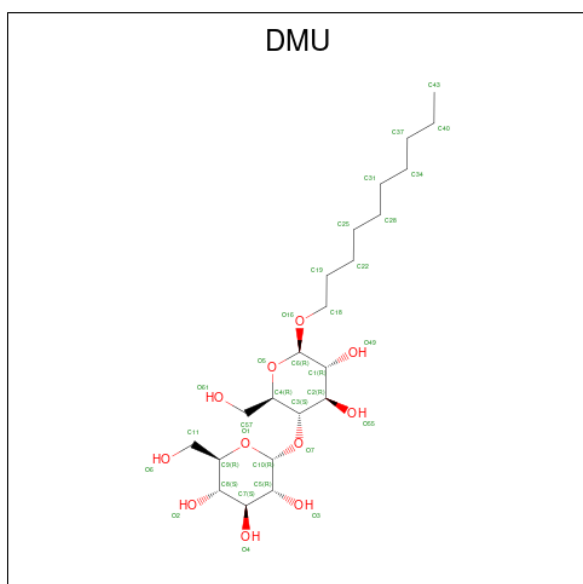
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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 (CCD ID: 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 (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



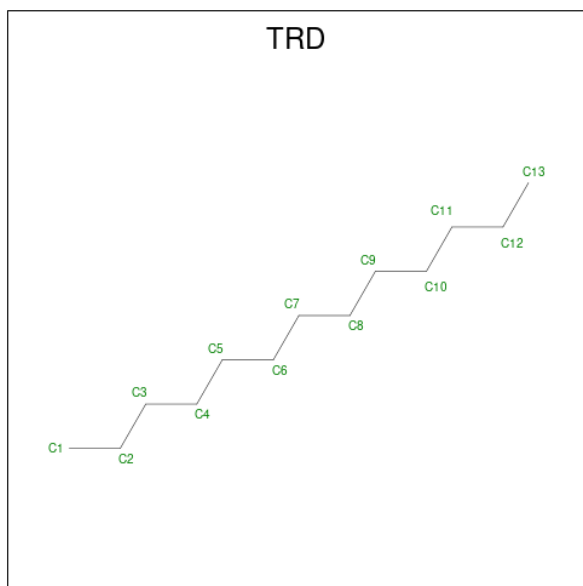
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			33	22	11		

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

- Molecule 9 is TRIDECANE (CCD ID: TRD) (formula: C₁₃H₂₈).



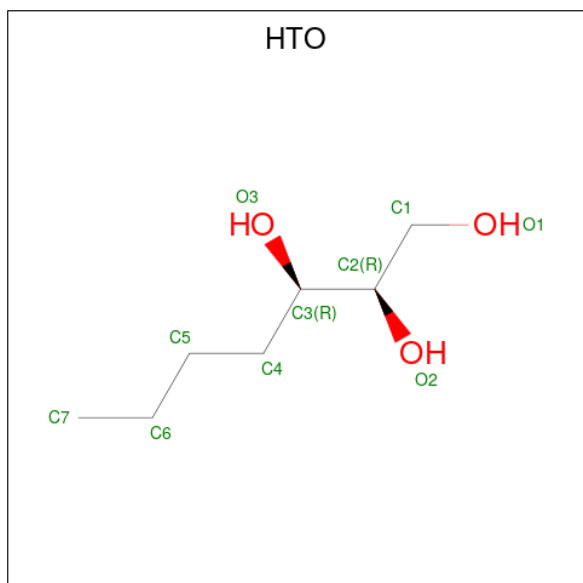
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C 13 13	0	0
9	A	1	Total C 13 13	0	0

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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 (CCD ID: 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 (CCD ID: 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

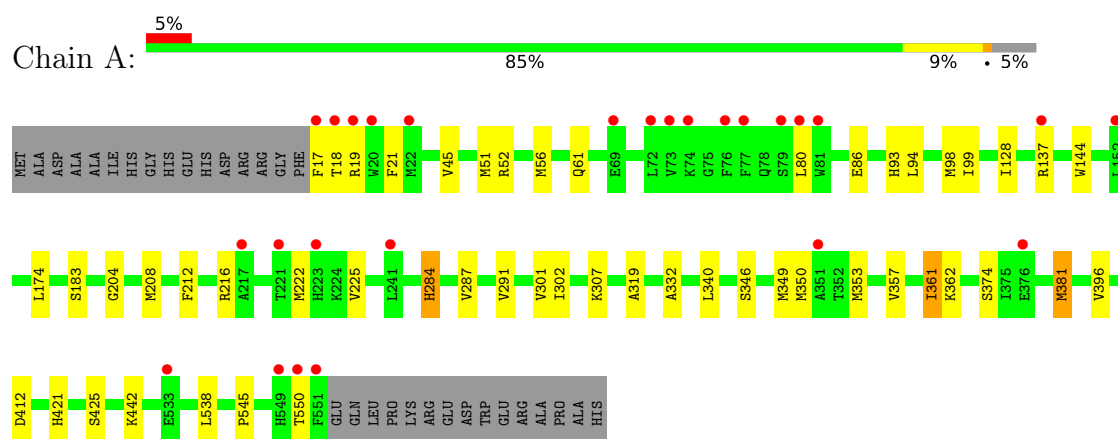
- Molecule 12 is water.

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

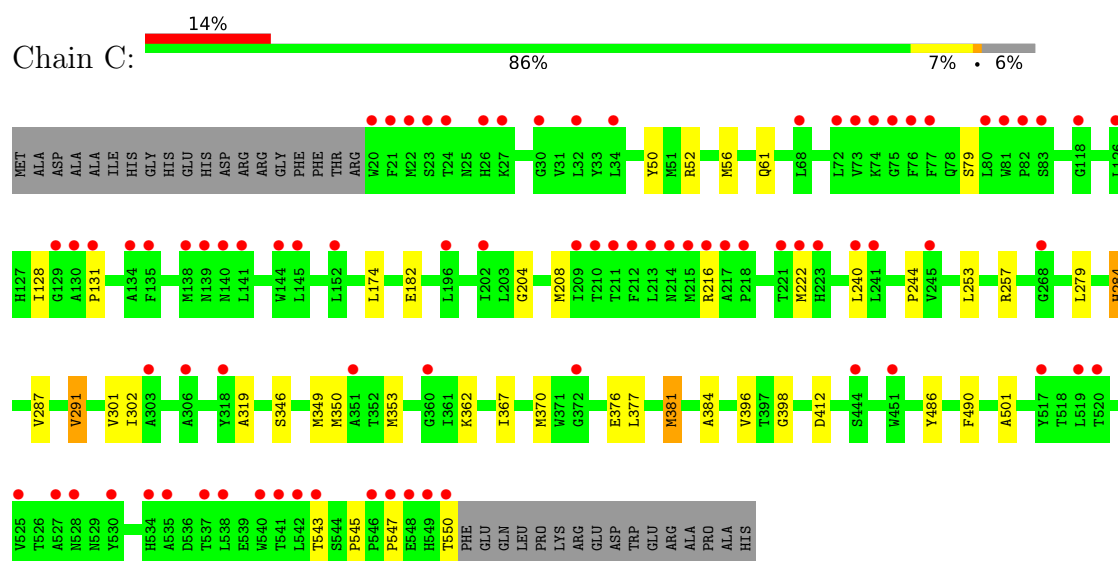
3 Residue-property plots [i](#)

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

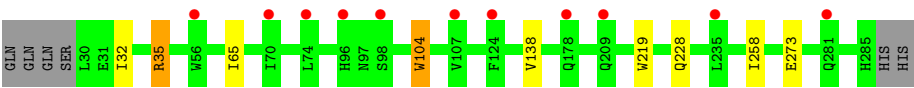


• Molecule 1: Cytochrome C oxidase subunit 1

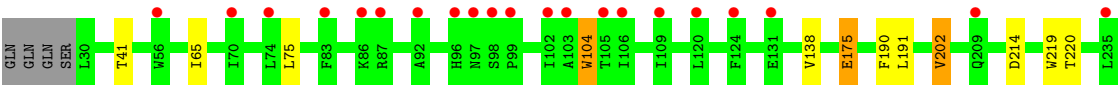
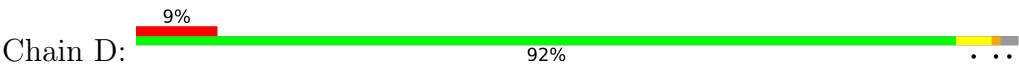


• Molecule 2: Cytochrome C oxidase subunit 2





● 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	124.61Å 131.47Å 176.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 50.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-2.15) 99.1 (50.00-2.15)	Depositor EDS
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 0.197 , 0.221	Depositor DCC
R_{free} test set	4375 reflections (2.81%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 61.4	EDS
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
F_o, F_c correlation	0.95	EDS
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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, HEA, DMU, CU1, UNX, CD, TRD, HTO, CA

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	0.72	0/4377	0.90	2/5973 (0.0%)
1	C	0.60	1/4326 (0.0%)	0.89	1/5905 (0.0%)
2	B	0.66	0/2096	0.81	0/2869
2	D	0.61	0/2096	0.83	1/2869 (0.0%)
All	All	0.65	1/12895 (0.0%)	0.87	4/17616 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	284	HIS	CE1-NE2	5.59	1.38	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	284	HIS	N-CA-CB	7.68	117.69	110.39
1	A	538	LEU	N-CA-C	6.14	118.78	111.71
2	D	202	VAL	CB-CA-C	-6.03	102.21	111.08
1	A	284	HIS	N-CA-CB	5.80	118.46	110.11

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	4218	0	4139	32	0
1	C	4172	0	4095	34	0
2	B	2031	0	1988	8	0
2	D	2031	0	1988	9	0
3	A	120	0	108	5	0
3	C	120	0	108	6	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	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	1	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	88	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 (88) 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
1:A:381:MET:HA	1:A:381:MET:HE2	1.56	0.85
1:A:21:PHE:HB3	1:A:144:TRP:HZ2	1.42	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:ILE:HG22	2:B:35:ARG:HD3	1.62	0.81
1:C:182:GLU:O	1:C:257:ARG:NH1	2.21	0.73
1:A:381:MET:HA	1:A:381:MET:CE	2.21	0.70
1:C:302:ILE:HA	1:C:381:MET:HE1	1.74	0.69
1:A:350:MET:HA	1:A:353:MET:HE3	1.74	0.69
1:C:56:MET:HE1	8:C:1005:DMU:H7	1.74	0.68
1:C:253:LEU:O	1:C:257:ARG:HG3	1.93	0.68
1:C:381:MET:HE2	1:C:381:MET:HA	1.74	0.67
1:A:301:VAL:HG12	1:A:381:MET:CE	2.25	0.67
1:A:302:ILE:HA	1:A:381:MET:HE1	1.76	0.67
1:C:349:MET:HG2	1:C:353:MET:HE2	1.76	0.67
1:C:50:TYR:OH	1:C:79:SER:HB2	1.96	0.66
1:C:543:THR:HG22	1:C:547:PRO:HD3	1.77	0.65
3:C:567:HEA:HBC1	3:C:567:HEA:HMC3	1.78	0.65
3:A:568:HEA:HBD2	3:A:568:HEA:HMD1	1.80	0.64
1:C:367:ILE:HA	1:C:370:MET:HE3	1.79	0.64
1:C:367:ILE:HA	1:C:370:MET:CE	2.28	0.63
1:C:381:MET:HA	1:C:381:MET:CE	2.29	0.63
7:A:573:UNX:UNK	12:A:666:HOH:O	1.81	0.61
1:C:350:MET:HA	1:C:353:MET:HE3	1.81	0.61
1:C:284:HIS:CD2	1:C:284:HIS:C	2.79	0.60
1:A:346:SER:O	1:A:350:MET:HG2	2.03	0.58
1:C:396:VAL:HB	2:D:65:ILE:HB	1.85	0.58
3:C:568:HEA:HMD1	3:C:568:HEA:HBD2	1.84	0.58
1:A:396:VAL:HB	2:B:65:ILE:HB	1.84	0.58
1:C:349:MET:O	1:C:353:MET:HG3	2.03	0.57
1:A:350:MET:HA	1:A:353:MET:CE	2.33	0.57
1:A:204:GLY:O	1:A:208:MET:HG2	2.04	0.56
1:C:543:THR:HG23	1:C:545:PRO:O	2.06	0.56
2:B:35:ARG:HD2	12:B:347:HOH:O	2.07	0.55
1:A:349:MET:HG2	1:A:353:MET:HE2	1.88	0.55
1:C:287:VAL:HB	3:C:568:HEA:HAC	1.89	0.55
1:A:17:PHE:C	1:A:19:ARG:H	2.15	0.55
1:A:357:VAL:O	1:A:361:ILE:HG12	2.07	0.54
1:A:21:PHE:HB3	1:A:144:TRP:CZ2	2.33	0.54
1:C:204:GLY:O	1:C:208:MET:HG2	2.09	0.53
1:C:398:GLY:C	3:C:568:HEA:HMB2	2.35	0.52
3:A:567:HEA:HMC1	3:A:567:HEA:HBC1	1.92	0.51
1:C:346:SER:O	1:C:350:MET:HG2	2.10	0.51
1:A:56:MET:HE1	8:A:577:DMU:H6	1.93	0.51
1:A:284:HIS:C	1:A:284:HIS:CD2	2.90	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:41:THR:OG1	9:D:1007:TRD:H12	2.12	0.50
1:A:442:LYS:O	1:A:545:PRO:HA	2.13	0.49
1:A:86[B]:GLU:H	1:A:86[B]:GLU:CD	2.21	0.49
2:D:104:TRP:CD1	2:D:104:TRP:C	2.91	0.48
1:C:52:ARG:HG3	1:C:501:ALA:CB	2.44	0.48
1:C:301:VAL:HG12	1:C:381:MET:CE	2.44	0.47
1:C:547:PRO:HD2	1:C:550:THR:CG2	2.44	0.47
3:C:567:HEA:HBC1	3:C:567:HEA:CMC	2.45	0.47
1:C:319:ALA:HB3	1:C:362:LYS:HE2	1.96	0.47
1:A:332:ALA:HB1	1:A:340:LEU:HD11	1.97	0.46
1:A:287:VAL:HB	3:A:568:HEA:HAC	1.97	0.46
1:C:128:ILE:HB	1:C:216:ARG:HG2	1.97	0.46
2:D:75:LEU:HD13	8:D:1003:DMU:H18	1.98	0.45
1:C:381:MET:HE2	1:C:384:ALA:HB3	1.98	0.45
8:A:577:DMU:H12	9:A:578:TRD:H92	1.99	0.45
1:C:131:PRO:HA	1:C:550:THR:O	2.17	0.44
2:D:220:THR:O	2:D:250:GLY:HA3	2.18	0.44
2:B:138:VAL:HG11	2:B:219:TRP:CD1	2.52	0.44
1:A:128:ILE:HB	1:A:216:ARG:HG2	2.00	0.44
1:A:45:VAL:HG21	3:A:567:HEA:H171	1.99	0.44
1:C:279:LEU:C	1:C:279:LEU:HD13	2.43	0.44
3:A:568:HEA:H212	3:A:568:HEA:H18	1.78	0.43
1:C:377:LEU:HD13	9:C:1010:TRD:H31	1.99	0.43
1:A:212:PHE:CE2	1:A:225:VAL:HG11	2.53	0.43
1:C:486:TYR:CD2	1:C:490:PHE:HB2	2.54	0.43
2:D:238:LEU:C	2:D:238:LEU:HD12	2.44	0.43
1:A:421:HIS:HA	1:A:425:SER:HB2	2.01	0.43
1:A:301:VAL:HG12	1:A:381:MET:HE3	1.98	0.43
1:A:350:MET:SD	9:B:289:TRD:H41	2.59	0.43
1:A:302:ILE:HG12	1:A:381:MET:HE1	2.01	0.42
2:D:138:VAL:HG11	2:D:219:TRP:CD1	2.52	0.42
1:A:94:LEU:O	1:A:98:MET:HG2	2.19	0.42
1:C:291:VAL:HB	3:C:568:HEA:HBC2	2.00	0.42
1:A:51:MET:HE3	1:A:99:ILE:HG22	2.02	0.42
1:C:240:LEU:O	1:C:244:PRO:HG2	2.19	0.42
2:B:273:GLU:HG3	12:B:348:HOH:O	2.20	0.41
1:A:307:LYS:HE2	1:A:374:SER:HB3	2.03	0.41
2:D:175:GLU:H	2:D:175:GLU:CD	2.28	0.41
1:A:319:ALA:HB3	1:A:362:LYS:HE2	2.01	0.41
2:B:104:TRP:CD1	2:B:104:TRP:C	2.99	0.41
1:A:93:HIS:HB2	2:B:258:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:284:HIS:O	1:C:287:VAL:HG22	2.21	0.40
1:C:301:VAL:HG12	1:C:381:MET:HE3	2.03	0.40
2:D:190:PHE:O	2:D:191:LEU:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	534/566 (94%)	524 (98%)	9 (2%)	1 (0%)	43	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	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	THR

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	436/459 (95%)	424 (97%)	12 (3%)	38	40
1	C	431/459 (94%)	424 (98%)	7 (2%)	55	61
2	B	216/221 (98%)	214 (99%)	2 (1%)	70	77
2	D	216/221 (98%)	212 (98%)	4 (2%)	50	56
All	All	1299/1360 (96%)	1274 (98%)	25 (2%)	50	56

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ARG
1	A	61	GLN
1	A	80	LEU
1	A	137	ARG
1	A	174	LEU
1	A	183	SER
1	A	222	MET
1	A	291	VAL
1	A	361	ILE
1	A	381	MET
1	A	412	ASP
1	A	550	THR
2	B	35	ARG
2	B	104	TRP
1	C	61	GLN
1	C	174	LEU
1	C	222	MET
1	C	291	VAL
1	C	376	GLU
1	C	381	MET
1	C	412	ASP
2	D	104	TRP
2	D	175	GLU
2	D	202	VAL
2	D	214	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	ASN
1	A	165	GLN

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Mol	Chain	Res	Type
2	B	170	ASN
2	B	251	GLN
1	C	25	ASN
1	C	140	ASN
1	C	465	ASN
2	D	127	GLN
2	D	170	ASN
2	D	179	GLN
2	D	237	GLN
2	D	251	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 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	C	1005	-	34,34,34	0.59	1 (2%)	45,45,45	0.85	1 (2%)
8	DMU	B	11	-	24,24,34	0.50	0	35,35,45	0.84	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEA	C	568	1	67,67,67	1.95	6 (8%)	81,103,103	1.57	18 (22%)
9	TRD	B	289	-	6,6,12	0.31	0	5,5,11	0.29	0
9	TRD	D	1008	-	6,6,12	0.28	0	5,5,11	0.34	0
8	DMU	D	1011	-	24,24,34	0.51	0	35,35,45	0.84	0
8	DMU	D	1003	-	34,34,34	0.56	0	45,45,45	0.59	0
8	DMU	A	577	-	34,34,34	0.60	1 (2%)	45,45,45	0.95	1 (2%)
9	TRD	C	1006	-	12,12,12	0.28	0	11,11,11	0.51	0
3	HEA	C	567	1	67,67,67	1.08	6 (8%)	81,103,103	0.95	0
3	HEA	A	568	1	67,67,67	1.75	7 (10%)	81,103,103	1.63	19 (23%)
9	TRD	A	581	-	12,12,12	0.25	0	11,11,11	0.52	0
8	DMU	C	1002	-	24,24,34	0.51	0	35,35,45	0.66	0
9	TRD	A	578	-	12,12,12	0.27	0	11,11,11	0.49	0
9	TRD	C	1001	-	12,12,12	0.28	0	11,11,11	0.45	0
8	DMU	A	574	-	34,34,34	0.52	0	45,45,45	1.03	3 (6%)
8	DMU	A	575	-	34,34,34	0.58	1 (2%)	45,45,45	0.99	3 (6%)
9	TRD	C	1010	-	8,8,12	0.29	0	7,7,11	0.39	0
9	TRD	C	1009	-	6,6,12	0.29	0	5,5,11	0.36	0
9	TRD	A	582	-	8,8,12	0.27	0	7,7,11	0.46	0
3	HEA	A	567	1	67,67,67	1.10	5 (7%)	81,103,103	1.08	6 (7%)
9	TRD	A	579	-	12,12,12	0.28	0	11,11,11	0.43	0
9	TRD	D	1007	-	12,12,12	0.22	0	11,11,11	0.60	0
10	HTO	B	1	-	9,9,9	0.44	0	10,10,10	0.67	0
8	DMU	A	576	-	22,22,34	0.57	1 (4%)	27,27,45	0.93	2 (7%)
8	DMU	B	288	-	34,34,34	0.57	0	45,45,45	0.69	0
9	TRD	A	580	-	6,6,12	0.25	0	5,5,11	0.42	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	C	1005	-	-	9/19/59/59	0/2/2/2
8	DMU	B	11	-	-	1/8/48/59	0/2/2/2
3	HEA	C	568	1	-	6/36/76/76	-
9	TRD	B	289	-	-	1/4/4/10	-
9	TRD	D	1008	-	-	1/4/4/10	-
8	DMU	D	1011	-	-	2/8/48/59	0/2/2/2
8	DMU	D	1003	-	-	5/19/59/59	0/2/2/2
8	DMU	A	577	-	-	10/19/59/59	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	TRD	C	1006	-	-	3/10/10/10	-
3	HEA	C	567	1	-	4/36/76/76	-
3	HEA	A	568	1	-	7/36/76/76	-
9	TRD	A	581	-	-	6/10/10/10	-
8	DMU	C	1002	-	-	2/8/48/59	0/2/2/2
9	TRD	A	578	-	-	7/10/10/10	-
9	TRD	C	1001	-	-	4/10/10/10	-
8	DMU	A	574	-	-	3/19/59/59	0/2/2/2
8	DMU	A	575	-	-	6/19/59/59	0/2/2/2
9	TRD	C	1010	-	-	4/6/6/10	-
9	TRD	C	1009	-	-	0/4/4/10	-
9	TRD	A	582	-	-	3/6/6/10	-
3	HEA	A	567	1	-	4/36/76/76	-
9	TRD	A	579	-	-	5/10/10/10	-
9	TRD	D	1007	-	-	8/10/10/10	-
10	HTO	B	1	-	1/1/2/2	4/10/10/10	-
8	DMU	A	576	-	-	9/13/33/59	0/1/1/2
8	DMU	B	288	-	-	5/19/59/59	0/2/2/2
9	TRD	A	580	-	-	1/4/4/10	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	568	HEA	FE-NB	9.76	2.25	1.94
3	A	568	HEA	FE-NA	7.14	2.18	1.95
3	A	568	HEA	FE-NB	6.87	2.16	1.94
3	C	568	HEA	FE-NC	6.76	2.17	1.95
3	C	568	HEA	C11-C3B	5.53	1.58	1.51
3	C	568	HEA	FE-NA	5.07	2.11	1.95
3	A	568	HEA	C11-C3B	4.76	1.57	1.51
3	A	568	HEA	FE-NC	4.00	2.08	1.95
3	A	567	HEA	CMA-C3A	2.93	1.51	1.45
3	A	568	HEA	CMD-C2D	2.86	1.56	1.50
3	A	567	HEA	CAC-C3C	2.86	1.55	1.47
3	C	567	HEA	C11-C3B	2.80	1.54	1.51
3	C	567	HEA	CMA-C3A	2.74	1.51	1.45
3	A	568	HEA	FE-ND	2.73	2.03	1.94
3	C	567	HEA	CMC-C2C	2.42	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	567	HEA	CMB-C2B	2.38	1.55	1.50
3	A	567	HEA	CMD-C2D	2.32	1.55	1.50
3	C	567	HEA	CAC-C3C	2.29	1.53	1.47
8	A	575	DMU	O16-C6	2.25	1.44	1.40
3	C	567	HEA	CMB-C2B	2.21	1.55	1.50
3	C	568	HEA	CMA-C3A	2.16	1.50	1.45
3	C	568	HEA	CAC-C3C	2.14	1.53	1.47
8	A	577	DMU	O16-C6	2.09	1.43	1.40
3	A	568	HEA	CMB-C2B	2.09	1.55	1.50
8	A	576	DMU	O16-C6	2.04	1.43	1.40
3	A	567	HEA	CMC-C2C	2.02	1.54	1.50
3	C	567	HEA	CMD-C2D	2.01	1.54	1.50
8	C	1005	DMU	O16-C6	2.00	1.43	1.40

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	568	HEA	C3C-C4C-NC	-5.08	105.52	109.80
3	A	568	HEA	C3C-C4C-NC	-4.84	105.72	109.80
8	A	575	DMU	O16-C6-C1	3.88	114.17	108.27
3	A	568	HEA	C2A-C1A-NA	-3.59	106.86	110.32
3	C	568	HEA	C4C-NC-C1C	3.24	111.10	105.82
3	A	567	HEA	C27-C19-C20	3.21	120.81	115.23
3	A	568	HEA	C4C-NC-C1C	3.17	110.99	105.82
3	A	568	HEA	C26-C15-C16	3.07	120.55	115.23
3	C	568	HEA	C2A-C1A-NA	-3.07	107.36	110.32
3	C	568	HEA	C4B-NB-C1B	3.01	108.78	105.21
3	A	568	HEA	CMB-C2B-C3B	-2.96	124.56	130.28
3	A	568	HEA	OMA-CMA-C3A	-2.95	118.96	125.62
3	A	567	HEA	C26-C15-C16	2.93	120.31	115.23
3	C	568	HEA	CMB-C2B-C3B	-2.83	124.80	130.28
3	A	568	HEA	C4A-C3A-C2A	2.79	109.24	106.81
3	A	567	HEA	C13-C12-C11	-2.79	109.93	114.39
3	A	568	HEA	C4A-NA-C1A	2.69	110.20	105.82
3	A	568	HEA	CBD-CAD-C3D	2.61	119.74	112.53
3	A	568	HEA	C27-C19-C20	2.60	119.75	115.23
3	A	568	HEA	C13-C14-C15	-2.57	121.75	127.62
3	C	568	HEA	C2B-C1B-NB	-2.53	106.98	109.90
3	C	568	HEA	C4A-NA-C1A	2.53	109.94	105.82
3	C	568	HEA	CBA-CAA-C2A	-2.50	105.61	112.53
8	A	575	DMU	C10-O1-C9	2.50	118.60	113.72
8	A	575	DMU	C10-O7-C3	-2.49	112.08	117.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	574	DMU	C10-O7-C3	-2.48	112.09	117.98
3	A	568	HEA	CHA-C4D-ND	2.48	127.10	124.42
8	A	577	DMU	O16-C6-C1	2.44	111.98	108.27
3	C	568	HEA	C17-C18-C19	-2.44	122.04	127.62
3	A	567	HEA	C17-C18-C19	-2.38	122.17	127.62
3	C	568	HEA	C2C-C1C-NC	-2.34	106.39	110.14
3	C	568	HEA	OMA-CMA-C3A	-2.34	120.35	125.62
3	A	568	HEA	CHC-C1C-NC	2.32	128.07	123.86
3	C	568	HEA	C4A-C3A-C2A	2.32	108.82	106.81
3	C	568	HEA	C1B-C2B-C3B	2.30	109.46	106.80
8	C	1005	DMU	C10-O1-C9	2.28	118.16	113.72
8	A	574	DMU	O2-C8-C9	2.27	114.92	109.32
3	A	568	HEA	C13-C12-C11	-2.27	110.77	114.39
3	C	568	HEA	C2D-C1D-ND	-2.25	107.25	109.84
3	A	568	HEA	CHB-C4A-NA	2.19	126.84	124.45
8	A	574	DMU	C7-C8-C9	-2.18	106.29	110.23
3	A	568	HEA	C2C-C1C-NC	-2.17	106.66	110.14
3	C	568	HEA	C26-C15-C16	2.17	118.99	115.23
3	C	568	HEA	CBD-CAD-C3D	2.15	118.47	112.53
8	A	576	DMU	O16-C6-C1	2.14	111.53	108.27
8	A	576	DMU	C18-O16-C6	-2.13	110.05	113.68
3	A	567	HEA	O2A-CGA-CBA	2.11	120.68	114.00
3	A	568	HEA	CBA-CAA-C2A	-2.10	106.73	112.53
3	C	568	HEA	C1D-C2D-C3D	2.10	109.19	106.98
3	A	567	HEA	O2D-CGD-CBD	2.09	120.61	114.00
3	C	568	HEA	C27-C19-C20	2.07	118.83	115.23
3	A	568	HEA	C12-C13-C14	-2.04	106.79	112.16
3	A	568	HEA	C17-C18-C19	-2.01	123.03	127.62

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	B	1	HTO	C2

All (120) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	568	HEA	C2A-C3A-CMA-OMA
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

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Mol	Chain	Res	Type	Atoms
3	A	568	HEA	C4D-C3D-CAD-CBD
3	C	568	HEA	C4D-C3D-CAD-CBD
8	A	576	DMU	O5-C4-C57-O61
8	C	1005	DMU	O1-C10-O7-C3
8	C	1002	DMU	O6-C11-C9-O1
8	D	1003	DMU	O6-C11-C9-O1
8	A	575	DMU	O6-C11-C9-O1
8	A	575	DMU	O5-C6-O16-C18
8	A	576	DMU	C3-C4-C57-O61
8	D	1003	DMU	O6-C11-C9-C8
8	A	575	DMU	C1-C6-O16-C18
8	A	577	DMU	C3-C4-C57-O61
8	C	1002	DMU	O6-C11-C9-C8
8	D	1011	DMU	O5-C4-C57-O61
8	A	576	DMU	C1-C6-O16-C18
10	B	1	HTO	O3-C3-C4-C5
8	A	576	DMU	O5-C6-O16-C18
8	A	577	DMU	O1-C10-O7-C3
8	A	575	DMU	C19-C18-O16-C6
8	C	1005	DMU	C19-C18-O16-C6
8	A	576	DMU	C19-C22-C25-C28
8	A	575	DMU	O6-C11-C9-C8
9	D	1008	TRD	C2-C3-C4-C5
8	B	288	DMU	C25-C28-C31-C34
9	C	1001	TRD	C5-C6-C7-C8
8	A	576	DMU	C28-C31-C34-C37
8	A	577	DMU	C28-C31-C34-C37
9	A	579	TRD	C4-C5-C6-C7
8	B	288	DMU	C28-C31-C34-C37
9	D	1007	TRD	C4-C5-C6-C7
9	C	1010	TRD	C3-C4-C5-C6
8	A	575	DMU	C28-C31-C34-C37
8	D	1003	DMU	C22-C25-C28-C31
8	B	11	DMU	O6-C11-C9-O1
9	D	1007	TRD	C6-C7-C8-C9
9	A	581	TRD	C9-C10-C11-C12
8	B	288	DMU	C22-C25-C28-C31
9	D	1007	TRD	C2-C3-C4-C5
8	D	1011	DMU	O6-C11-C9-O1
8	C	1005	DMU	C18-C19-C22-C25
8	C	1005	DMU	C28-C31-C34-C37
9	A	578	TRD	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
10	B	1	HTO	C2-C3-C4-C5
9	A	581	TRD	C5-C6-C7-C8
8	A	577	DMU	C2-C3-O7-C10
9	A	579	TRD	C2-C3-C4-C5
8	A	577	DMU	C4-C3-O7-C10
9	C	1001	TRD	C3-C4-C5-C6
9	D	1007	TRD	C5-C6-C7-C8
9	A	582	TRD	C2-C3-C4-C5
9	C	1001	TRD	C4-C5-C6-C7
9	D	1007	TRD	C10-C11-C12-C13
9	A	582	TRD	C6-C7-C8-C9
9	A	579	TRD	C6-C7-C8-C9
9	A	578	TRD	C11-C10-C9-C8
9	A	578	TRD	C9-C10-C11-C12
9	A	578	TRD	C3-C4-C5-C6
9	A	578	TRD	C5-C6-C7-C8
9	C	1001	TRD	C1-C2-C3-C4
9	A	582	TRD	C1-C2-C3-C4
8	A	574	DMU	C25-C28-C31-C34
9	C	1006	TRD	C5-C6-C7-C8
8	D	1003	DMU	C25-C28-C31-C34
8	A	577	DMU	O5-C4-C57-O61
8	A	574	DMU	C31-C34-C37-C40
9	D	1007	TRD	C11-C10-C9-C8
9	A	581	TRD	C6-C7-C8-C9
8	A	577	DMU	O5-C6-O16-C18
9	C	1006	TRD	C7-C8-C9-C10
9	C	1010	TRD	C4-C5-C6-C7
8	A	576	DMU	O16-C18-C19-C22
9	A	580	TRD	C4-C5-C6-C7
3	C	568	HEA	C19-C20-C21-C22
8	A	577	DMU	C1-C6-O16-C18
9	B	289	TRD	C4-C5-C6-C7
3	A	568	HEA	C4A-C3A-CMA-OMA
8	C	1005	DMU	C31-C34-C37-C40
9	A	581	TRD	C3-C4-C5-C6
9	A	579	TRD	C5-C6-C7-C8
3	A	568	HEA	C19-C20-C21-C22
8	C	1005	DMU	C3-C4-C57-O61
9	A	581	TRD	C2-C3-C4-C5
3	A	567	HEA	CAD-CBD-CGD-O2D
9	A	579	TRD	C11-C10-C9-C8

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Mol	Chain	Res	Type	Atoms
3	C	567	HEA	CAD-CBD-CGD-O1D
8	C	1005	DMU	C2-C3-O7-C10
3	A	567	HEA	CAD-CBD-CGD-O1D
3	A	568	HEA	CAA-CBA-CGA-O2A
8	A	576	DMU	C31-C34-C37-C40
9	C	1010	TRD	C6-C7-C8-C9
9	D	1007	TRD	C3-C4-C5-C6
3	C	568	HEA	CAA-CBA-CGA-O2A
3	C	567	HEA	CAD-CBD-CGD-O2D
3	C	568	HEA	CAA-CBA-CGA-O1A
8	A	577	DMU	C5-C10-O7-C3
9	A	581	TRD	C7-C8-C9-C10
3	A	568	HEA	CAA-CBA-CGA-O1A
8	A	576	DMU	C18-C19-C22-C25
8	D	1003	DMU	C28-C31-C34-C37
8	B	288	DMU	C19-C22-C25-C28
8	C	1005	DMU	C4-C3-O7-C10
9	D	1007	TRD	C9-C10-C11-C12
8	A	574	DMU	C18-C19-C22-C25
8	B	288	DMU	C3-C4-C57-O61
8	A	577	DMU	C31-C34-C37-C40
9	A	578	TRD	C1-C2-C3-C4
3	C	568	HEA	C4C-C3C-CAC-CBC
3	C	567	HEA	CAA-CBA-CGA-O1A
3	C	567	HEA	CAA-CBA-CGA-O2A
3	A	567	HEA	CAA-CBA-CGA-O1A
9	A	578	TRD	C6-C7-C8-C9
9	C	1010	TRD	C5-C6-C7-C8
9	C	1006	TRD	C10-C11-C12-C13
8	C	1005	DMU	C19-C22-C25-C28
3	A	567	HEA	CAA-CBA-CGA-O2A

There are no ring outliers.

11 monomers are involved in 18 short contacts:

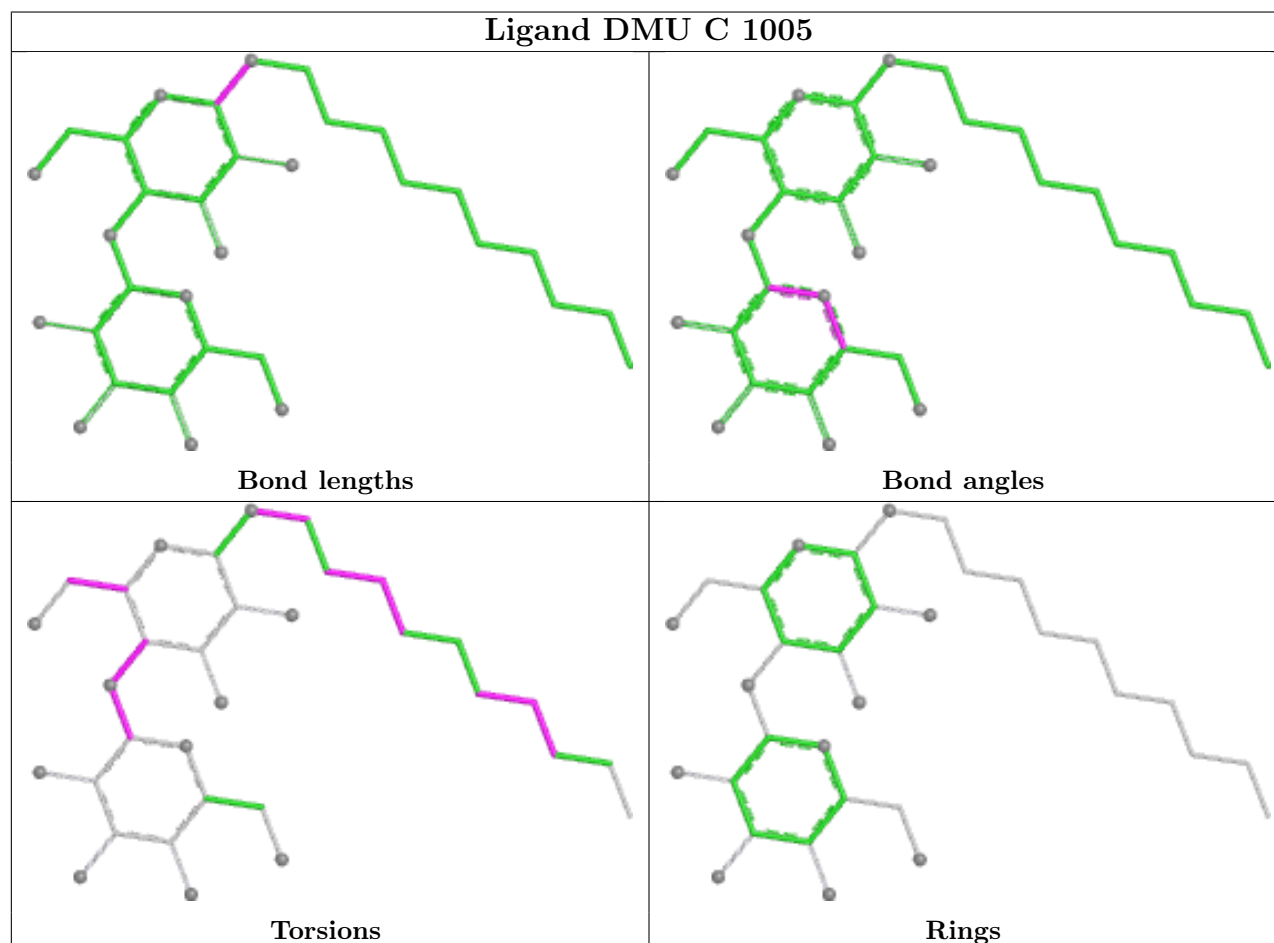
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	1005	DMU	1	0
3	C	568	HEA	4	0
9	B	289	TRD	1	0
8	D	1003	DMU	1	0
8	A	577	DMU	2	0
3	C	567	HEA	2	0

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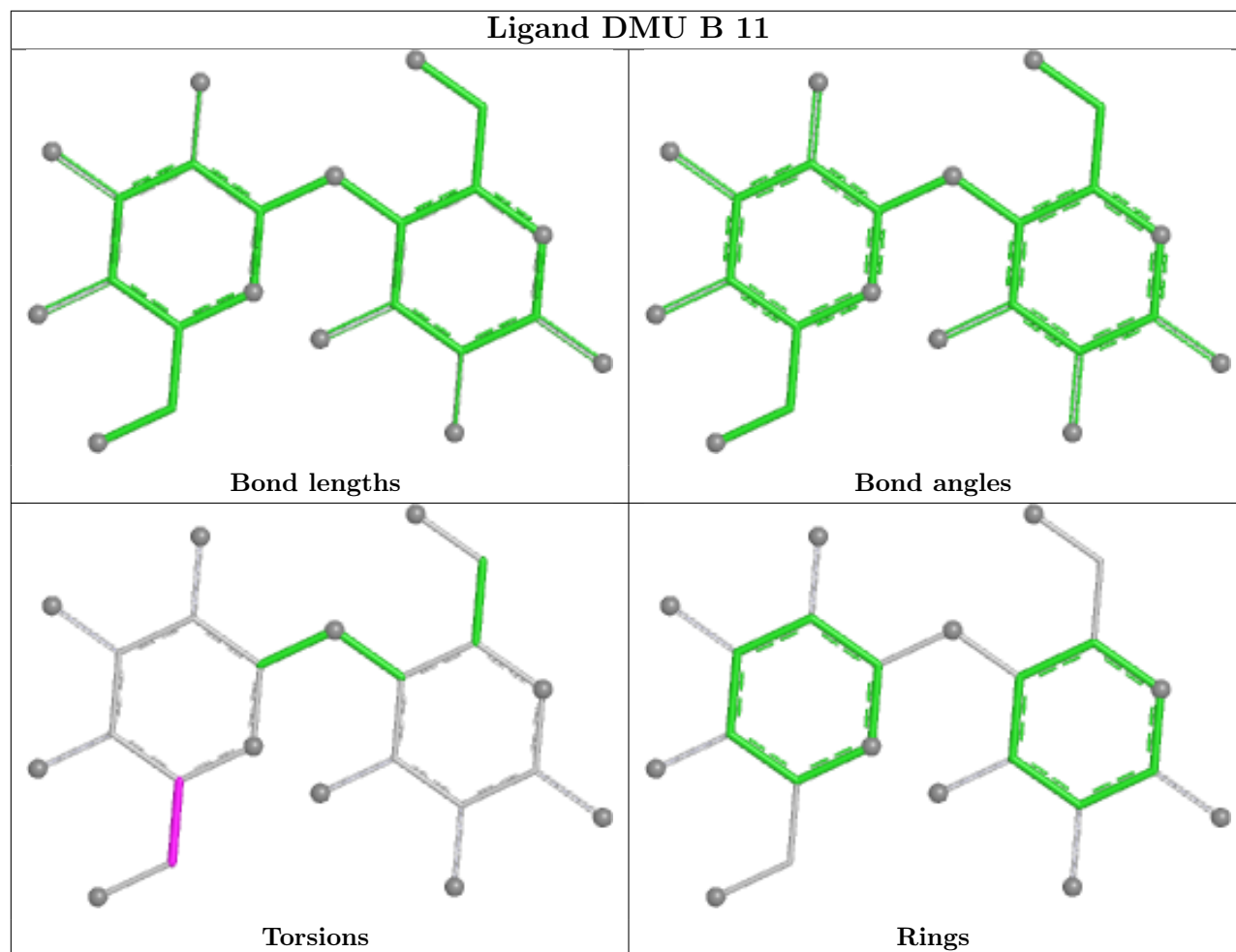
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	568	HEA	3	0
9	A	578	TRD	1	0
9	C	1010	TRD	1	0
3	A	567	HEA	2	0
9	D	1007	TRD	1	0

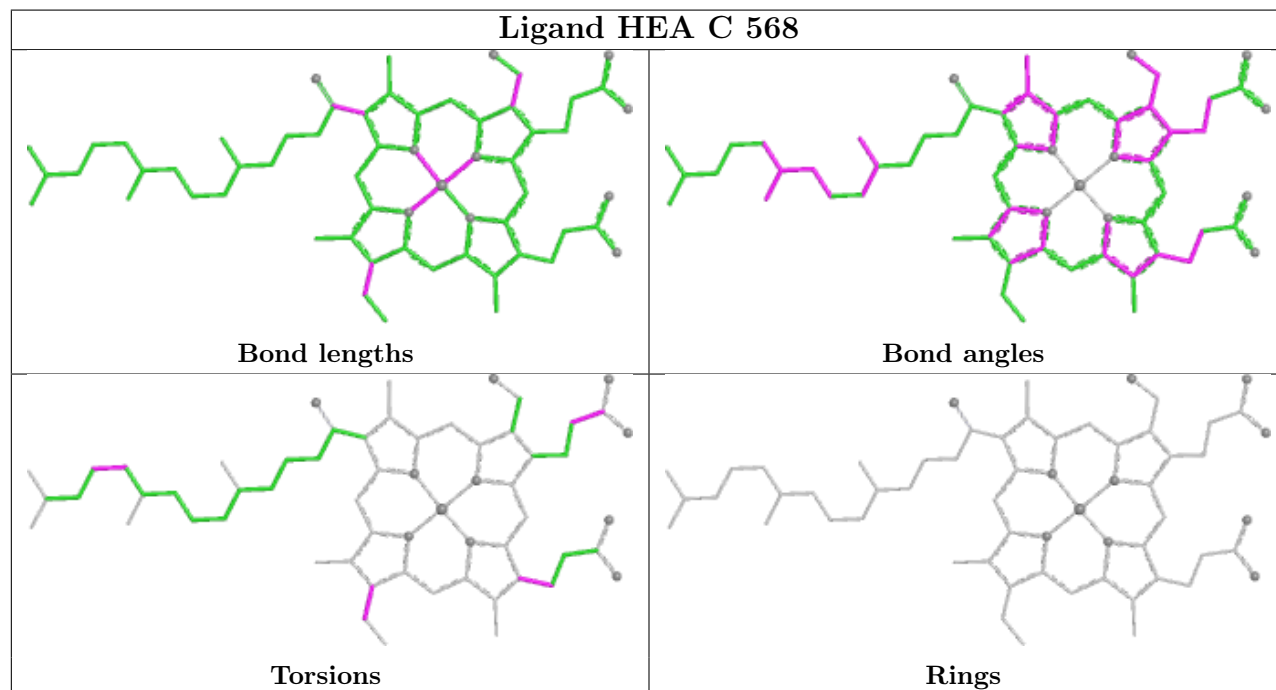
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



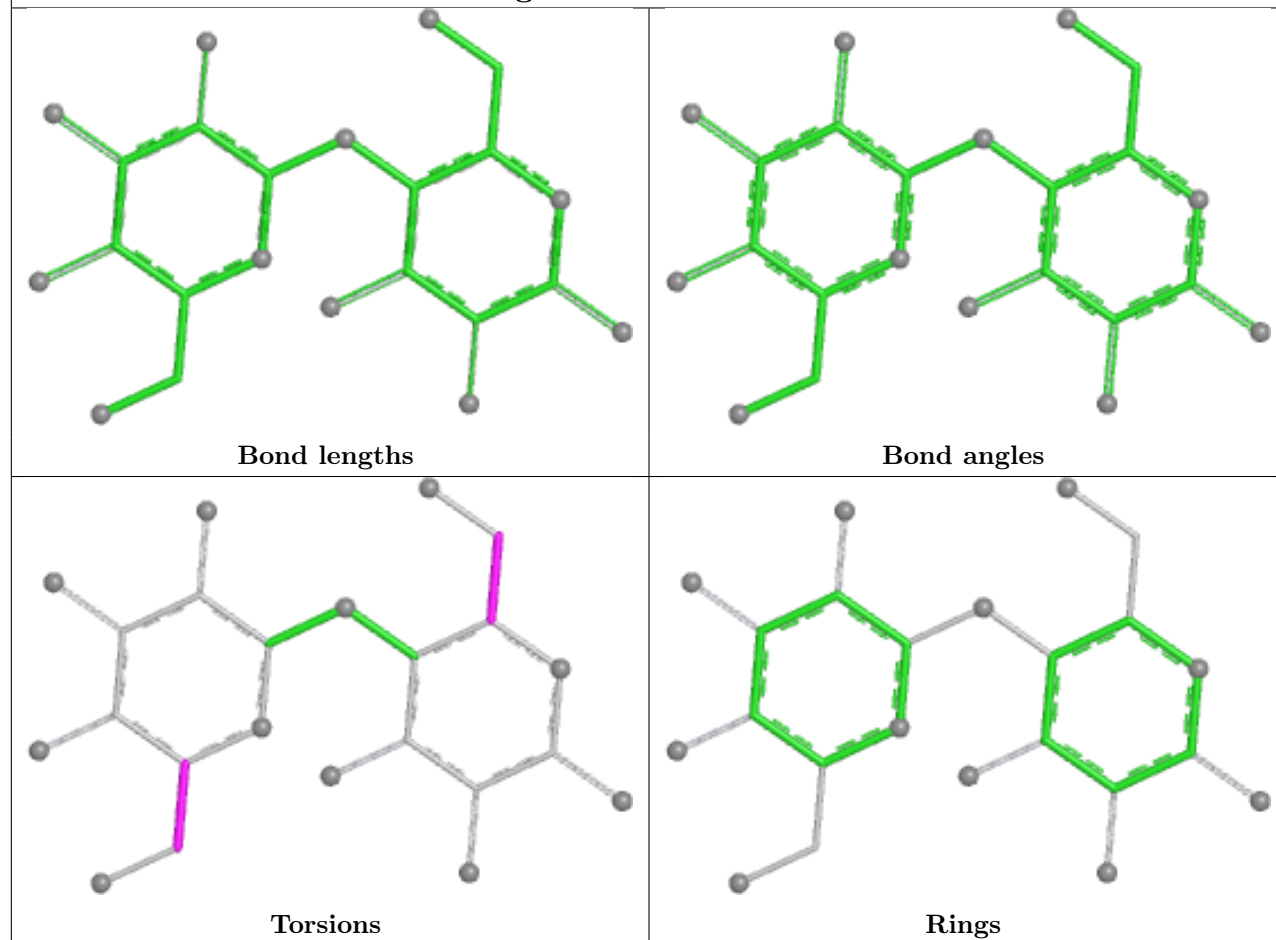
Ligand DMU B 11

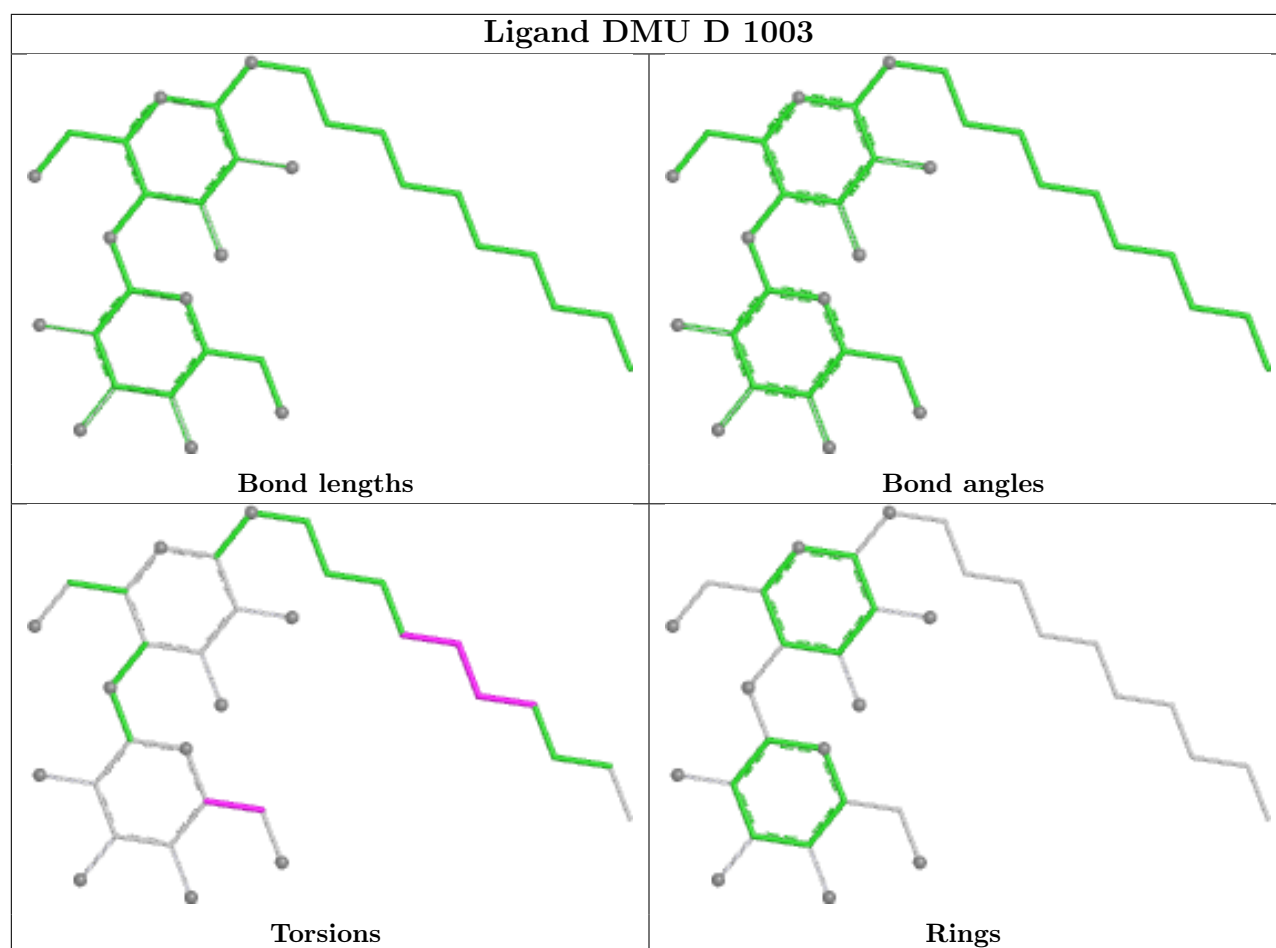


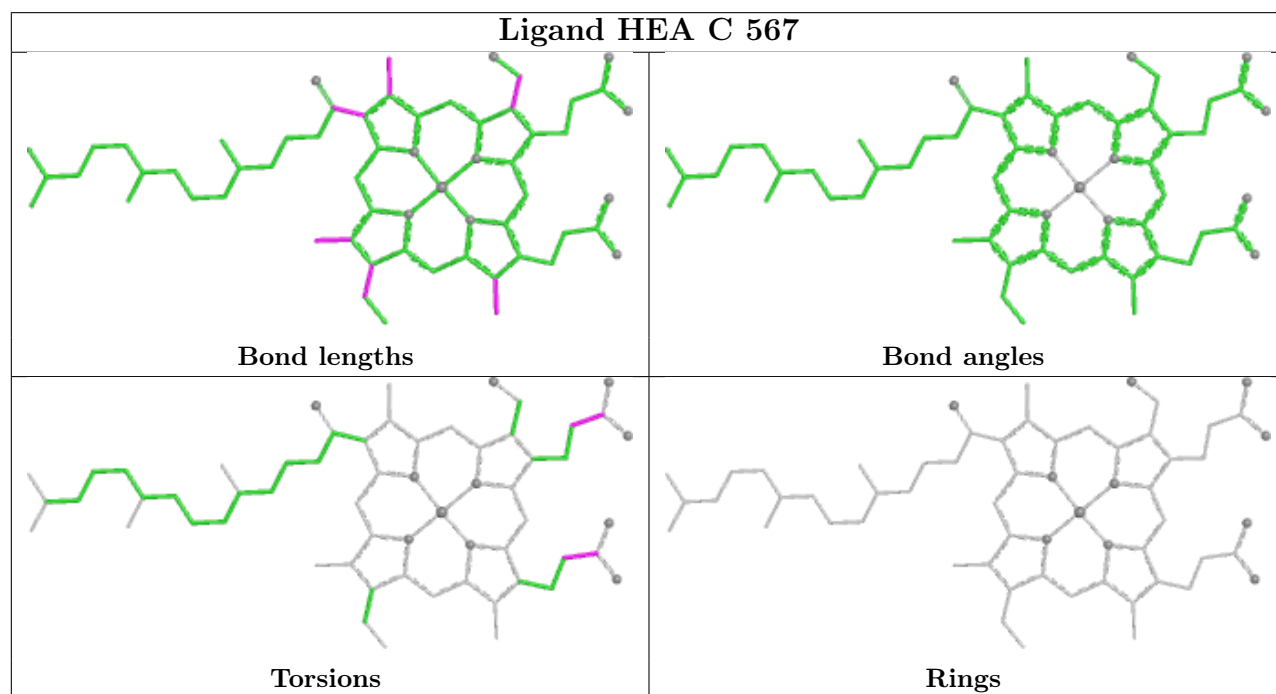
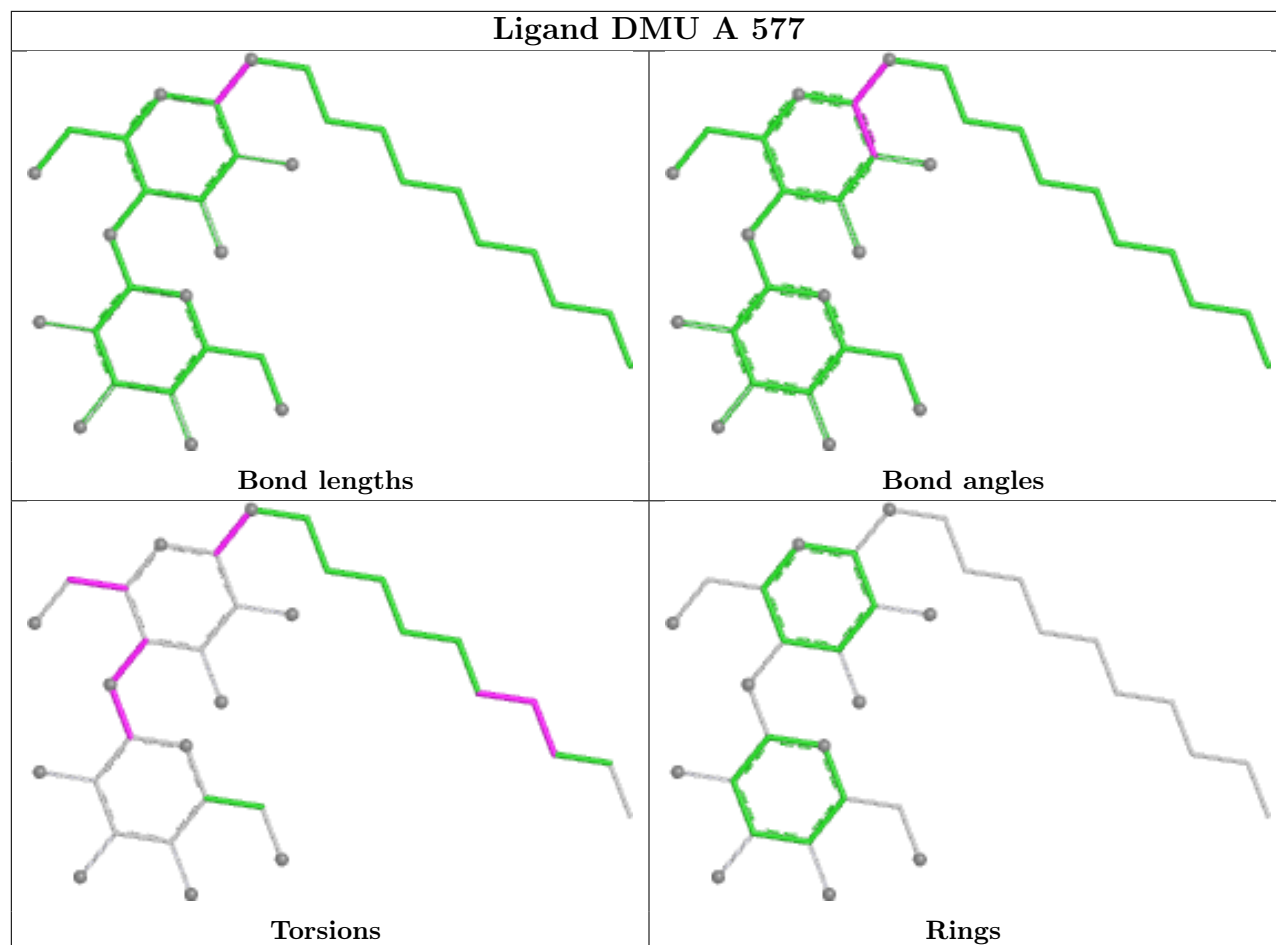
Ligand HEA C 568

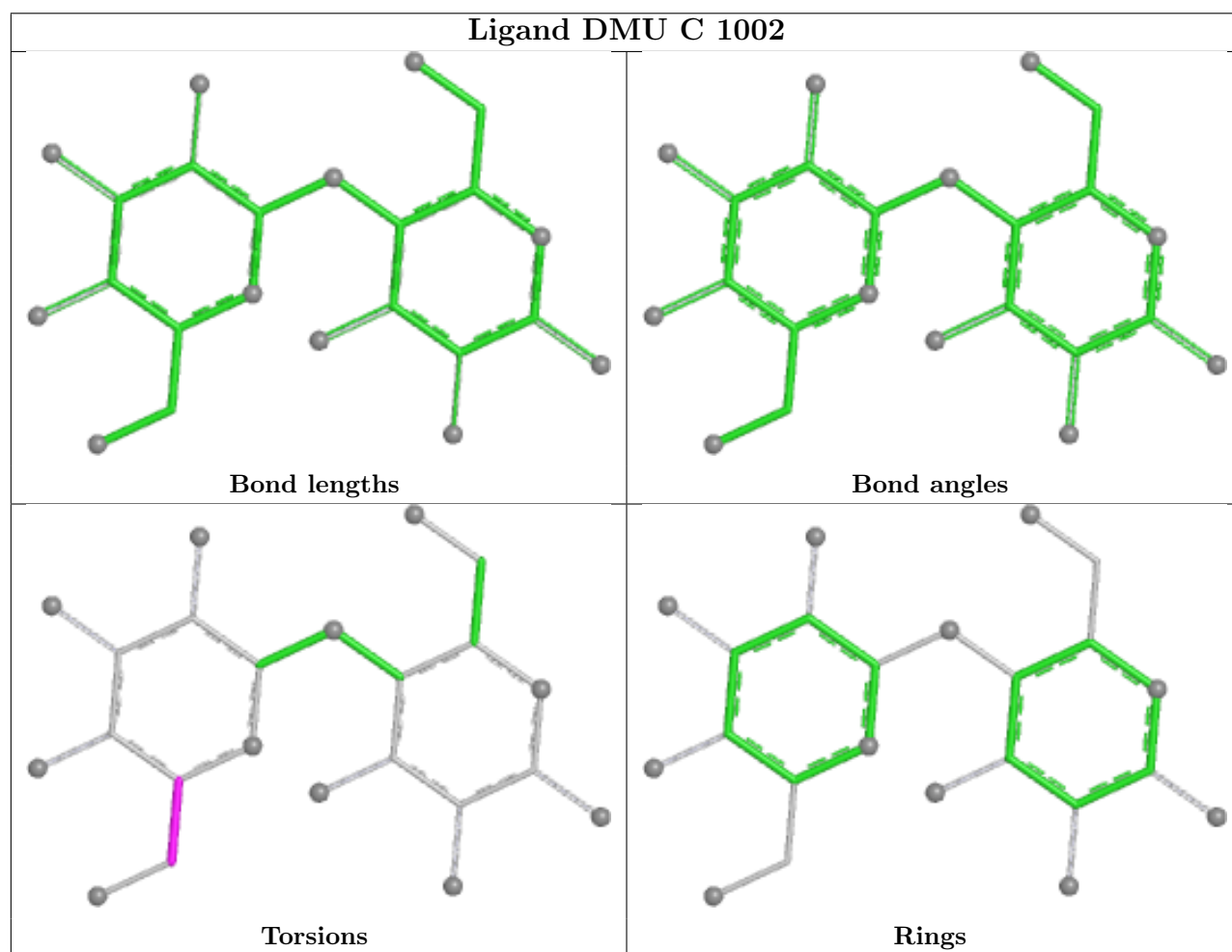
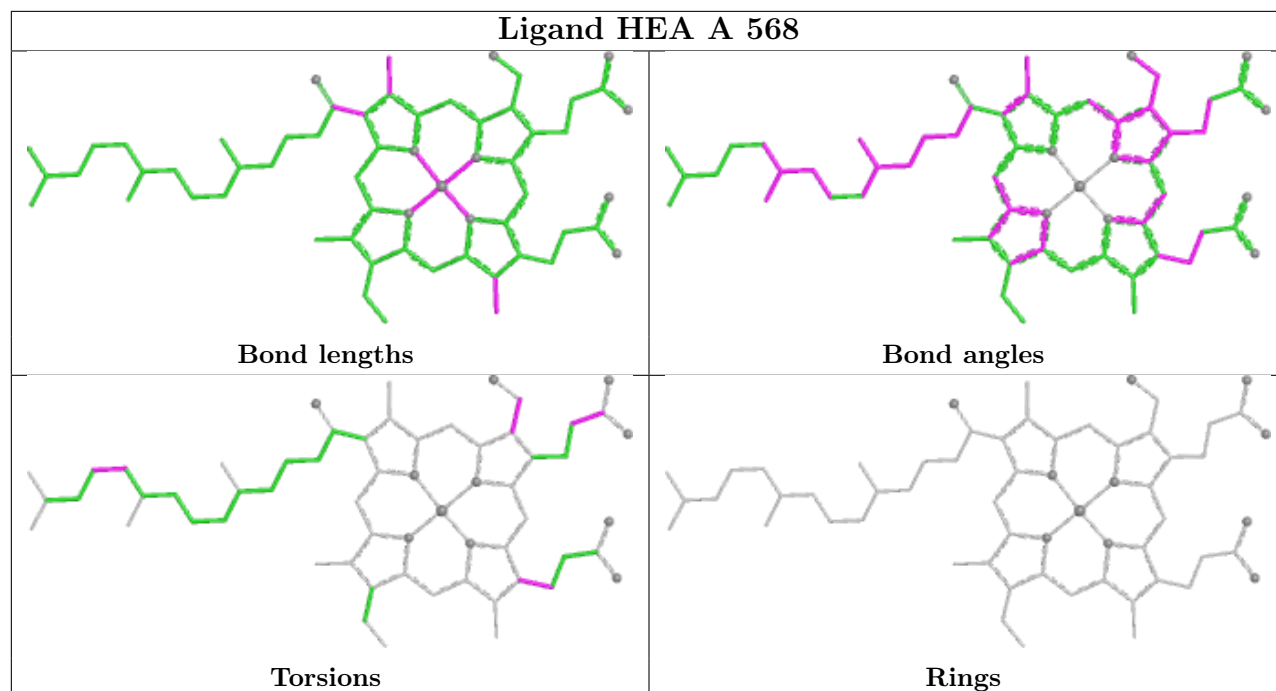


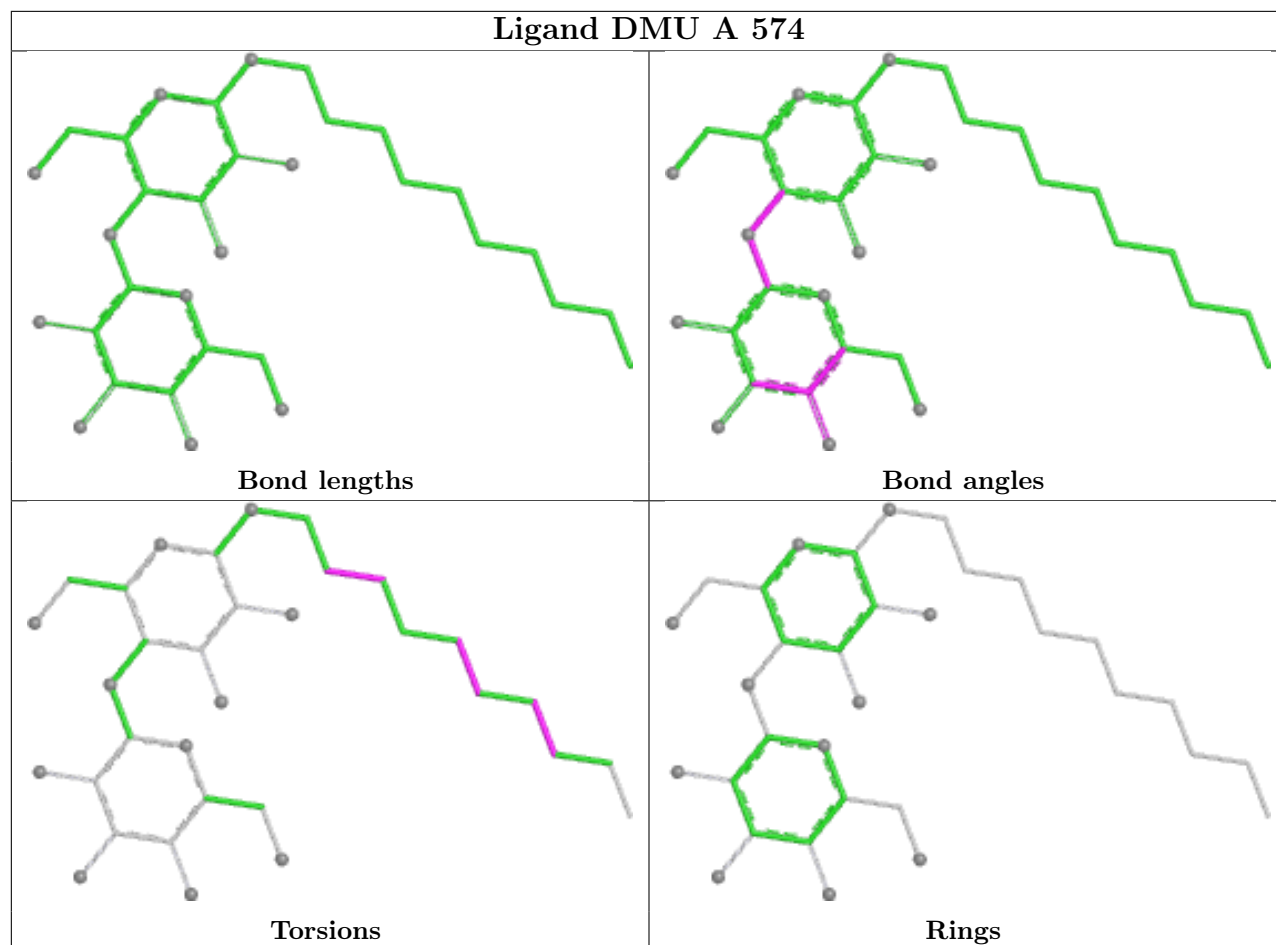
Ligand DMU D 1011

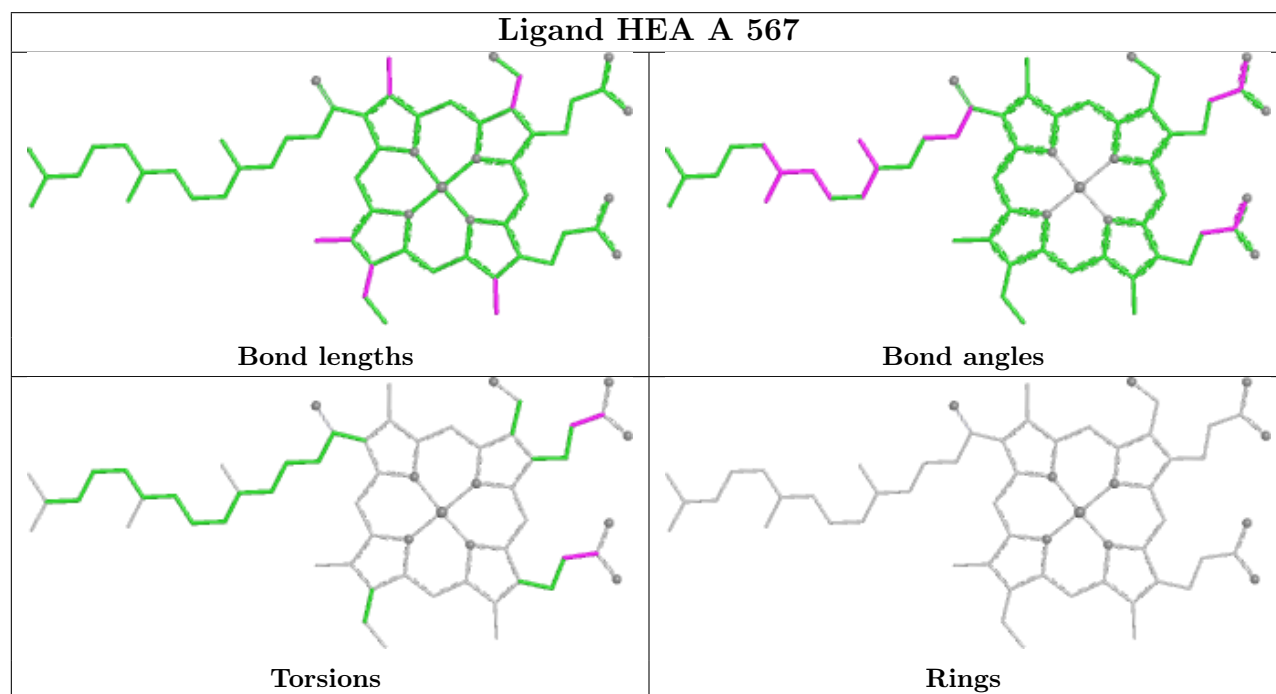
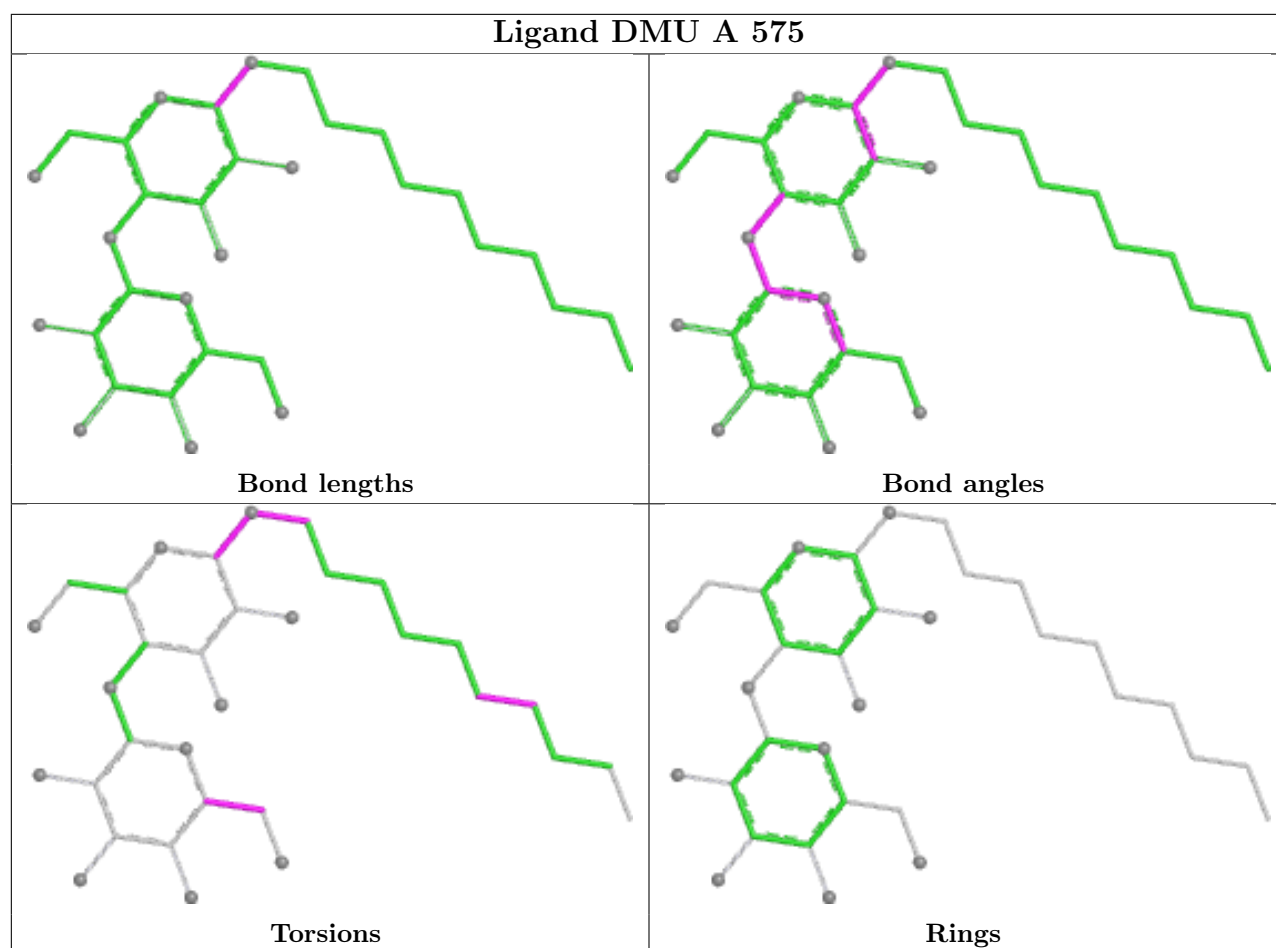


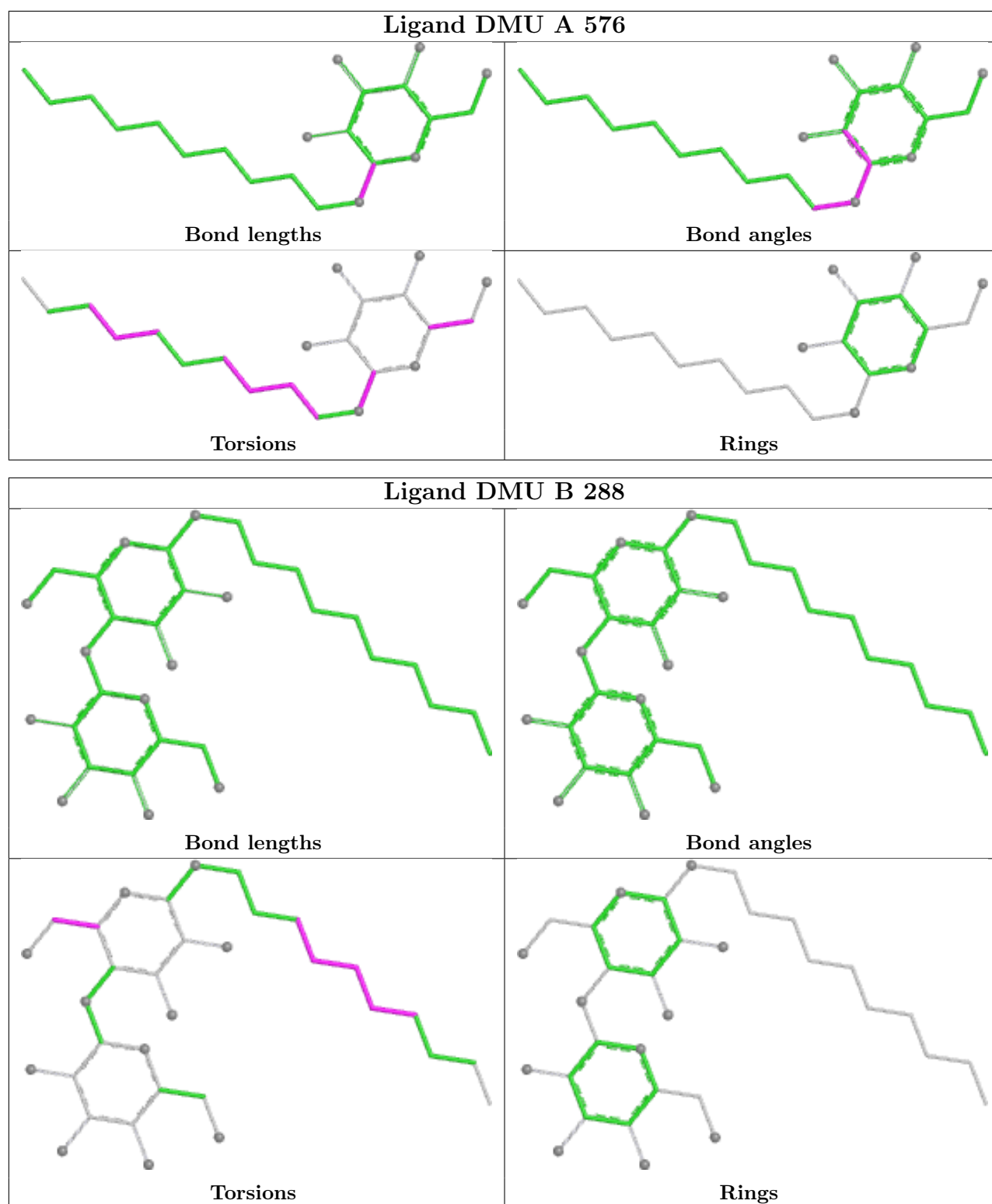












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	535/566 (94%)	0.25	26 (4%) 35 39	25, 37, 55, 74	7 (1%)
1	C	531/566 (93%)	1.02	82 (15%) 5 5	29, 52, 73, 96	5 (0%)
2	B	256/262 (97%)	0.33	11 (4%) 40 45	22, 41, 55, 62	3 (1%)
2	D	256/262 (97%)	0.56	23 (8%) 15 16	24, 45, 64, 73	3 (1%)
All	All	1578/1656 (95%)	0.57	142 (8%) 15 16	22, 43, 66, 96	18 (1%)

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	72	LEU	6.0
1	C	550	THR	5.5
2	B	56	TRP	5.4
1	A	20	TRP	5.1
1	A	81	TRP	5.1
1	C	549	HIS	5.1
1	C	20	TRP	4.6
1	A	551	PHE	4.6
2	D	109	ILE	4.4
1	A	22	MET	4.2
1	C	222	MET	4.0
1	A	18	THR	3.9
1	C	543	THR	3.8
1	C	73	VAL	3.7
1	C	318	TYR	3.7
1	C	76	PHE	3.6
1	C	138	MET	3.6
1	C	213	LEU	3.6
1	C	75	GLY	3.6
1	C	77	PHE	3.5
1	A	17	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	360	GLY	3.5
1	A	550	THR	3.5
2	D	74	LEU	3.4
1	C	126	LEU	3.3
1	C	145	LEU	3.3
2	D	105	THR	3.3
1	C	134	ALA	3.3
1	C	548	GLU	3.3
2	D	56	TRP	3.2
1	C	81	TRP	3.1
1	C	22	MET	3.1
1	C	196	LEU	3.1
1	C	129	GLY	3.1
2	B	70	ILE	3.1
1	C	214	ASN	3.0
1	C	80	LEU	3.0
1	C	546	PRO	3.0
1	C	217	ALA	3.0
2	D	98	SER	3.0
1	C	541	THR	3.0
2	B	281	GLN	2.9
1	A	19	ARG	2.9
2	D	235	LEU	2.8
1	C	547	PRO	2.8
2	B	209	GLN	2.8
1	C	118	GLY	2.8
2	D	86	LYS	2.8
2	D	284	HIS	2.8
1	C	215	MET	2.8
1	C	30	GLY	2.8
1	C	351	ALA	2.8
1	C	444	SER	2.8
1	C	221	THR	2.8
1	C	540	TRP	2.8
1	C	23	SER	2.7
1	C	152	LEU	2.7
1	A	69	GLU	2.7
1	C	525	VAL	2.7
2	D	102	ILE	2.7
1	C	451	TRP	2.7
2	D	209	GLN	2.7
1	A	223	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	303	ALA	2.6
1	A	549	HIS	2.6
2	B	235	LEU	2.6
1	C	268	GLY	2.6
1	A	241	LEU	2.6
1	C	32	LEU	2.6
1	C	218	PRO	2.6
1	C	542	LEU	2.6
1	C	74	LYS	2.6
1	C	139	ASN	2.6
1	A	72	LEU	2.6
1	A	79	SER	2.6
2	D	106	ILE	2.5
2	B	98	SER	2.5
2	D	120	LEU	2.5
2	B	124	PHE	2.5
1	C	520	THR	2.5
1	C	240	LEU	2.5
1	C	21	PHE	2.5
2	D	83	PHE	2.5
1	C	223	HIS	2.5
1	C	534	HIS	2.5
1	A	351	ALA	2.5
1	A	152	LEU	2.5
1	C	202	ILE	2.5
2	B	178	GLN	2.4
1	C	517	TYR	2.4
1	C	306	ALA	2.4
2	D	124	PHE	2.4
1	C	209	ILE	2.4
1	C	144	TRP	2.4
1	C	530	TYR	2.4
1	C	537	THR	2.4
1	C	141	LEU	2.4
2	D	70	ILE	2.4
1	A	74	LYS	2.4
1	C	131	PRO	2.4
1	A	533	GLU	2.3
2	D	131	GLU	2.3
1	A	80	LEU	2.3
1	C	372	GLY	2.3
1	C	519	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	24	THR	2.3
1	C	68	LEU	2.3
1	C	140	ASN	2.3
1	C	26	HIS	2.2
2	D	281	GLN	2.2
1	C	212	PHE	2.2
2	B	74	LEU	2.2
2	B	96	HIS	2.2
1	C	135	PHE	2.2
2	D	97	ASN	2.2
1	A	73	VAL	2.2
1	A	376	GLU	2.2
1	C	27	LYS	2.2
1	A	76	PHE	2.2
1	C	82	PRO	2.2
1	C	130	ALA	2.2
1	C	535	ALA	2.2
1	C	83	SER	2.2
2	D	87	ARG	2.2
1	C	211	THR	2.1
1	A	77	PHE	2.1
2	D	92	ALA	2.1
1	C	210	THR	2.1
2	D	96	HIS	2.1
1	C	245	VAL	2.1
1	C	34	LEU	2.1
1	C	538	LEU	2.1
1	C	528	ASN	2.1
1	A	137	ARG	2.1
1	A	221	THR	2.1
1	C	527	ALA	2.1
1	C	241	LEU	2.0
2	B	107	VAL	2.0
1	A	217	ALA	2.0
2	D	103	ALA	2.0
1	C	216	ARG	2.0
2	D	99	PRO	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($\text{\AA}^2$)	Q<0.9
8	DMU	C	1002	23/33	0.63	0.23	98,99,100,100	23
9	TRD	C	1001	13/13	0.72	0.38	75,76,77,77	0
9	TRD	B	289	7/13	0.73	0.31	62,63,66,66	0
9	TRD	C	1006	13/13	0.76	0.30	70,75,81,81	0
8	DMU	D	1011	23/33	0.78	0.47	68,70,72,72	23
9	TRD	A	578	13/13	0.80	0.26	67,67,71,72	0
9	TRD	A	581	13/13	0.81	0.25	56,62,69,70	0
9	TRD	D	1008	7/13	0.82	0.30	67,68,68,68	0
8	DMU	D	1003	33/33	0.83	0.18	88,93,98,99	0
8	DMU	A	577	33/33	0.83	0.18	43,52,55,56	33
8	DMU	A	575	33/33	0.83	0.17	67,74,77,79	0
9	TRD	C	1010	9/13	0.83	0.21	67,68,69,70	0
8	DMU	C	1005	33/33	0.83	0.19	53,58,62,63	33
9	TRD	A	582	9/13	0.84	0.25	65,66,67,67	0
8	DMU	B	11	23/33	0.84	0.19	72,73,75,75	23
9	TRD	C	1009	7/13	0.85	0.21	65,66,67,67	0
9	TRD	A	579	13/13	0.85	0.22	47,50,56,58	0
8	DMU	A	576	22/33	0.85	0.17	46,65,73,74	0
9	TRD	D	1007	13/13	0.87	0.22	53,55,56,57	0
7	UNX	C	573	1/1	0.87	0.29	46,46,46,46	0
8	DMU	B	288	33/33	0.89	0.14	71,74,79,79	0
10	HTO	B	1	10/10	0.91	0.18	55,60,64,64	0
9	TRD	A	580	7/13	0.92	0.18	58,61,62,62	0
7	UNX	A	573	1/1	0.93	0.34	29,29,29,29	0
8	DMU	A	574	33/33	0.93	0.10	29,39,53,56	0
3	HEA	C	568	60/60	0.96	0.10	36,42,54,56	0
3	HEA	A	568	60/60	0.97	0.09	31,34,51,52	0
3	HEA	C	567	60/60	0.98	0.07	32,36,48,49	0
11	CD	D	9	1/1	0.98	0.09	49,49,49,49	1
5	MG	C	571	1/1	0.99	0.09	14,14,14,14	0
6	CA	C	572	1/1	0.99	0.03	43,43,43,43	0
3	HEA	A	567	60/60	0.99	0.05	24,26,30,31	0

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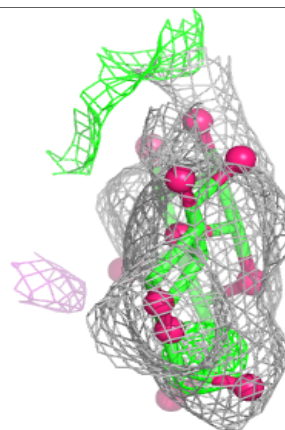
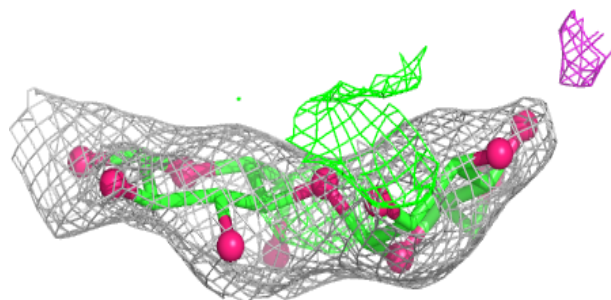
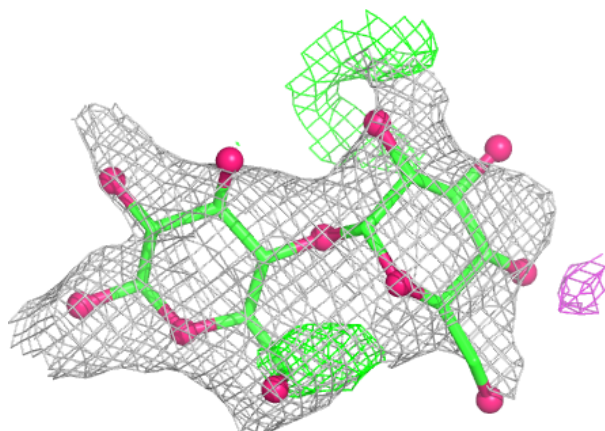
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	CD	B	8	1/1	0.99	0.02	44,44,44,44	0
11	CD	B	9	1/1	0.99	0.09	40,40,40,40	1
11	CD	D	8	1/1	0.99	0.02	42,42,42,42	0
4	CU1	C	570	1/1	0.99	0.02	42,42,42,42	0
4	CU1	D	3	1/1	1.00	0.01	35,35,35,35	0
4	CU1	D	4	1/1	1.00	0.01	35,35,35,35	0
5	MG	A	571	1/1	1.00	0.10	9,9,9,9	0
4	CU1	B	3	1/1	1.00	0.01	29,29,29,29	0
6	CA	A	572	1/1	1.00	0.01	29,29,29,29	0
4	CU1	B	4	1/1	1.00	0.02	29,29,29,29	0
4	CU1	A	570	1/1	1.00	0.02	35,35,35,35	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.

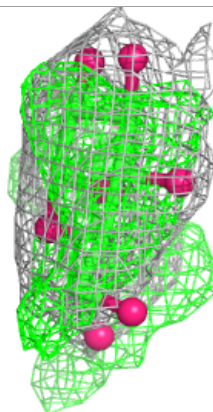
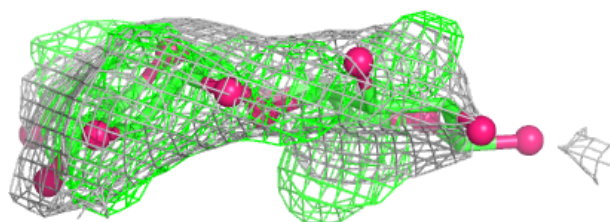
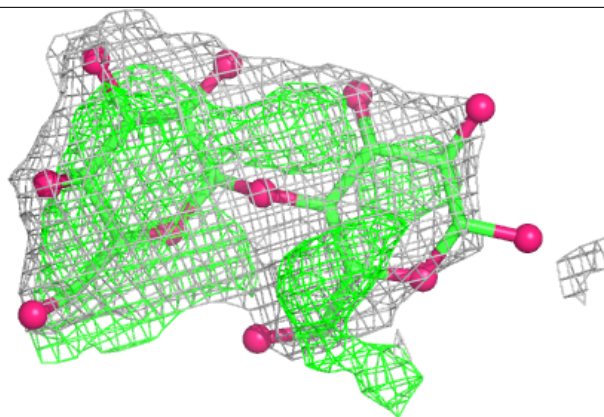
Electron density around DMU C 1002:

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

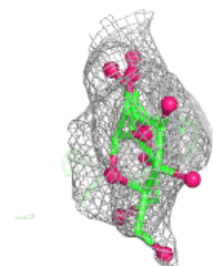
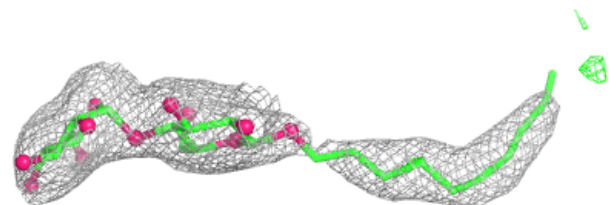
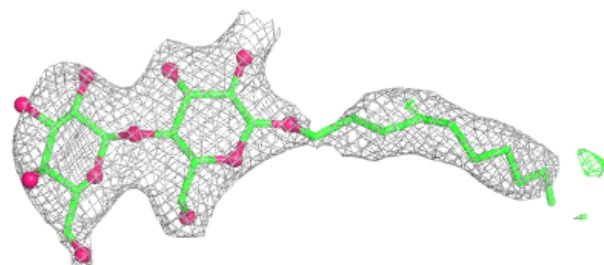


Electron density around DMU D 1011:

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

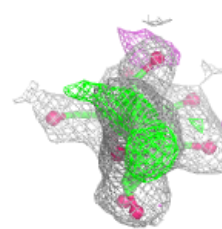
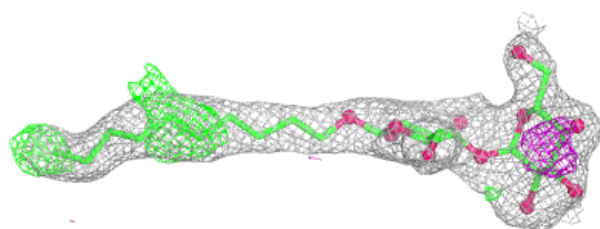
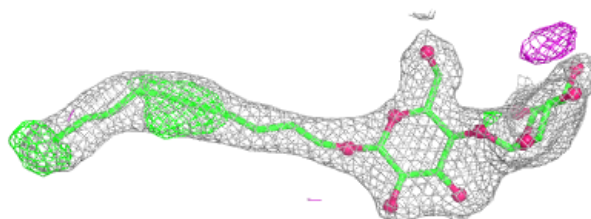
**Electron density around DMU D 1003:**

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

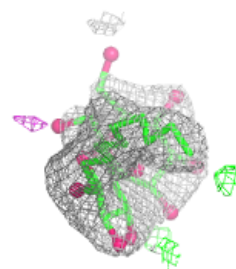
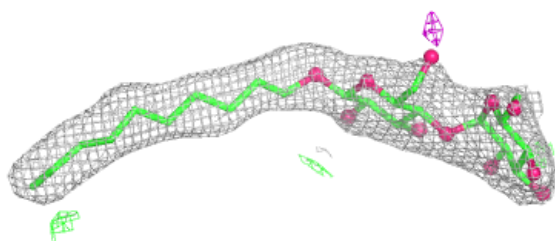
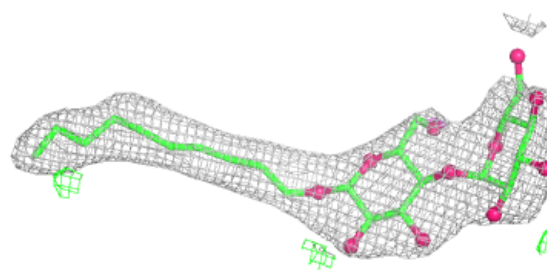


Electron density around DMU A 577:

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

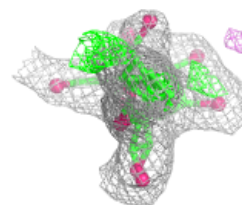
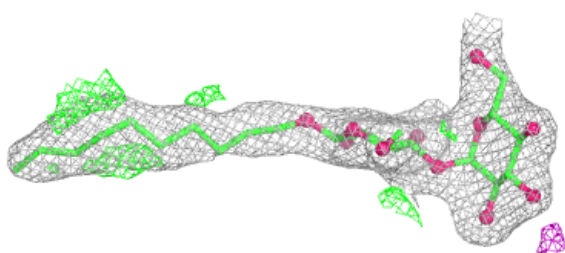
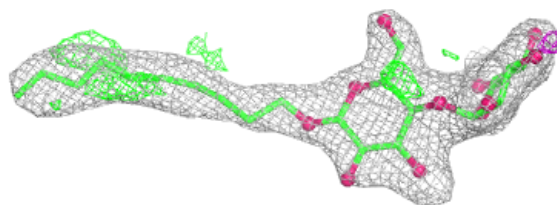
**Electron density around DMU A 575:**

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

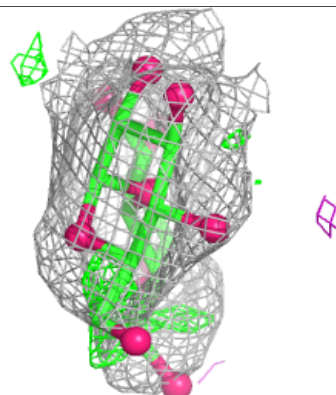
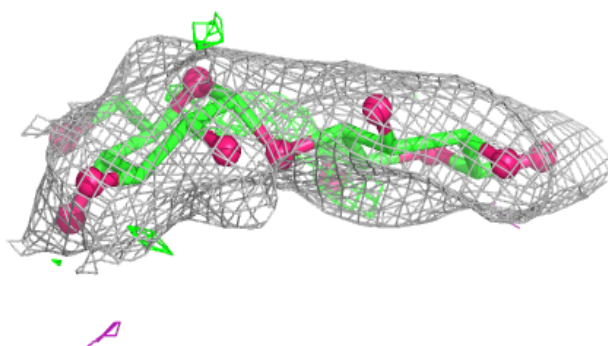
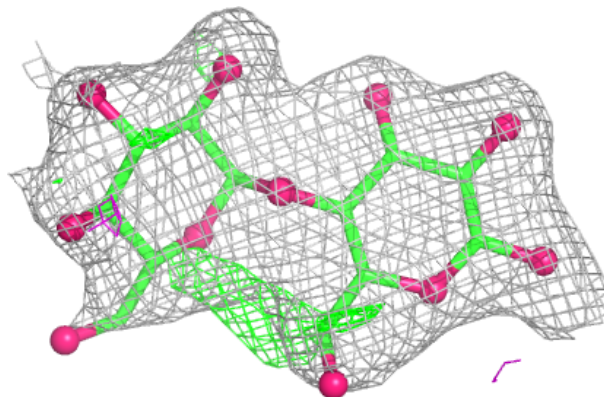


Electron density around DMU C 1005:

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

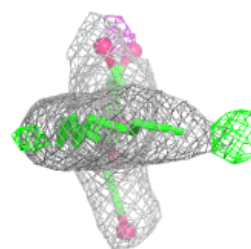
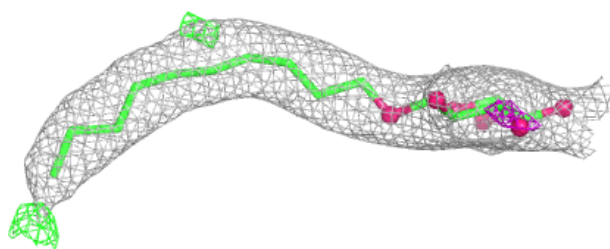
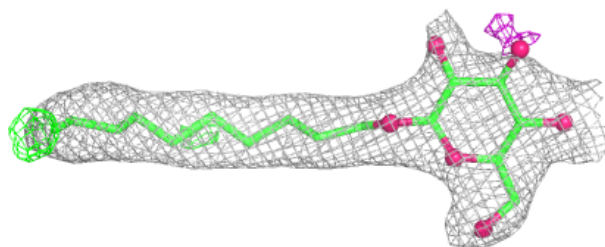
**Electron density around DMU B 11:**

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

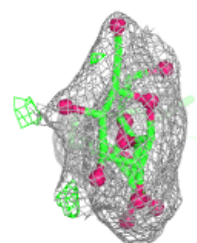
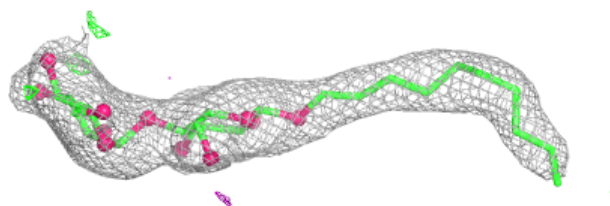
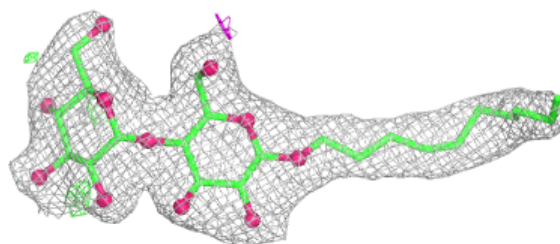


Electron density around DMU A 576:

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

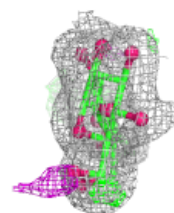
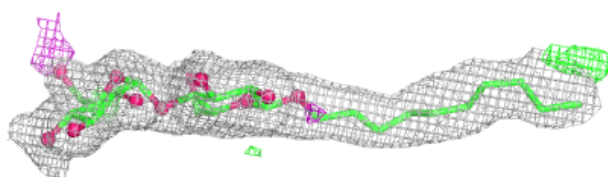
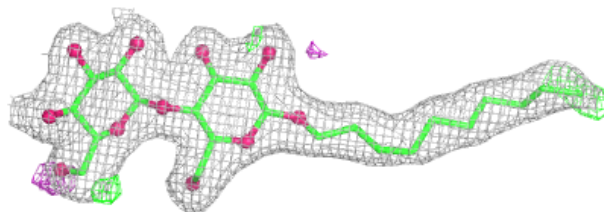
**Electron density around DMU B 288:**

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

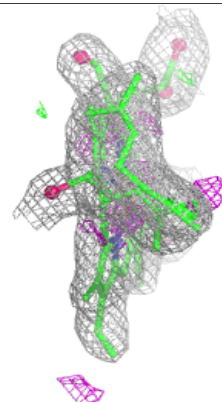
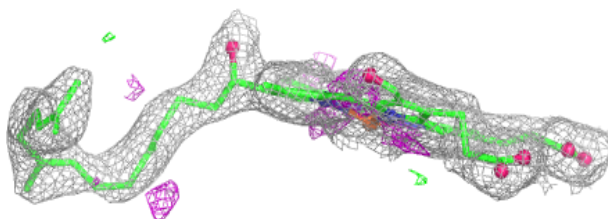
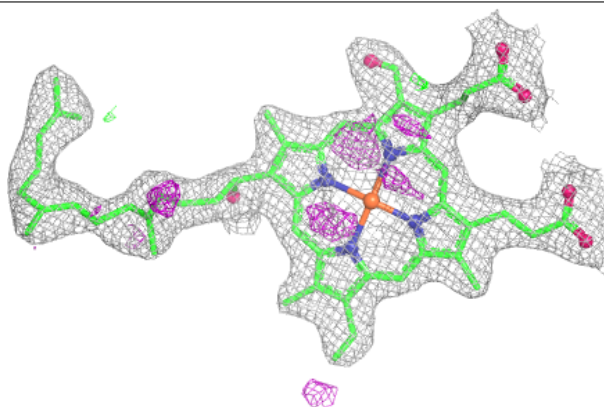


Electron density around DMU A 574:

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

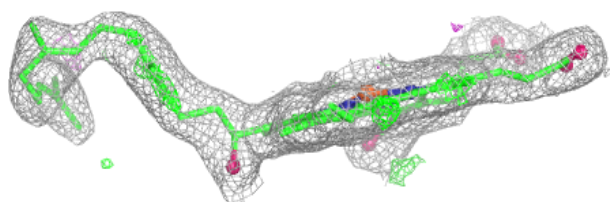
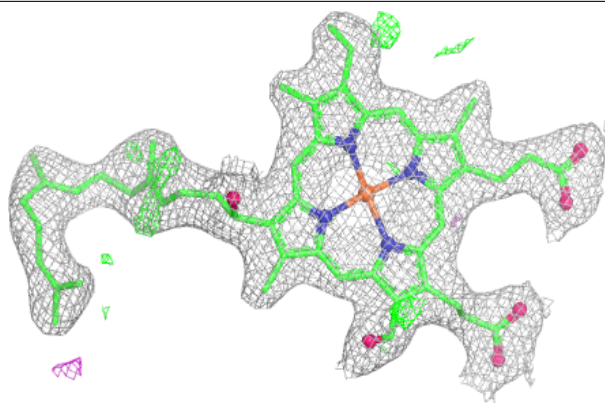
**Electron density around HEA C 568:**

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

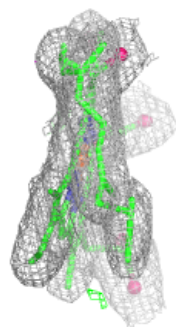
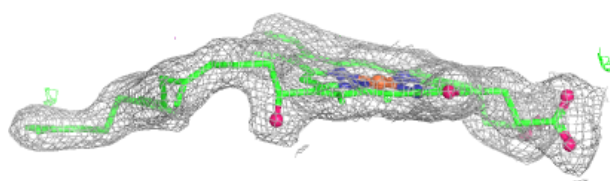
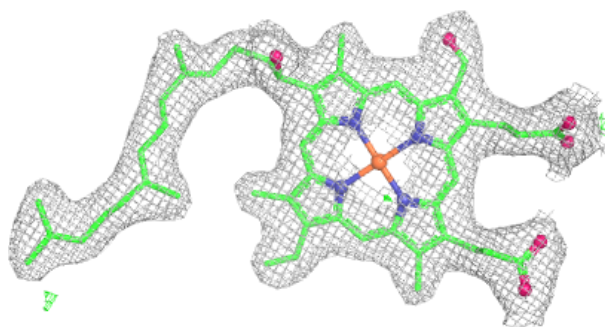


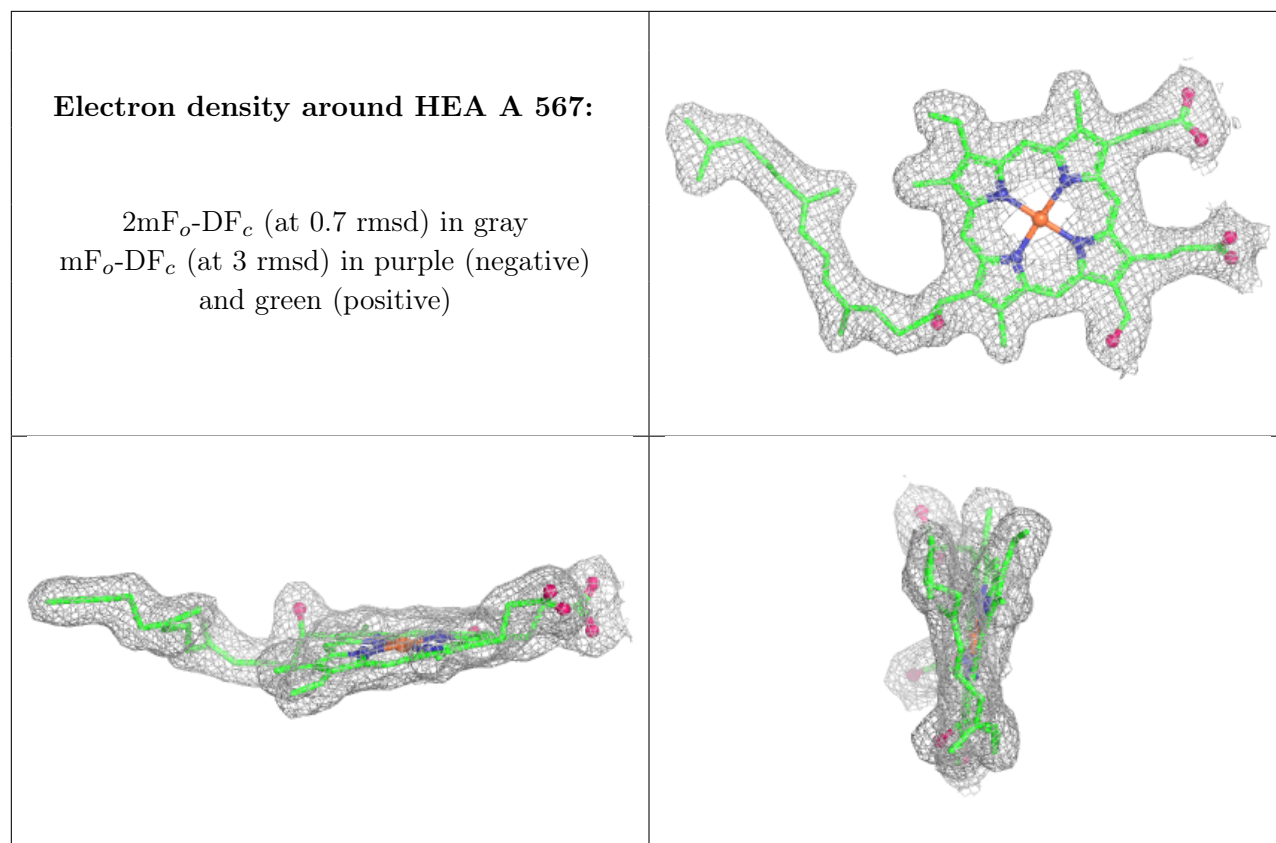
Electron density around HEA A 568:

$2mF_o-DF_c$ (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)





6.5 Other polymers [i](#)

There are no such residues in this entry.