



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 05:40 PM EDT

PDB ID : 4PV1 / pdb_00004pv1
Title : Cytochrome B6F structure from *M. lamosus* with the quinone analog inhibitor stigmatellin
Authors : Hasan, S.S.; Yamashita, E.; Cramer, W.A.
Deposited on : 2014-03-14
Resolution : 3.00 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

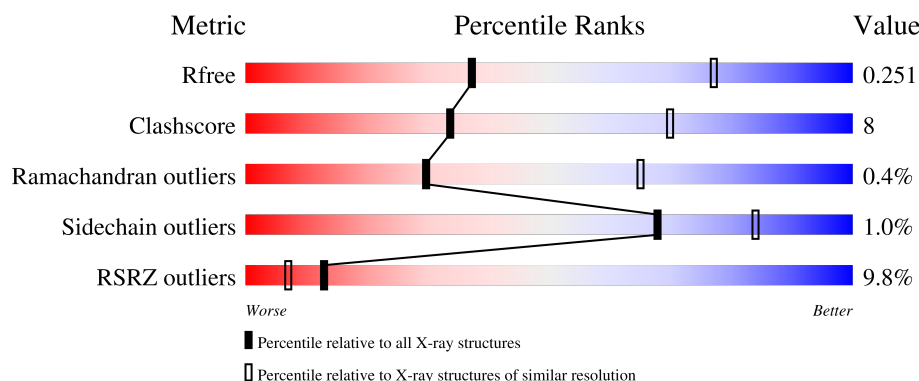
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	215	0% 85% 14% .
2	B	160	6% 85% 14% .
3	C	289	11% 83% 16% .
4	D	179	18% 71% 17% 12%
5	E	32	6% 78% 9% 12%

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Mol	Chain	Length	Quality of chain
6	F	35	
7	G	37	
8	H	29	

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
11	HEC	A	303	X	-	-	-
11	HEC	A	304	X	-	-	-
11	HEC	A	305	X	-	-	-
11	HEC	C	301	X	-	-	-
13	SMA	A	308	X	-	-	-

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 8049 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 b6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	5	0	0
			1698	1132	270	286	10			

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	159	Total	C	N	O	S	2	0	0
			1241	836	192	208	5			

- Molecule 3 is a protein called Apocytochrome f.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	288	Total	C	N	O	S	0	0	0
			2216	1415	369	424	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	11	PRO	GLU	conflict	UNP P83793

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	158	Total	C	N	O	S	0	0	0
			1221	783	210	221	7			

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	28	Total	C	N	O	0	0	0
			215	156	29	30			

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	31	Total	C	N	O	S	0	0	0
			234	160	34	39	1			

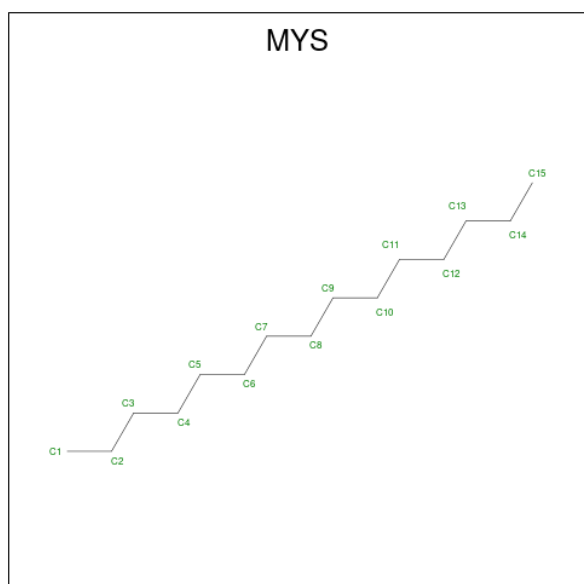
- Molecule 7 is a protein called Cytochrome b6-f complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	37	Total	C	N	O	S	4	0	0
			283	188	44	50	1			

- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	28	Total	C	N	O	S	0	0	0
			222	151	35	35	1			

- Molecule 9 is PENTADECANE (CCD ID: MYS) (formula: C₁₅H₃₂).

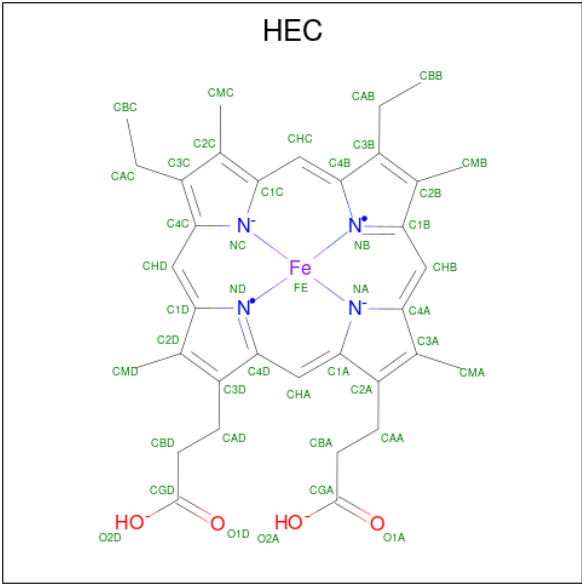


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	C	0	0
			15	15		

- Molecule 10 is CADMIUM ION (CCD ID: CD) (formula: Cd).

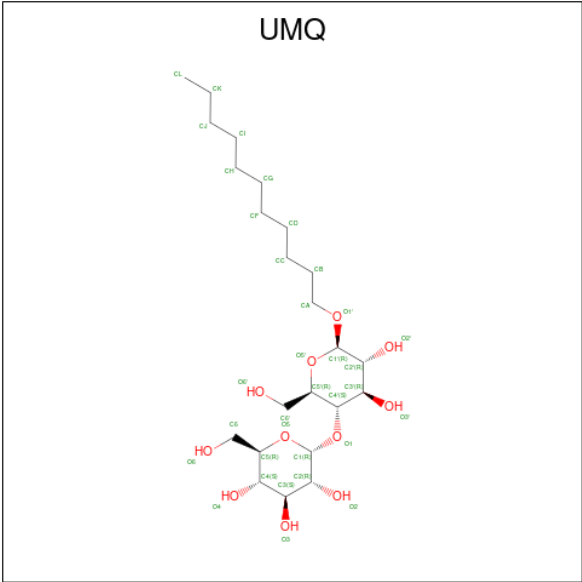
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total Cd 1 1	0	0
10	B	1	Total Cd 1 1	0	0

- Molecule 11 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₆FeN₄O₄).



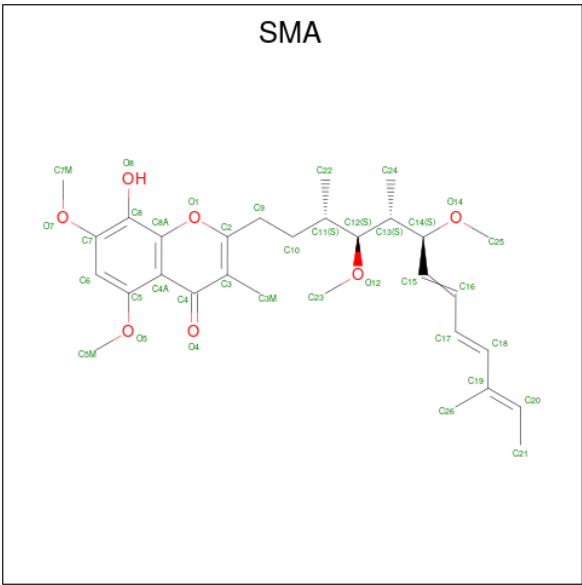
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total C Fe N O 43 34 1 4 4	0	0
11	A	1	Total C Fe N O 43 34 1 4 4	0	0
11	A	1	Total C Fe N O 43 34 1 4 4	0	0
11	C	1	Total C Fe N O 43 34 1 4 4	0	0

- Molecule 12 is UNDECYL-MALTOSIDE (CCD ID: UMQ) (formula: C₂₃H₄₄O₁₁).



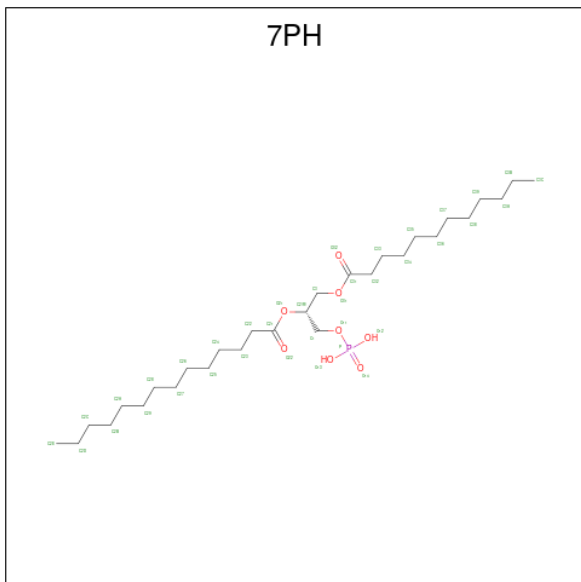
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	6	0
			34	23	11		
12	A	1	Total	C	O	2	0
			34	23	11		
12	B	1	Total	C	O	0	0
			34	23	11		

- Molecule 13 is STIGMATELLIN A (CCD ID: SMA) (formula: C₃₀H₄₂O₇).



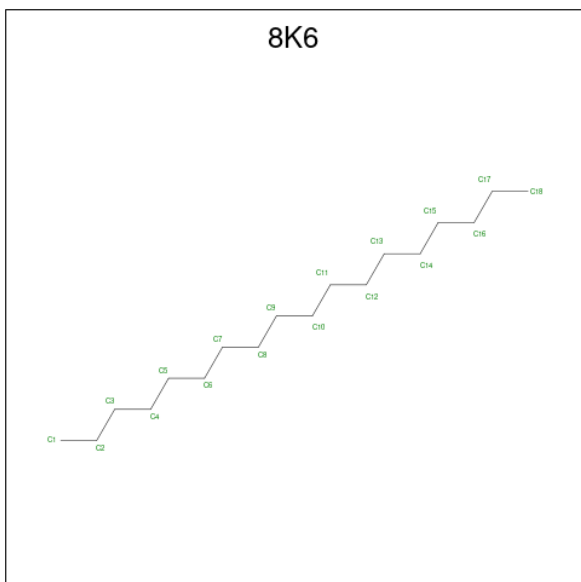
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	A	1	Total	C	O	3	0
			37	30	7		

- Molecule 14 is (1R)-2-(dodecanoyloxy)-1-[(phosphonoxy)methyl]ethyl tetradecanoate (CCD ID: 7PH) (formula: $C_{29}H_{57}O_8P$).



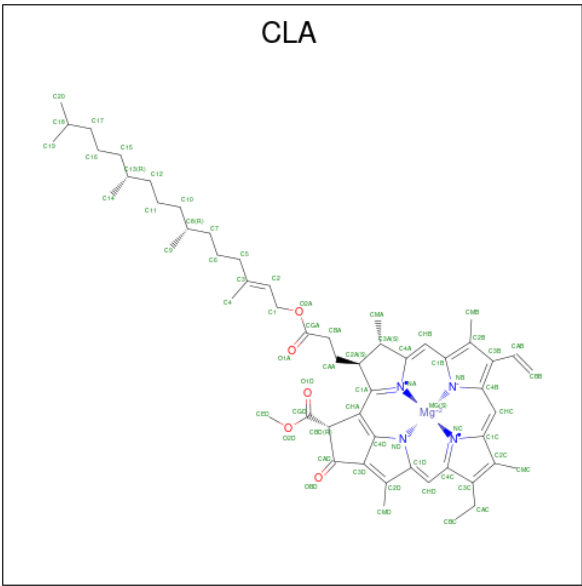
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	A	1	Total	C	O	3	0
			32	27	5		

- Molecule 15 is Octadecane (CCD ID: 8K6) (formula: $C_{18}H_{38}$).



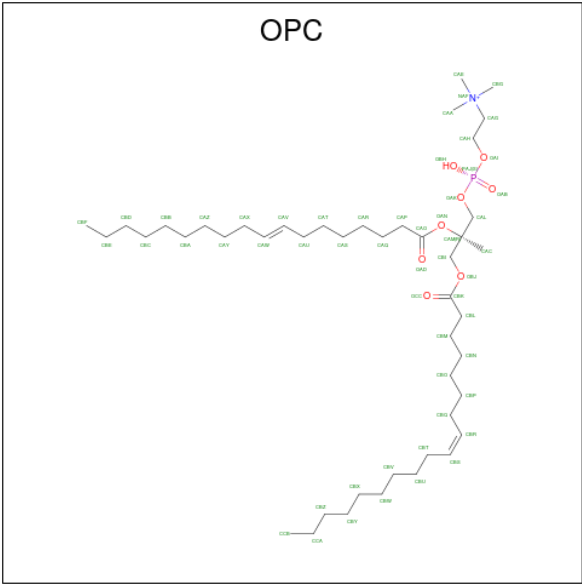
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	B	1	Total	C	0	0
			18	18		

- Molecule 16 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
16	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 17 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (CCD ID: OPC) (formula: C₄₅H₈₇NO₈P).



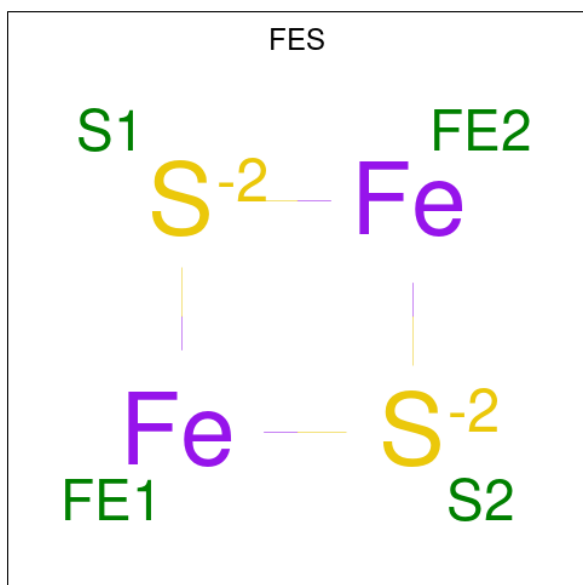
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

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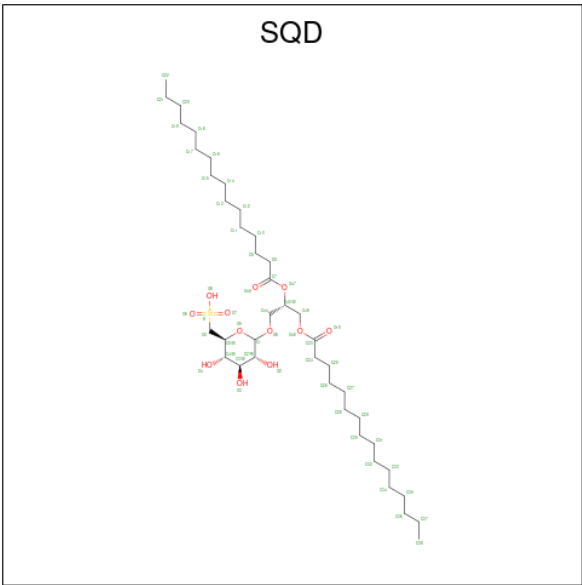
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	D	1	Total	C	N	O	P	1	0
			54	44	1	8	1		
17	E	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 18 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



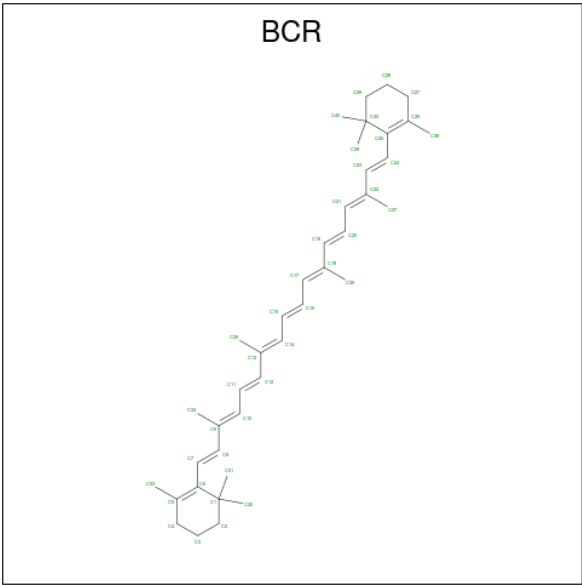
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 19 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (CCD ID: SQD) (formula: $\text{C}_{41}\text{H}_{78}\text{O}_{12}\text{S}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	D	1	Total	C	O	S	30	0
			54	41	12	1		

- Molecule 20 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	G	1	Total	C	14	0
			40	40		

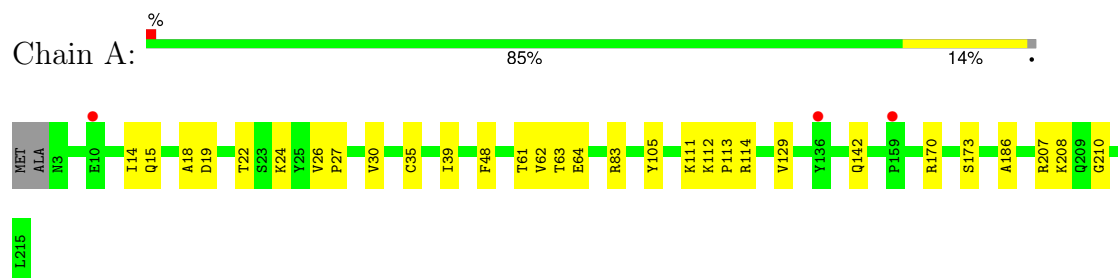
- Molecule 21 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	A	8	Total 8	O 8	0	0
21	B	5	Total 5	O 5	0	0
21	C	2	Total 2	O 2	0	0
21	G	1	Total 1	O 1	0	0

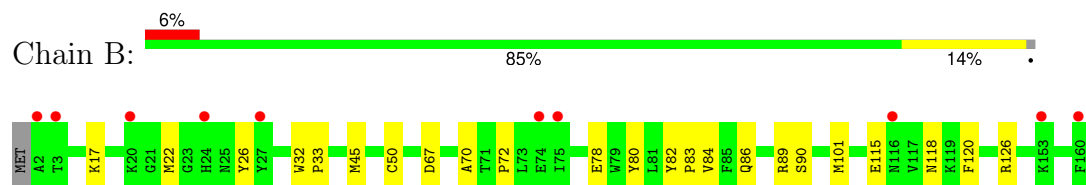
3 Residue-property plots

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

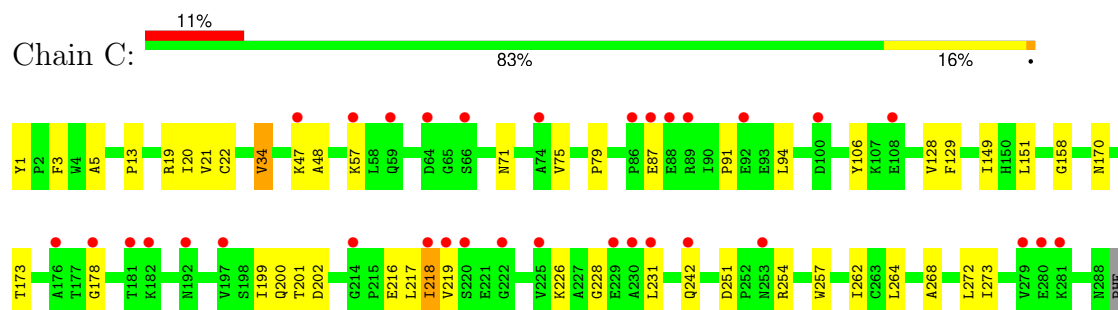
• Molecule 1: Cytochrome b6



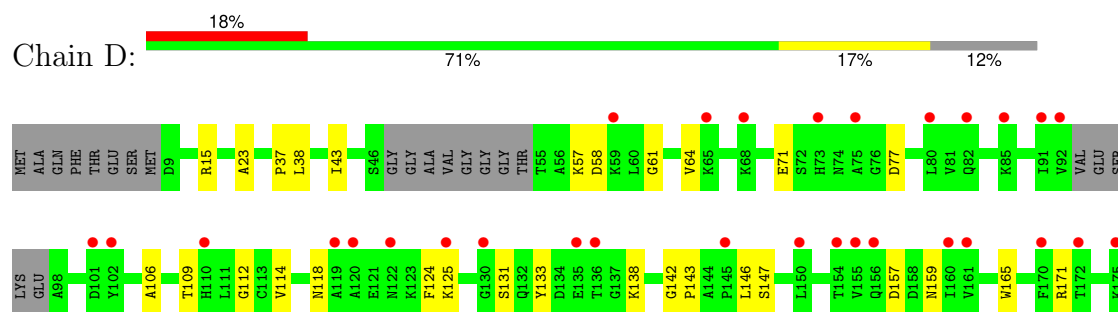
• Molecule 2: Cytochrome b6-f complex subunit 4



• Molecule 3: Apocytochrome f

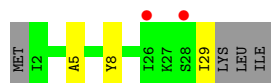
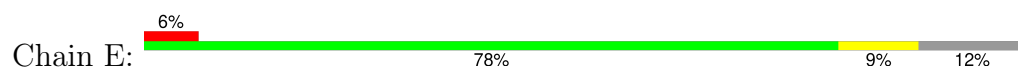


• Molecule 4: Cytochrome b6-f complex iron-sulfur subunit

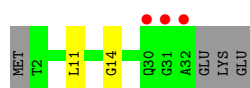
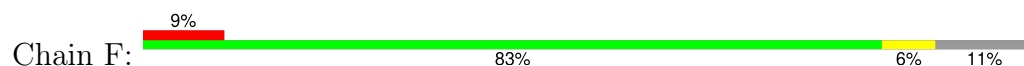




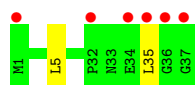
- Molecule 5: Cytochrome b6-f complex subunit 6



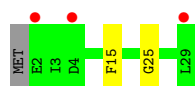
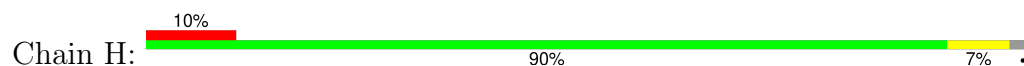
- Molecule 6: Cytochrome b6-f complex subunit 7



- Molecule 7: Cytochrome b6-f complex subunit 5



- Molecule 8: Cytochrome b6-f complex subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	159.09Å 159.09Å 361.32Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.34 – 3.00 48.34 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.2 (48.34-3.00) 83.5 (48.34-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.75 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.4_1496), REFMAC	Depositor
R, R_{free}	0.216 , 0.247 0.223 , 0.251	Depositor DCC
R_{free} test set	2560 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	85.7	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 92.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8049	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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: 8K6, CLA, SMA, CD, SQD, BCR, HEC, UMQ, 7PH, FES, MYS, OPC

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	0.29	0/1750	0.73	0/2388
2	B	0.30	0/1280	0.76	0/1755
3	C	0.29	0/2264	0.73	1/3082 (0.0%)
4	D	0.27	0/1252	0.74	3/1705 (0.2%)
5	E	0.26	0/220	0.71	0/297
6	F	0.24	0/238	0.65	0/321
7	G	0.27	0/289	0.74	0/391
8	H	0.26	0/228	0.64	0/313
All	All	0.28	0/7521	0.73	4/10252 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	43	ILE	CA-C-N	6.14	124.14	119.66
4	D	43	ILE	C-N-CA	6.14	124.14	119.66
4	D	157	ASP	CB-CA-C	-5.80	109.91	116.63
3	C	226	LYS	CB-CA-C	-5.21	109.58	115.79

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	1698	0	1719	29	1
2	B	1241	0	1296	19	0
3	C	2216	0	2232	29	1
4	D	1221	0	1206	18	0
5	E	215	0	237	3	0
6	F	234	0	248	2	0
7	G	283	0	289	1	0
8	H	222	0	227	2	0
9	A	15	0	32	3	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
11	A	129	0	96	7	0
11	C	43	0	31	5	0
12	A	68	0	87	10	0
12	B	34	0	44	10	0
13	A	37	0	41	7	0
14	A	32	0	45	3	0
15	B	18	0	38	0	0
16	B	65	0	72	5	0
17	B	54	0	83	5	0
17	D	54	0	83	4	0
17	E	54	0	83	12	0
18	D	4	0	0	0	0
19	D	54	0	78	1	0
20	G	40	0	56	1	0
21	A	8	0	0	0	0
21	B	5	0	0	1	0
21	C	2	0	0	0	0
21	G	1	0	0	0	0
All	All	8049	0	8323	125	1

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 8.

All (125) 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)
12:B:203:UMQ:O5'	12:B:203:UMQ:C5'	1.63	1.46
1:A:35:CYS:SG	11:A:305:HEC:CAB	2.04	1.44
12:B:203:UMQ:O5'	12:B:203:UMQ:C1'	1.69	1.41
12:A:307:UMQ:O5'	12:A:307:UMQ:C1'	1.69	1.40
1:A:35:CYS:SG	11:A:305:HEC:CBB	2.18	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:CYS:SG	11:A:305:HEC:HBB2	1.73	1.26
12:B:203:UMQ:C5'	12:B:203:UMQ:C1'	2.48	0.91
12:A:307:UMQ:C1'	12:A:307:UMQ:C5'	2.48	0.91
9:A:301:MYS:H101	9:A:301:MYS:H52	1.52	0.90
1:A:83:ARG:NH1	11:A:303:HEC:O2D	2.04	0.89
1:A:35:CYS:SG	11:A:305:HEC:C3B	2.64	0.86
17:E:101:OPC:HBI1	17:E:101:OPC:HAQ1	1.57	0.85
1:A:114:ARG:NH1	1:A:210:GLY:O	2.10	0.85
1:A:186:ALA:HB2	9:A:301:MYS:H81	1.61	0.83
1:A:208:LYS:NZ	12:A:306:UMQ:H61	1.98	0.79
2:B:78:GLU:OE2	2:B:80:TYR:OH	2.03	0.76
4:D:165:TRP:HB3	4:D:178:TRP:HE1	1.50	0.74
3:C:251:ASP:HB3	3:C:254:ARG:HD3	1.67	0.74
1:A:24:LYS:HG3	13:A:308:SMA:H4	1.71	0.73
1:A:208:LYS:HZ2	12:A:306:UMQ:H61	1.59	0.68
17:E:101:OPC:HBF2	6:F:14:GLY:HA3	1.76	0.67
5:E:5:ALA:HA	17:E:101:OPC:HAW	1.78	0.66
1:A:22:THR:HG21	12:B:203:UMQ:H2'1	1.78	0.66
4:D:57:LYS:HB3	4:D:61:GLY:HA2	1.79	0.65
14:A:309:7PH:H2CA	4:D:37:PRO:HG2	1.79	0.64
3:C:5:ALA:HB2	11:C:301:HEC:HBB3	1.78	0.64
2:B:45:MET:HE1	3:C:268:ALA:HB3	1.80	0.63
3:C:178:GLY:HA3	3:C:199:ILE:HG23	1.80	0.63
3:C:91:PRO:HG2	3:C:94:LEU:HB2	1.80	0.63
9:A:301:MYS:H101	9:A:301:MYS:C5	2.28	0.62
13:A:308:SMA:H36	13:A:308:SMA:H14	1.82	0.61
12:A:306:UMQ:O5'	12:A:306:UMQ:C6'	2.48	0.61
17:E:101:OPC:HBW1	8:H:15:PHE:CD1	2.35	0.61
4:D:124:PHE:HB2	4:D:133:TYR:HB2	1.83	0.60
4:D:131:SER:HA	4:D:142:GLY:HA3	1.82	0.60
1:A:39:ILE:HD11	20:G:101:BCR:H312	1.83	0.59
11:A:305:HEC:HBD1	11:A:305:HEC:HHA	1.85	0.58
1:A:142:GLN:NE2	2:B:70:ALA:O	2.36	0.58
3:C:19:ARG:O	3:C:242:GLN:NE2	2.35	0.58
4:D:38:LEU:HD21	17:D:203:OPC:HAL2	1.85	0.58
1:A:142:GLN:HG3	2:B:72:PRO:HG3	1.86	0.57
1:A:113:PRO:HG3	2:B:22:MET:HE2	1.85	0.57
5:E:8:TYR:CE2	17:E:101:OPC:HAZ1	2.39	0.56
4:D:109:THR:HG21	4:D:146:LEU:HB2	1.87	0.56
3:C:57:LYS:NZ	3:C:57:LYS:HB3	2.20	0.56
1:A:207:ARG:NH1	13:A:308:SMA:O4	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:48:ALA:HB3	3:C:129:PHE:HB2	1.88	0.56
1:A:105:TYR:O	2:B:126:ARG:NH2	2.34	0.55
1:A:129:VAL:HG21	16:B:204:CLA:H43	1.88	0.55
3:C:79:PRO:HD3	3:C:149:ILE:HG12	1.87	0.55
3:C:272:LEU:HD23	4:D:23:ALA:HB1	1.89	0.54
17:E:101:OPC:HBI1	17:E:101:OPC:CAQ	2.35	0.54
2:B:17:LYS:NZ	2:B:26:TYR:OH	2.40	0.53
4:D:118:ASN:HD22	4:D:125:LYS:HD3	1.74	0.53
3:C:34:VAL:HB	3:C:151:LEU:HD22	1.90	0.53
1:A:61:THR:HG22	1:A:63:THR:H	1.73	0.53
17:D:203:OPC:HBI2	17:D:203:OPC:HBO1	1.90	0.53
16:B:204:CLA:HAC1	17:B:205:OPC:HBW1	1.91	0.52
2:B:84:VAL:HG13	2:B:101:MET:HG2	1.92	0.51
1:A:15:GLN:NE2	1:A:19:ASP:OD1	2.44	0.51
12:B:203:UMQ:O5'	12:B:203:UMQ:C6'	2.48	0.51
13:A:308:SMA:C25	12:B:203:UMQ:HL1	2.41	0.51
4:D:138:LYS:HD2	4:D:171:ARG:HG3	1.93	0.50
2:B:86:GLN:HE22	2:B:89:ARG:HH21	1.58	0.50
4:D:77:ASP:N	4:D:77:ASP:OD1	2.44	0.50
16:B:204:CLA:OBD	21:B:305:HOH:O	2.19	0.50
3:C:200:GLN:HG3	3:C:201:THR:H	1.77	0.49
3:C:47:LYS:HG3	3:C:128:VAL:HG13	1.94	0.49
4:D:106:ALA:HB1	4:D:114:VAL:HG13	1.94	0.49
3:C:1:TYR:H2	11:C:301:HEC:C4A	2.20	0.49
17:B:205:OPC:HBL2	17:B:205:OPC:HAS1	1.94	0.49
1:A:18:ALA:HB2	12:A:307:UMQ:HD2	1.95	0.48
14:A:309:7PH:H24A	3:C:254:ARG:HA	1.95	0.48
1:A:208:LYS:HZ3	12:A:306:UMQ:H61	1.76	0.48
12:A:306:UMQ:O5'	12:A:306:UMQ:C4'	2.62	0.48
4:D:146:LEU:HD13	4:D:177:TRP:CG	2.49	0.48
3:C:22:CYS:HB2	11:C:301:HEC:HBB2	1.96	0.47
3:C:231:LEU:H	3:C:231:LEU:HD23	1.79	0.47
1:A:27:PRO:HG2	1:A:30:VAL:HG23	1.95	0.47
2:B:50:CYS:HB3	17:E:101:OPC:HBX1	1.95	0.47
3:C:173:THR:HB	3:C:228:GLY:HA2	1.95	0.47
13:A:308:SMA:H43	12:B:203:UMQ:CL	2.45	0.47
4:D:131:SER:HB3	4:D:143:PRO:HD2	1.97	0.47
1:A:61:THR:HB	1:A:64:GLU:HB2	1.97	0.46
2:B:118:ASN:HD21	2:B:120:PHE:HB2	1.80	0.46
3:C:201:THR:OG1	3:C:202:ASP:N	2.48	0.46
17:E:101:OPC:HBN1	6:F:11:LEU:HD12	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:216:GLU:HG3	3:C:217:LEU:H	1.81	0.46
4:D:58:ASP:HB3	4:D:64:VAL:HG22	1.98	0.46
16:B:204:CLA:HBB2	17:B:205:OPC:HBM2	1.98	0.46
14:A:309:7PH:H26	3:C:257:TRP:HB2	1.97	0.45
2:B:115:GLU:HG2	17:B:205:OPC:HBI2	1.99	0.45
1:A:111:LYS:NZ	2:B:120:PHE:O	2.34	0.45
3:C:218:ILE:HD12	3:C:219:VAL:HG23	1.98	0.45
13:A:308:SMA:H43	12:B:203:UMQ:HL2	1.99	0.45
3:C:71:ASN:HB2	11:C:301:HEC:CGA	2.48	0.44
1:A:142:GLN:OE1	2:B:67:ASP:N	2.47	0.44
17:E:101:OPC:HBP2	17:E:101:OPC:HBS	1.68	0.44
17:E:101:OPC:HAZ2	17:E:101:OPC:HBC1	1.58	0.44
3:C:218:ILE:H	3:C:218:ILE:HG13	1.67	0.44
17:D:203:OPC:HAA2	17:D:203:OPC:HAH2	1.72	0.44
12:B:203:UMQ:HF1	12:B:203:UMQ:HI1	1.76	0.43
17:E:101:OPC:HAE2	17:E:101:OPC:HAH1	1.63	0.43
2:B:118:ASN:ND2	2:B:120:PHE:HB2	2.34	0.43
3:C:13:PRO:HB3	3:C:106:TYR:CE1	2.54	0.43
3:C:158:GLY:H	11:C:301:HEC:C3D	2.32	0.43
16:B:204:CLA:CBB	17:B:205:OPC:HBM2	2.50	0.42
17:E:101:OPC:HBP1	7:G:5:LEU:HD11	2.00	0.42
12:A:306:UMQ:HA2	12:A:306:UMQ:H2'1	1.67	0.42
12:A:306:UMQ:O5'	12:A:306:UMQ:C2'	2.67	0.42
3:C:170:ASN:OD1	3:C:170:ASN:N	2.51	0.42
13:A:308:SMA:H40	12:B:203:UMQ:HL1	2.02	0.42
2:B:33:PRO:HG3	19:D:202:SQD:H4	2.02	0.41
1:A:170:ARG:NH1	1:A:173:SER:C	2.78	0.41
4:D:15:ARG:HH12	5:E:29:ILE:HG22	1.85	0.41
2:B:86:GLN:OE1	2:B:90:SER:OG	2.39	0.41
3:C:1:TYR:HB3	3:C:3:PHE:CE1	2.56	0.40
4:D:64:VAL:N	4:D:159:ASN:OD1	2.54	0.40
1:A:48:PHE:HE2	17:D:203:OPC:HAQ2	1.87	0.40
1:A:62:VAL:HG23	1:A:63:THR:HG23	2.03	0.40
11:A:303:HEC:HHC	11:A:303:HEC:CBB	2.51	0.40
2:B:32:TRP:HA	2:B:33:PRO:HA	1.81	0.40
4:D:138:LYS:HA	4:D:147:SER:HB3	2.03	0.40
2:B:82:TYR:HB2	2:B:83:PRO:HD3	2.04	0.40
3:C:273:ILE:HD12	8:H:25:GLY:HA3	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:LYS:NZ	3:C:87:GLU:OE1[8_665]	2.19	0.01

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	211/215 (98%)	201 (95%)	10 (5%)	0	100	100
2	B	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
3	C	286/289 (99%)	256 (90%)	28 (10%)	2 (1%)	18	53
4	D	152/179 (85%)	127 (84%)	23 (15%)	2 (1%)	9	38
5	E	26/32 (81%)	26 (100%)	0	0	100	100
6	F	29/35 (83%)	27 (93%)	2 (7%)	0	100	100
7	G	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
8	H	26/29 (90%)	26 (100%)	0	0	100	100
All	All	922/976 (94%)	846 (92%)	72 (8%)	4 (0%)	30	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	71	GLU
4	D	112	GLY
3	C	20	ILE
3	C	21	VAL

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	183/184 (100%)	181 (99%)	2 (1%)	65	83
2	B	136/137 (99%)	136 (100%)	0	100	100
3	C	242/243 (100%)	237 (98%)	5 (2%)	47	75
4	D	132/146 (90%)	132 (100%)	0	100	100
5	E	21/25 (84%)	21 (100%)	0	100	100
6	F	23/27 (85%)	23 (100%)	0	100	100
7	G	28/28 (100%)	27 (96%)	1 (4%)	31	65
8	H	23/24 (96%)	23 (100%)	0	100	100
All	All	788/814 (97%)	780 (99%)	8 (1%)	68	84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ILE
1	A	26	VAL
3	C	34	VAL
3	C	75	VAL
3	C	218	ILE
3	C	262	ILE
3	C	264	LEU
7	G	35	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	6	GLN
3	C	125	GLN
3	C	200	GLN
6	F	30	GLN
8	H	27	ASN

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 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	$\# Z > 2$
9	MYS	A	301	-	14,14,14	0.08	0	13,13,13	0.80	0
14	7PH	A	309	-	31,31,37	1.29	2 (6%)	33,33,42	1.21	2 (6%)
19	SQD	D	202	-	52,54,54	0.96	3 (5%)	62,65,65	1.41	9 (14%)
11	HEC	C	301	3	50,50,50	1.97	9 (18%)	68,82,82	1.62	9 (13%)
13	SMA	A	308	11	38,38,38	2.79	14 (36%)	47,52,52	1.94	9 (19%)
17	OPC	B	205	-	53,53,54	1.06	2 (3%)	59,61,64	1.00	2 (3%)
17	OPC	D	203	-	53,53,54	1.05	3 (5%)	59,61,64	0.99	3 (5%)
11	HEC	A	304	1	50,50,50	2.01	9 (18%)	68,82,82	1.52	4 (5%)
12	UMQ	B	203	-	35,35,35	3.68	17 (48%)	46,46,46	2.07	5 (10%)
15	8K6	B	201	-	17,17,17	0.07	0	16,16,16	0.86	0
18	FES	D	201	4	0,4,4	-	-	-	-	-
11	HEC	A	303	1	50,50,50	2.01	8 (16%)	68,82,82	1.63	11 (16%)
12	UMQ	A	307	-	35,35,35	3.67	17 (48%)	46,46,46	2.12	5 (10%)
20	BCR	G	101	-	41,41,41	1.14	2 (4%)	56,56,56	1.19	6 (10%)
16	CLA	B	204	21	69,73,73	1.19	7 (10%)	82,113,113	1.26	5 (6%)
11	HEC	A	305	21,13	50,50,50	2.03	9 (18%)	68,82,82	1.58	7 (10%)
12	UMQ	A	306	-	35,35,35	3.67	17 (48%)	46,46,46	2.16	7 (15%)
17	OPC	E	101	-	53,53,54	1.05	3 (5%)	59,61,64	1.02	3 (5%)

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
9	MYS	A	301	-	-	3/12/12/12	-
14	7PH	A	309	-	-	7/33/33/39	-
19	SQD	D	202	-	-	18/49/69/69	0/1/1/1
13	SMA	A	308	11	1/1/5/10	19/34/34/34	0/2/2/2
11	HEC	C	301	3	1/1/3/7	6/14/54/54	-
17	OPC	B	205	-	-	22/57/57/60	-
17	OPC	D	203	-	-	30/57/57/60	-
11	HEC	A	304	1	1/1/3/7	6/14/54/54	-
12	UMQ	B	203	-	-	8/20/60/60	0/2/2/2
15	8K6	B	201	-	-	5/15/15/15	-
18	FES	D	201	4	-	-	0/1/1/1
11	HEC	A	303	1	1/1/3/7	5/14/54/54	-
12	UMQ	A	307	-	-	1/20/60/60	0/2/2/2
20	BCR	G	101	-	-	12/29/63/63	0/2/2/2
16	CLA	B	204	21	-	12/39/115/115	-
11	HEC	A	305	21,13	1/1/3/7	6/14/54/54	-
12	UMQ	A	306	-	-	9/20/60/60	0/2/2/2
17	OPC	E	101	-	-	30/57/57/60	-

All (122) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	203	UMQ	O5'-C1'	10.73	1.69	1.41
12	A	307	UMQ	O5'-C1'	10.72	1.69	1.41
12	A	306	UMQ	O5'-C1'	10.71	1.69	1.41
12	B	203	UMQ	O3'-C3'	8.10	1.63	1.43
12	A	307	UMQ	O3'-C3'	8.10	1.63	1.43
11	C	301	HEC	C3D-C2D	8.03	1.54	1.36
12	A	306	UMQ	O3'-C3'	8.01	1.62	1.43
11	A	305	HEC	C3D-C2D	7.98	1.54	1.36
11	A	304	HEC	C3D-C2D	7.96	1.53	1.36
13	A	308	SMA	O1-C2	7.91	1.45	1.36
12	A	306	UMQ	O5'-C5'	7.86	1.63	1.44
11	A	303	HEC	C3D-C2D	7.84	1.53	1.36
12	B	203	UMQ	O5'-C5'	7.81	1.63	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	307	UMQ	O5'-C5'	7.80	1.63	1.44
13	A	308	SMA	O1-C8A	7.37	1.48	1.38
13	A	308	SMA	C3-C2	6.16	1.46	1.34
12	B	203	UMQ	O5-C5	5.94	1.58	1.44
12	A	307	UMQ	O5-C5	5.90	1.58	1.44
12	A	306	UMQ	O5-C5	5.87	1.58	1.44
12	A	306	UMQ	C6-C5	-5.85	1.32	1.51
12	A	307	UMQ	C6-C5	-5.85	1.32	1.51
12	B	203	UMQ	C6-C5	-5.82	1.32	1.51
13	A	308	SMA	C20-C19	5.26	1.37	1.33
12	B	203	UMQ	O1'-C1'	-4.96	1.31	1.40
12	A	307	UMQ	O1'-C1'	-4.94	1.32	1.40
11	A	305	HEC	FE-ND	4.87	2.09	1.94
11	A	303	HEC	FE-NB	4.87	2.09	1.94
12	A	306	UMQ	O1'-C1'	-4.82	1.32	1.40
12	A	307	UMQ	C3'-C4'	-4.58	1.39	1.52
12	A	306	UMQ	C3'-C4'	-4.58	1.39	1.52
12	B	203	UMQ	C3'-C4'	-4.57	1.39	1.52
11	A	304	HEC	FE-NB	4.54	2.08	1.94
13	A	308	SMA	C18-C19	4.46	1.55	1.46
11	A	303	HEC	FE-ND	4.40	2.08	1.94
11	A	305	HEC	FE-NB	4.35	2.08	1.94
11	C	301	HEC	FE-NB	4.29	2.08	1.94
14	A	309	7PH	O31-C31	4.28	1.45	1.33
12	B	203	UMQ	O2-C2	4.27	1.53	1.43
12	A	306	UMQ	O2-C2	4.27	1.53	1.43
12	A	307	UMQ	O2-C2	4.27	1.53	1.43
11	C	301	HEC	FE-ND	4.24	2.07	1.94
12	B	203	UMQ	C3-C2	-4.23	1.41	1.52
12	A	306	UMQ	C3-C2	-4.21	1.41	1.52
12	A	307	UMQ	C3-C2	-4.20	1.41	1.52
11	C	301	HEC	CBB-CAB	-4.15	1.33	1.51
11	A	303	HEC	CBB-CAB	-4.10	1.34	1.51
11	A	305	HEC	CBC-CAC	-4.08	1.34	1.51
14	A	309	7PH	O21-C21	4.07	1.45	1.34
11	A	304	HEC	CBB-CAB	-4.06	1.34	1.51
11	A	304	HEC	CBC-CAC	-4.05	1.34	1.51
11	A	303	HEC	CBC-CAC	-4.05	1.34	1.51
11	C	301	HEC	CBC-CAC	-4.05	1.34	1.51
11	A	305	HEC	CBB-CAB	-4.05	1.34	1.51
11	A	304	HEC	FE-ND	4.01	2.07	1.94
17	B	205	OPC	OBJ-CBK	3.81	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	E	101	OPC	OBJ-CBK	3.77	1.44	1.33
17	D	203	OPC	OBJ-CBK	3.74	1.44	1.33
12	A	306	UMQ	C4-C5	3.71	1.60	1.53
12	B	203	UMQ	C4-C5	3.70	1.60	1.53
11	A	304	HEC	FE-NA	3.70	2.07	1.95
11	A	303	HEC	FE-NA	3.68	2.07	1.95
12	A	307	UMQ	C4-C5	3.62	1.60	1.53
12	A	307	UMQ	C3'-C2'	-3.62	1.43	1.52
20	G	101	BCR	C1-C6	-3.61	1.49	1.53
11	A	305	HEC	FE-NA	3.60	2.07	1.95
13	A	308	SMA	C17-C16	3.58	1.55	1.44
16	B	204	CLA	C1D-ND	3.56	1.42	1.37
12	A	306	UMQ	C3'-C2'	-3.55	1.43	1.52
12	B	203	UMQ	C3'-C2'	-3.52	1.43	1.52
20	G	101	BCR	C30-C25	-3.33	1.49	1.53
11	A	304	HEC	FE-NC	3.33	2.06	1.95
12	B	203	UMQ	O3-C3	3.20	1.50	1.43
12	A	307	UMQ	O3-C3	3.19	1.50	1.43
16	B	204	CLA	C4B-NB	3.19	1.42	1.37
12	A	306	UMQ	O3-C3	3.18	1.50	1.43
19	D	202	SQD	O48-C23	3.16	1.42	1.33
17	D	203	OPC	OAN-CAO	3.13	1.43	1.34
17	B	205	OPC	OAN-CAO	3.13	1.43	1.34
17	E	101	OPC	OAN-CAO	3.13	1.43	1.34
11	A	305	HEC	FE-NC	3.11	2.05	1.95
12	A	307	UMQ	C6'-C5'	-2.96	1.41	1.51
12	B	203	UMQ	C6'-C5'	-2.95	1.41	1.51
12	A	306	UMQ	C6'-C5'	-2.95	1.41	1.51
19	D	202	SQD	O47-C7	2.93	1.42	1.34
12	B	203	UMQ	O1-C4'	2.92	1.51	1.43
13	A	308	SMA	O7-C7	2.91	1.41	1.37
12	A	306	UMQ	O1-C4'	2.91	1.51	1.43
13	A	308	SMA	O5-C5	2.87	1.41	1.37
11	C	301	HEC	FE-NA	2.85	2.04	1.95
12	A	307	UMQ	O1-C4'	2.82	1.51	1.43
11	A	303	HEC	FE-NC	2.75	2.04	1.95
11	C	301	HEC	FE-NC	2.73	2.04	1.95
16	B	204	CLA	C1B-C2B	2.62	1.49	1.43
12	B	203	UMQ	C1-C2	-2.54	1.45	1.52
12	A	306	UMQ	C1-C2	-2.52	1.45	1.52
12	A	307	UMQ	C1-C2	-2.51	1.45	1.52
16	B	204	CLA	C3B-C4B	2.45	1.49	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	203	UMQ	O2'-C2'	2.43	1.49	1.43
12	A	307	UMQ	O2'-C2'	2.43	1.49	1.43
12	A	306	UMQ	O2'-C2'	2.40	1.48	1.43
13	A	308	SMA	C24-C13	-2.38	1.48	1.53
16	B	204	CLA	CHC-C1C	2.30	1.43	1.38
13	A	308	SMA	C4A-C4	2.29	1.52	1.46
13	A	308	SMA	O8-C8	2.28	1.42	1.36
11	A	305	HEC	CMB-C2B	2.17	1.55	1.50
17	E	101	OPC	CAG-NAF	-2.15	1.44	1.51
11	A	305	HEC	CMC-C2C	2.13	1.55	1.50
13	A	308	SMA	C9-C2	2.12	1.55	1.49
11	A	304	HEC	CMB-C2B	2.12	1.55	1.50
11	C	301	HEC	CMC-C2C	2.11	1.55	1.50
17	D	203	OPC	CAG-NAF	-2.10	1.45	1.51
16	B	204	CLA	CMB-C2B	-2.10	1.46	1.50
13	A	308	SMA	C26-C19	-2.07	1.46	1.50
11	A	303	HEC	CMC-C2C	2.07	1.55	1.50
16	B	204	CLA	MG-NB	-2.07	2.01	2.05
12	B	203	UMQ	O5-C1	2.06	1.47	1.41
13	A	308	SMA	C14-C15	2.05	1.57	1.50
11	A	304	HEC	CMC-C2C	2.05	1.55	1.50
11	C	301	HEC	CMD-C2D	2.03	1.54	1.50
12	A	306	UMQ	O5-C1	2.01	1.47	1.41
12	A	307	UMQ	O5-C1	2.00	1.47	1.41
19	D	202	SQD	O2-C2	-2.00	1.38	1.43

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	307	UMQ	C1'-O5'-C5'	-8.81	96.52	113.72
12	A	306	UMQ	C1'-O5'-C5'	-8.77	96.59	113.72
12	B	203	UMQ	C1'-O5'-C5'	-8.70	96.73	113.72
12	B	203	UMQ	C2'-C3'-C4'	6.96	125.47	109.68
13	A	308	SMA	O7-C7-C8	-6.87	107.34	114.53
12	A	306	UMQ	C2'-C3'-C4'	6.85	125.23	109.68
12	A	307	UMQ	C2'-C3'-C4'	6.56	124.57	109.68
16	B	204	CLA	C4A-NA-C1A	6.24	109.53	106.68
11	A	305	HEC	C1D-ND-C4D	5.60	111.83	105.21
11	A	304	HEC	C1D-ND-C4D	5.50	111.73	105.21
11	A	303	HEC	C1D-ND-C4D	5.44	111.64	105.21
11	C	301	HEC	C1D-ND-C4D	5.41	111.61	105.21
13	A	308	SMA	O1-C2-C9	4.79	120.28	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	308	SMA	O7-C7-C6	4.72	132.20	124.08
11	A	303	HEC	CBC-CAC-C3C	4.69	125.15	112.42
11	C	301	HEC	CBC-CAC-C3C	4.68	125.11	112.42
11	A	305	HEC	CBC-CAC-C3C	4.63	124.98	112.42
11	A	305	HEC	CBB-CAB-C3B	4.62	124.96	112.42
11	A	304	HEC	CBB-CAB-C3B	4.57	124.80	112.42
11	A	304	HEC	CBC-CAC-C3C	4.48	124.56	112.42
12	A	307	UMQ	O5-C5-C4	-4.44	101.70	109.70
12	A	306	UMQ	C1-O1-C4'	-4.37	107.61	117.98
12	A	306	UMQ	O5-C5-C4	-4.13	102.25	109.70
17	B	205	OPC	OAN-CAO-CAP	4.11	120.37	111.48
19	D	202	SQD	O9-S-O7	-3.96	100.96	113.82
11	A	303	HEC	CBB-CAB-C3B	3.95	123.12	112.42
12	A	307	UMQ	C1-O1-C4'	-3.94	108.64	117.98
11	C	301	HEC	CBB-CAB-C3B	3.89	122.97	112.42
12	B	203	UMQ	O5-C5-C4	-3.77	102.90	109.70
14	A	309	7PH	O21-C21-C22	3.77	119.63	111.48
17	E	101	OPC	OAN-CAO-CAP	3.74	119.58	111.48
17	D	203	OPC	OAN-CAO-CAP	3.71	119.51	111.48
11	C	301	HEC	CAB-C3B-C4B	3.70	129.61	124.79
19	D	202	SQD	O47-C7-C8	3.68	119.45	111.48
12	B	203	UMQ	C1-O1-C4'	-3.34	110.06	117.98
19	D	202	SQD	O7-S-C6	3.24	111.60	106.76
11	A	303	HEC	CAB-C3B-C4B	3.20	128.95	124.79
19	D	202	SQD	O9-S-C6	3.11	111.40	106.76
16	B	204	CLA	O2D-CGD-O1D	-3.10	117.82	123.85
13	A	308	SMA	C5M-O5-C5	-3.06	113.03	117.51
16	B	204	CLA	C3B-C4B-NB	-3.02	107.84	110.53
13	A	308	SMA	C14-C15-C16	-2.86	120.09	125.88
20	G	101	BCR	C33-C5-C6	-2.82	121.40	124.48
17	D	203	OPC	OBJ-CBK-CBL	2.70	120.06	111.83
17	E	101	OPC	OBJ-CBK-CBL	2.68	120.02	111.83
11	C	301	HEC	CAB-C3B-C2B	-2.67	122.65	127.56
20	G	101	BCR	C27-C26-C25	2.65	126.28	122.70
11	A	305	HEC	C2A-C1A-NA	-2.61	107.80	110.32
11	A	305	HEC	CAD-C3D-C4D	2.60	129.23	124.70
11	A	304	HEC	C2A-C1A-NA	-2.60	107.81	110.32
13	A	308	SMA	C7M-O7-C7	-2.58	113.73	117.51
19	D	202	SQD	C44-O6-C1	2.54	119.23	113.80
11	A	303	HEC	C2A-C1A-NA	-2.53	107.88	110.32
17	B	205	OPC	OBJ-CBK-CBL	2.52	119.53	111.83
11	C	301	HEC	C4B-NB-C1B	2.49	108.16	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	C	301	HEC	C2A-C1A-NA	-2.43	107.97	110.32
12	A	306	UMQ	C3-C4-C5	2.42	114.62	110.23
11	A	303	HEC	CAC-C3C-C2C	2.40	130.69	126.89
11	C	301	HEC	C3B-C4B-NB	-2.40	107.54	110.17
14	A	309	7PH	O31-C31-C32	2.40	119.15	111.83
12	A	306	UMQ	C1-C2-C3	2.39	115.03	110.01
12	A	307	UMQ	C1-C2-C3	2.38	115.02	110.01
16	B	204	CLA	CHB-C4A-NA	2.38	127.83	124.40
11	A	303	HEC	C4B-NB-C1B	2.36	108.01	105.21
19	D	202	SQD	O48-C23-C24	2.36	119.03	111.83
19	D	202	SQD	O6-C1-C2	2.35	111.85	108.27
12	B	203	UMQ	C3-C4-C5	2.32	114.44	110.23
11	A	303	HEC	CAB-C3B-C2B	-2.29	123.35	127.56
13	A	308	SMA	C17-C18-C19	-2.28	120.12	126.36
13	A	308	SMA	O1-C2-C3	-2.27	119.82	121.81
19	D	202	SQD	O8-S-C6	2.25	110.31	105.97
11	A	303	HEC	CAD-C3D-C4D	2.20	128.53	124.70
13	A	308	SMA	C3M-C3-C2	-2.16	120.07	123.28
11	A	303	HEC	CAC-C3C-C4C	-2.15	121.95	124.91
19	D	202	SQD	O5-C5-C4	2.14	113.55	109.70
11	A	303	HEC	C3B-C4B-NB	-2.13	107.83	110.17
11	C	301	HEC	CAC-C3C-C2C	2.12	130.25	126.89
12	A	306	UMQ	O5'-C1'-C2'	2.06	114.61	110.37
20	G	101	BCR	C7-C8-C9	-2.06	123.19	126.23
20	G	101	BCR	C24-C23-C22	-2.05	123.20	126.23
11	A	305	HEC	CAC-C3C-C2C	2.05	130.13	126.89
11	A	305	HEC	C4B-NB-C1B	2.05	107.63	105.21
20	G	101	BCR	C2-C1-C6	2.04	113.40	110.44
16	B	204	CLA	O2A-CGA-O1A	-2.01	118.60	123.63
20	G	101	BCR	C10-C11-C12	-2.01	117.38	123.20
17	E	101	OPC	CAH-CAG-NAF	-2.00	109.39	115.82
17	D	203	OPC	CAH-CAG-NAF	-2.00	109.40	115.82

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	303	HEC	NA
11	A	304	HEC	NA
11	A	305	HEC	NA
11	C	301	HEC	NA
13	A	308	SMA	C12

All (199) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	303	HEC	C2B-C3B-CAB-CBB
11	A	303	HEC	C4B-C3B-CAB-CBB
11	C	301	HEC	C2B-C3B-CAB-CBB
11	C	301	HEC	C4B-C3B-CAB-CBB
12	A	306	UMQ	O5'-C1'-O1'-CA
13	A	308	SMA	C22-C11-C12-O12
13	A	308	SMA	C14-C15-C16-C17
13	A	308	SMA	C17-C18-C19-C20
13	A	308	SMA	C17-C18-C19-C26
14	A	309	7PH	O11-C1-C2-C3
14	A	309	7PH	O11-C1-C2-O21
17	B	205	OPC	CAL-OAK-PAJ-OBH
17	B	205	OPC	CAL-OAK-PAJ-OAI
17	D	203	OPC	CAH-OAI-PAJ-OAK
17	D	203	OPC	CAH-OAI-PAJ-OBH
17	E	101	OPC	CAP-CAO-OAN-CAM
19	D	202	SQD	O6-C44-C45-O47
20	G	101	BCR	C6-C7-C8-C9
20	G	101	BCR	C7-C8-C9-C10
20	G	101	BCR	C7-C8-C9-C34
20	G	101	BCR	C19-C20-C21-C22
17	D	203	OPC	OCC-CBK-OBJ-CBI
11	A	303	HEC	C4C-C3C-CAC-CBC
11	A	304	HEC	C4C-C3C-CAC-CBC
11	A	305	HEC	C4C-C3C-CAC-CBC
11	C	301	HEC	C4C-C3C-CAC-CBC
11	A	304	HEC	C4B-C3B-CAB-CBB
11	A	305	HEC	C4B-C3B-CAB-CBB
11	A	304	HEC	C2B-C3B-CAB-CBB
11	A	305	HEC	C2B-C3B-CAB-CBB
17	E	101	OPC	OAD-CAO-OAN-CAM
11	A	303	HEC	C2C-C3C-CAC-CBC
11	A	304	HEC	C2C-C3C-CAC-CBC
11	A	305	HEC	C2C-C3C-CAC-CBC
11	C	301	HEC	C2C-C3C-CAC-CBC
13	A	308	SMA	C8-C7-O7-C7M
14	A	309	7PH	C32-C31-O31-C3
17	D	203	OPC	CBL-CBK-OBJ-CBI
13	A	308	SMA	C15-C16-C17-C18
12	B	203	UMQ	O5-C1-O1-C4'
12	B	203	UMQ	C3'-C4'-O1-C1
12	A	306	UMQ	O5-C1-O1-C4'

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Mol	Chain	Res	Type	Atoms
12	A	306	UMQ	C2'-C1'-O1'-CA
13	A	308	SMA	C6-C7-O7-C7M
13	A	308	SMA	C6-C5-O5-C5M
14	A	309	7PH	O32-C31-O31-C3
12	B	203	UMQ	O1'-CA-CB-CC
12	B	203	UMQ	C5'-C4'-O1-C1
17	E	101	OPC	CBK-CBL-CBM-CBN
16	B	204	CLA	C15-C16-C17-C18
17	D	203	OPC	OAD-CAO-OAN-CAM
13	A	308	SMA	C4A-C5-O5-C5M
17	E	101	OPC	CBL-CBK-OBJ-CBI
12	A	306	UMQ	O5-C5-C6-O6
12	B	203	UMQ	O5-C5-C6-O6
17	D	203	OPC	CAP-CAO-OAN-CAM
19	D	202	SQD	C2-C1-O6-C44
11	A	303	HEC	C2A-CAA-CBA-CGA
20	G	101	BCR	C11-C10-C9-C8
17	B	205	OPC	CAP-CAO-OAN-CAM
17	B	205	OPC	CBT-CBU-CBV-CBW
19	D	202	SQD	C12-C13-C14-C15
15	B	201	8K6	C6-C7-C8-C9
17	D	203	OPC	CAR-CAS-CAT-CAU
17	B	205	OPC	CAR-CAS-CAT-CAU
19	D	202	SQD	C9-C10-C11-C12
17	E	101	OPC	CBW-CBX-CBY-CBZ
17	E	101	OPC	CAP-CAQ-CAR-CAS
19	D	202	SQD	C27-C28-C29-C30
16	B	204	CLA	C3A-C2A-CAA-CBA
17	D	203	OPC	CBA-CBB-CBC-CBD
12	A	306	UMQ	O1'-CA-CB-CC
12	A	306	UMQ	C4-C5-C6-O6
20	G	101	BCR	C1-C6-C7-C8
20	G	101	BCR	C5-C6-C7-C8
17	D	203	OPC	CBQ-CBR-CBS-CBT
12	B	203	UMQ	C4-C5-C6-O6
17	D	203	OPC	CBW-CBX-CBY-CBZ
17	E	101	OPC	CBU-CBV-CBW-CBX
17	B	205	OPC	OAD-CAO-OAN-CAM
17	E	101	OPC	CAQ-CAR-CAS-CAT
20	G	101	BCR	C18-C19-C20-C21
9	A	301	MYS	C5-C6-C7-C8
17	D	203	OPC	CAY-CAZ-CBA-CBB

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Mol	Chain	Res	Type	Atoms
19	D	202	SQD	O5-C1-O6-C44
12	A	306	UMQ	C3'-C4'-O1-C1
14	A	309	7PH	C32-C33-C34-C35
17	B	205	OPC	CAS-CAT-CAU-CAV
17	B	205	OPC	CBO-CBP-CBQ-CBR
17	D	203	OPC	CAS-CAT-CAU-CAV
17	D	203	OPC	CBO-CBP-CBQ-CBR
17	E	101	OPC	CAS-CAT-CAU-CAV
17	E	101	OPC	CBO-CBP-CBQ-CBR
13	A	308	SMA	C11-C12-C13-C24
17	E	101	OPC	OCC-CBK-OBJ-CBI
17	D	203	OPC	CAP-CAQ-CAR-CAS
12	A	306	UMQ	C5'-C4'-O1-C1
12	B	203	UMQ	O5'-C5'-C6'-O6'
17	D	203	OPC	CBM-CBN-CBO-CBP
17	E	101	OPC	CAY-CAZ-CBA-CBB
19	D	202	SQD	C30-C31-C32-C33
17	D	203	OPC	CBR-CBS-CBT-CBU
11	A	305	HEC	C2D-C3D-CAD-CBD
11	A	305	HEC	C4D-C3D-CAD-CBD
17	B	205	OPC	CBM-CBN-CBO-CBP
16	B	204	CLA	C1A-C2A-CAA-CBA
17	E	101	OPC	CBT-CBU-CBV-CBW
19	D	202	SQD	C28-C29-C30-C31
19	D	202	SQD	C7-C8-C9-C10
17	D	203	OPC	CBK-CBL-CBM-CBN
19	D	202	SQD	O6-C44-C45-C46
17	D	203	OPC	CBS-CBT-CBU-CBV
9	A	301	MYS	C9-C10-C11-C12
17	D	203	OPC	CBU-CBV-CBW-CBX
17	D	203	OPC	CAW-CAX-CAY-CAZ
17	E	101	OPC	CBS-CBT-CBU-CBV
17	B	205	OPC	CBL-CBK-OBJ-CBI
12	A	306	UMQ	CA-CB-CC-CD
16	B	204	CLA	C4-C3-C5-C6
19	D	202	SQD	C18-C19-C20-C21
12	A	307	UMQ	CB-CA-O1'-C1'
16	B	204	CLA	C4B-C3B-CAB-CBB
17	B	205	OPC	CBA-CBB-CBC-CBD
13	A	308	SMA	O12-C12-C13-C24
16	B	204	CLA	C2-C3-C5-C6
16	B	204	CLA	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
17	E	101	OPC	CAZ-CBA-CBB-CBC
15	B	201	8K6	C12-C13-C14-C15
17	B	205	OPC	CAY-CAZ-CBA-CBB
11	A	304	HEC	C1A-C2A-CAA-CBA
20	G	101	BCR	C11-C10-C9-C34
17	D	203	OPC	CBI-CAM-OAN-CAO
17	E	101	OPC	CBL-CBM-CBN-CBO
13	A	308	SMA	C24-C13-C14-C15
13	A	308	SMA	C24-C13-C14-O14
17	D	203	OPC	NAF-CAG-CAH-OAI
17	E	101	OPC	NAF-CAG-CAH-OAI
17	E	101	OPC	CBP-CBQ-CBR-CBS
13	A	308	SMA	O12-C12-C13-C14
17	D	203	OPC	CAQ-CAR-CAS-CAT
13	A	308	SMA	C11-C12-C13-C14
17	B	205	OPC	CBU-CBV-CBW-CBX
15	B	201	8K6	C9-C10-C11-C12
16	B	204	CLA	C12-C13-C15-C16
9	A	301	MYS	C7-C8-C9-C10
17	D	203	OPC	CBL-CBM-CBN-CBO
14	A	309	7PH	C36-C37-C38-C39
17	E	101	OPC	CAL-CAM-CBI-OBJ
17	D	203	OPC	CBY-CBZ-CCA-CCB
17	B	205	OPC	CAL-OAK-PAJ-OAB
17	E	101	OPC	CAL-OAK-PAJ-OAB
19	D	202	SQD	C11-C10-C9-C8
19	D	202	SQD	C16-C17-C18-C19
15	B	201	8K6	C11-C12-C13-C14
17	E	101	OPC	CAM-CAL-OAK-PAJ
19	D	202	SQD	O47-C45-C46-O48
16	B	204	CLA	C10-C11-C12-C13
17	E	101	OPC	CAT-CAU-CAV-CAW
17	B	205	OPC	CAP-CAQ-CAR-CAS
11	A	304	HEC	C3A-C2A-CAA-CBA
13	A	308	SMA	C12-C13-C14-O14
17	B	205	OPC	CAT-CAU-CAV-CAW
17	E	101	OPC	CAL-CAM-OAN-CAO
17	E	101	OPC	CBA-CBB-CBC-CBD
17	B	205	OPC	CAH-CAG-NAF-CAE
20	G	101	BCR	C23-C24-C25-C30
17	E	101	OPC	CBV-CBW-CBX-CBY
14	A	309	7PH	O21-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
17	B	205	OPC	OAN-CAO-CAP-CAQ
12	B	203	UMQ	CF-CG-CH-CI
19	D	202	SQD	C10-C11-C12-C13
16	B	204	CLA	C14-C13-C15-C16
17	B	205	OPC	CBS-CBT-CBU-CBV
19	D	202	SQD	C19-C20-C21-C22
17	E	101	OPC	CBR-CBS-CBT-CBU
17	E	101	OPC	CAV-CAW-CAX-CAY
17	E	101	OPC	CAG-CAH-OAI-PAJ
13	A	308	SMA	C22-C11-C12-C13
17	D	203	OPC	CAT-CAU-CAV-CAW
20	G	101	BCR	C23-C24-C25-C26
13	A	308	SMA	C3-C2-C9-C10
16	B	204	CLA	CAA-CBA-CGA-O2A
17	D	203	OPC	CAV-CAW-CAX-CAY
17	B	205	OPC	CAH-CAG-NAF-CAA
11	C	301	HEC	C2D-C3D-CAD-CBD
15	B	201	8K6	C13-C14-C15-C16
17	B	205	OPC	CAH-CAG-NAF-CBG
17	E	101	OPC	OAN-CAO-CAP-CAQ
17	E	101	OPC	OAD-CAO-CAP-CAQ
16	B	204	CLA	CAA-CBA-CGA-O1A
17	D	203	OPC	OAD-CAO-CAP-CAQ
17	D	203	OPC	OAN-CAO-CAP-CAQ
13	A	308	SMA	C10-C11-C12-C13
11	C	301	HEC	CAA-CBA-CGA-O2A
19	D	202	SQD	O49-C7-C8-C9
17	B	205	OPC	CBR-CBS-CBT-CBU
20	G	101	BCR	C22-C23-C24-C25
17	D	203	OPC	CBT-CBU-CBV-CBW
19	D	202	SQD	O47-C7-C8-C9

There are no ring outliers.

15 monomers are involved in 66 short contacts:

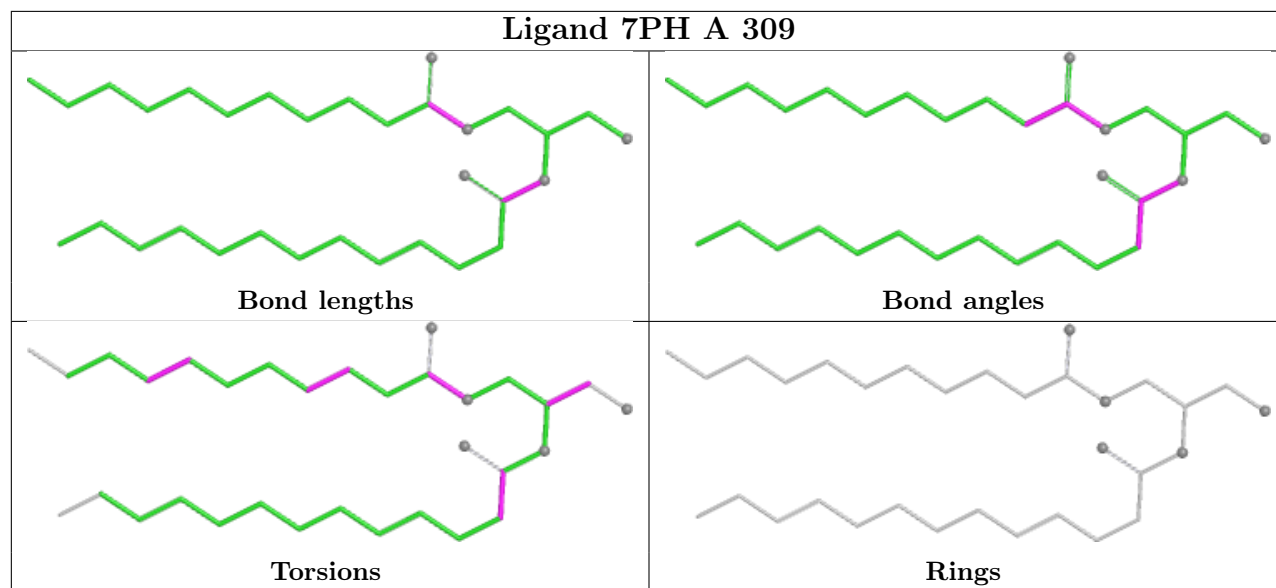
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	301	MYS	3	0
14	A	309	7PH	3	0
19	D	202	SQD	1	0
11	C	301	HEC	5	0
13	A	308	SMA	7	0
17	B	205	OPC	5	0

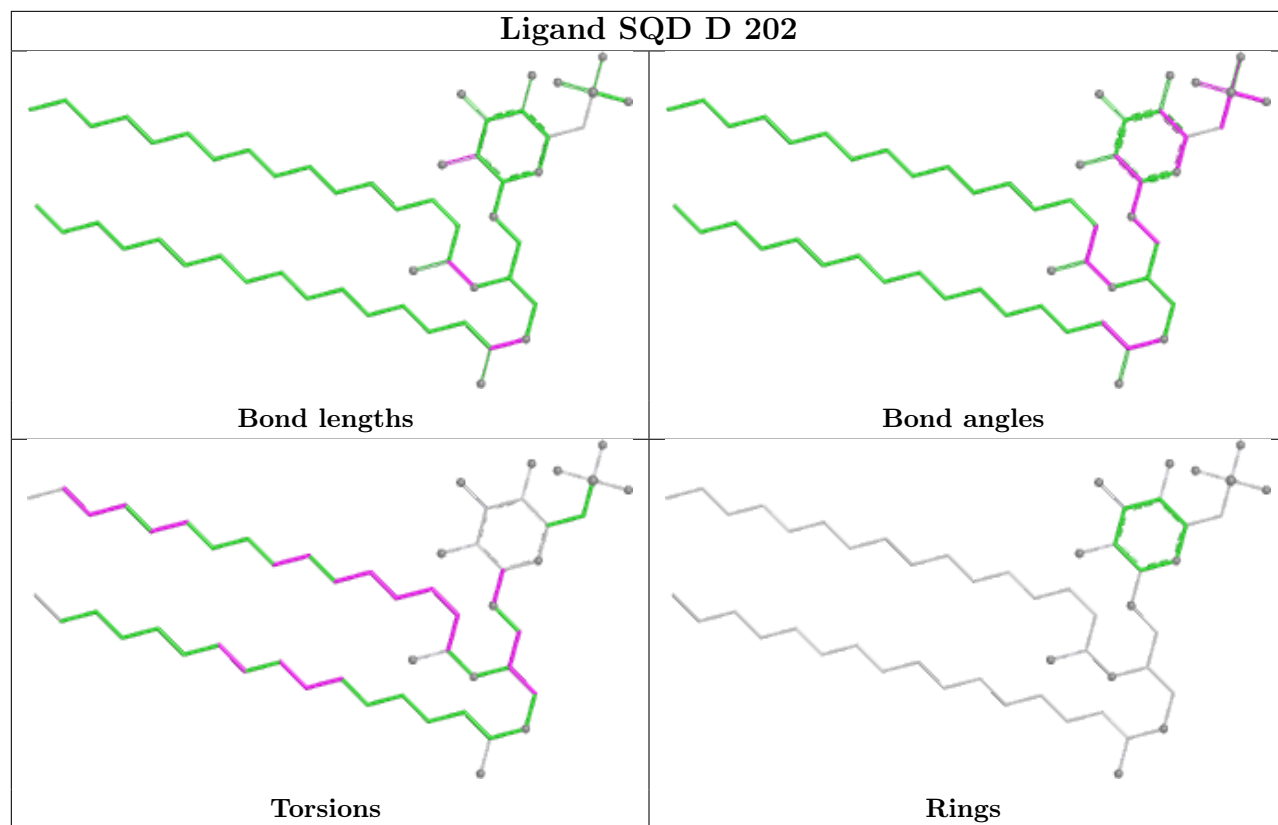
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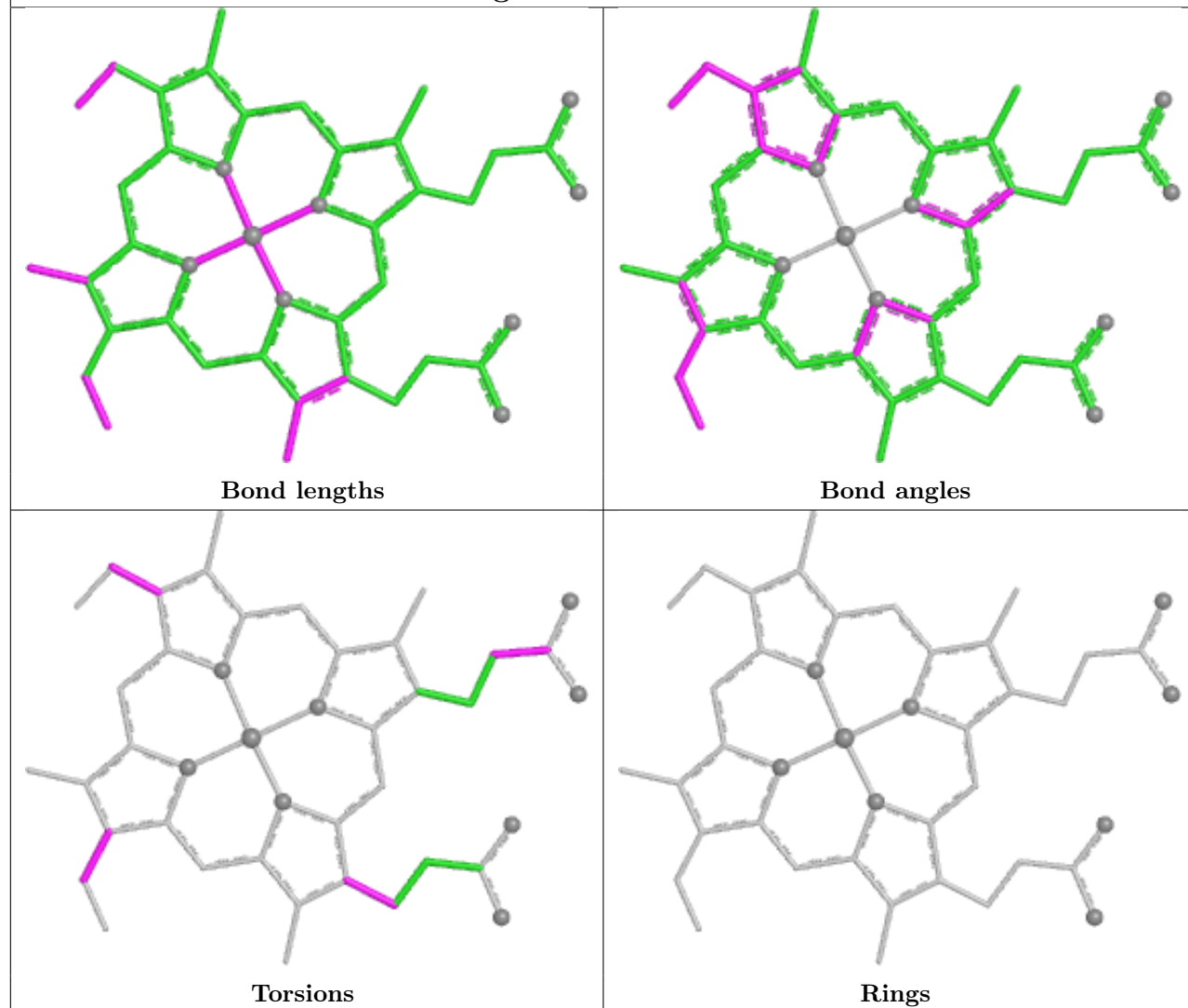
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	D	203	OPC	4	0
12	B	203	UMQ	10	0
11	A	303	HEC	2	0
12	A	307	UMQ	3	0
20	G	101	BCR	1	0
16	B	204	CLA	5	0
11	A	305	HEC	5	0
12	A	306	UMQ	7	0
17	E	101	OPC	12	0

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.

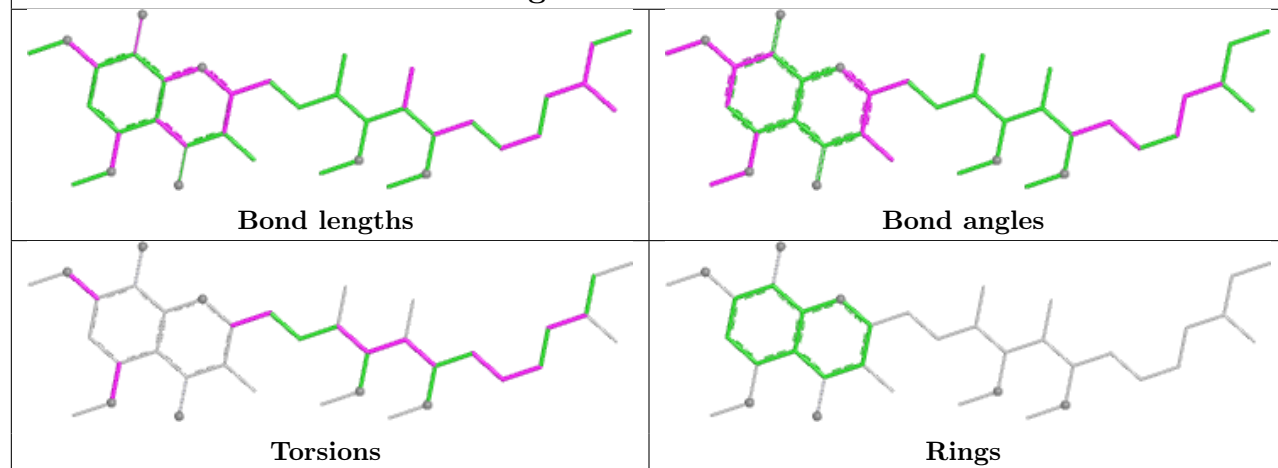


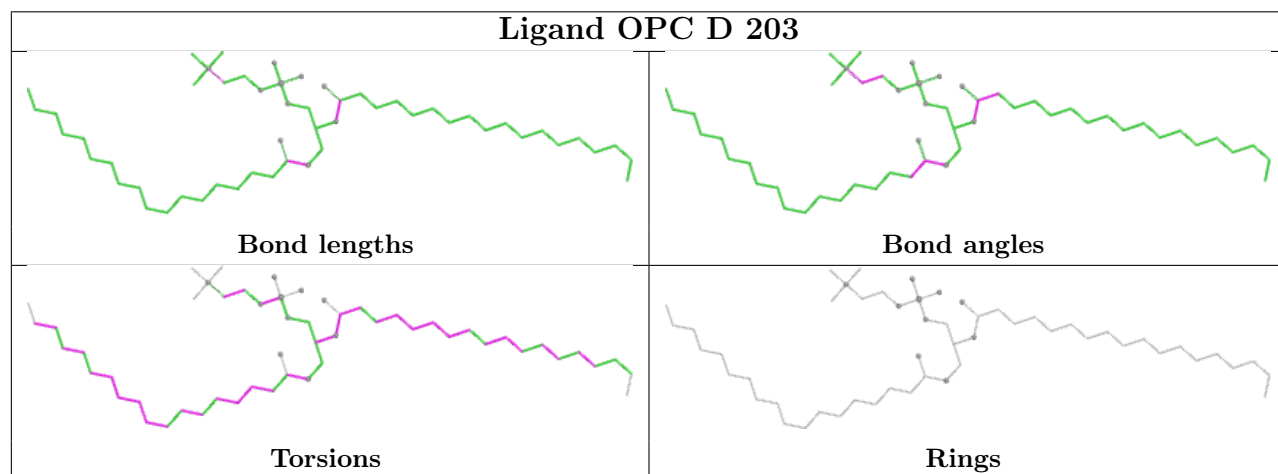
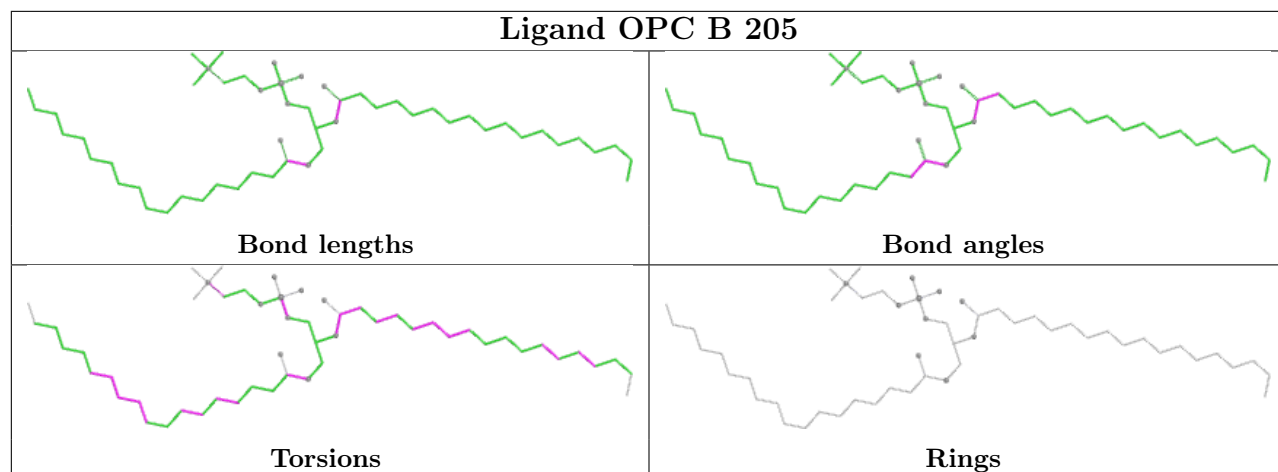


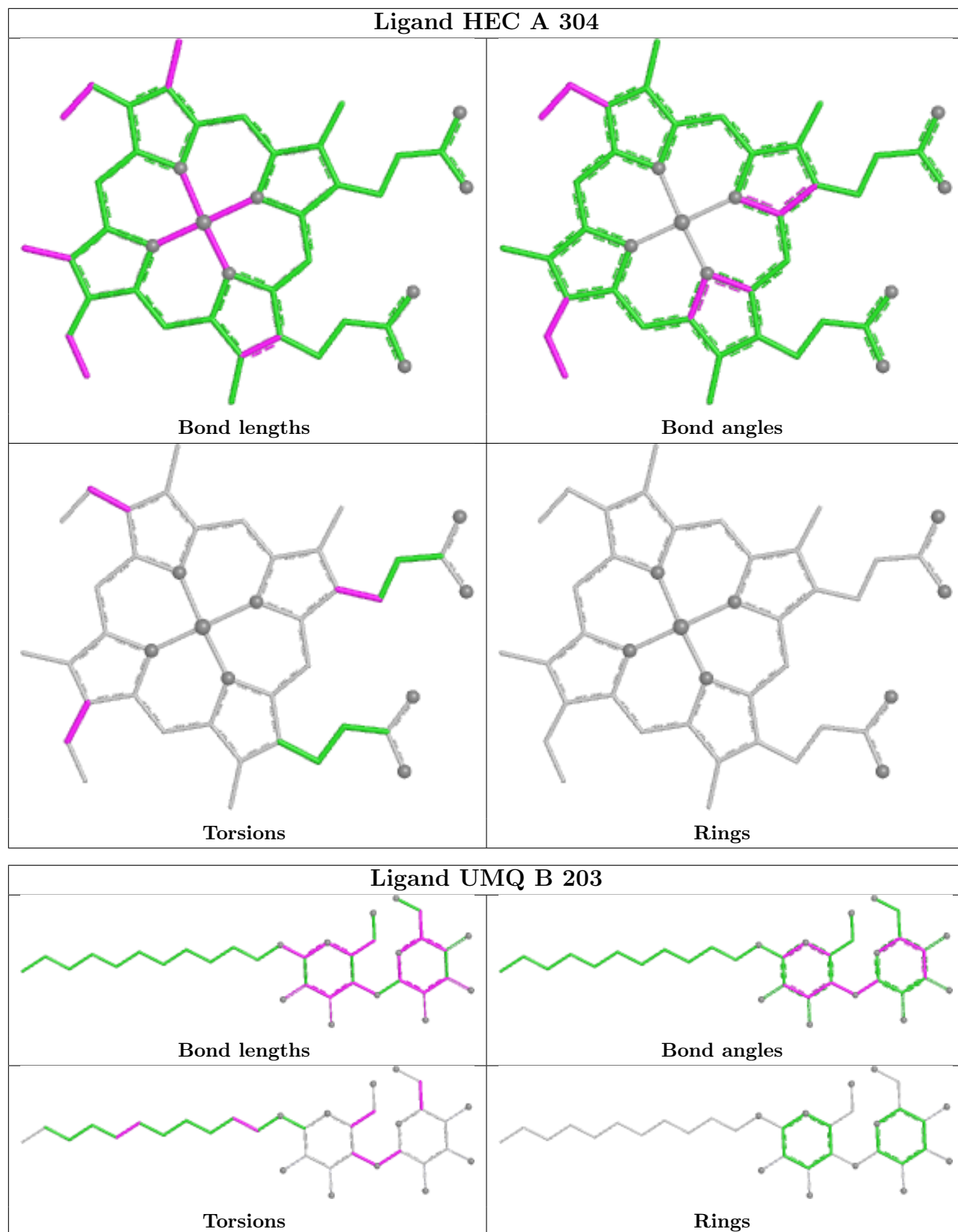
Ligand HEC C 301

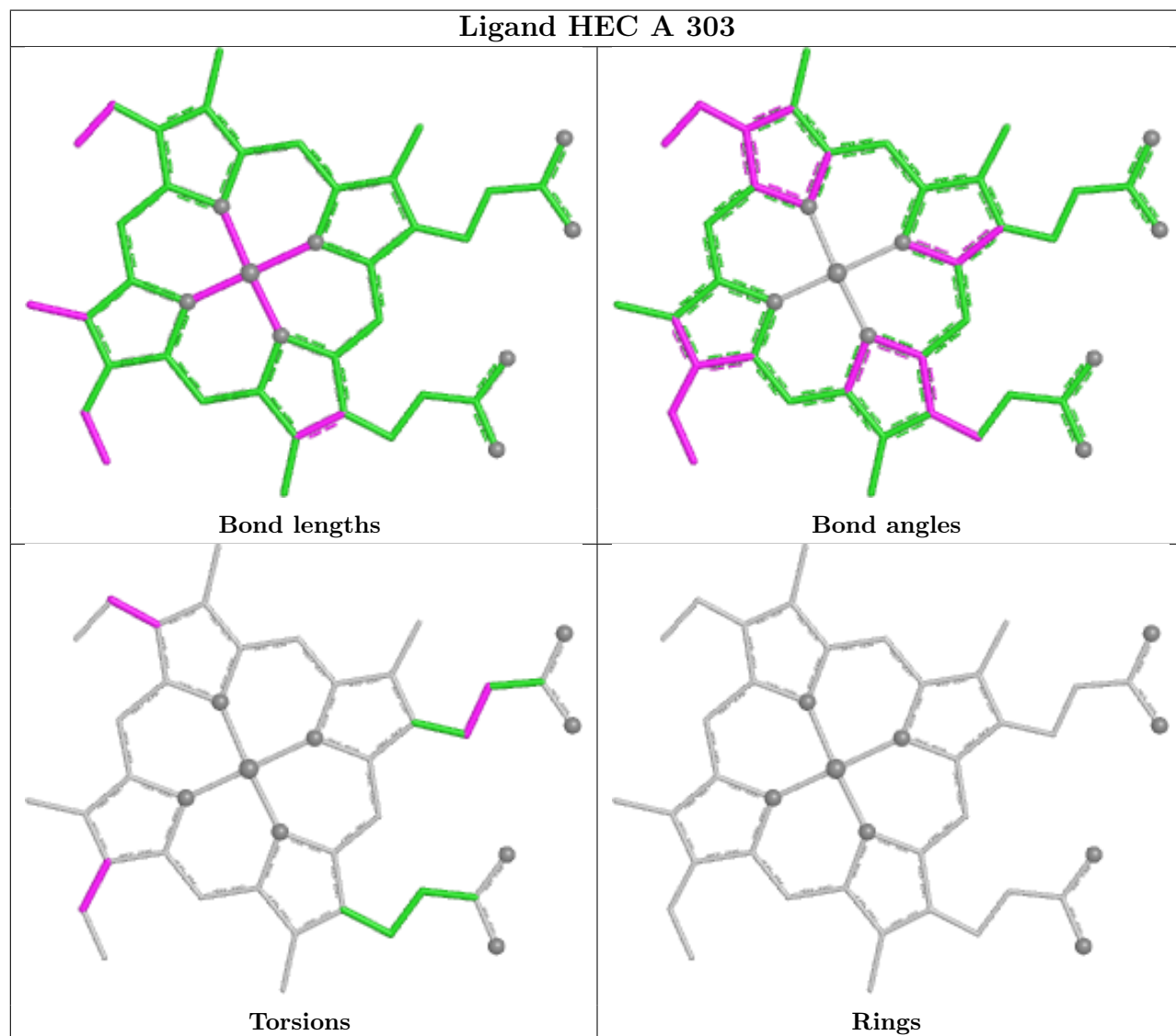
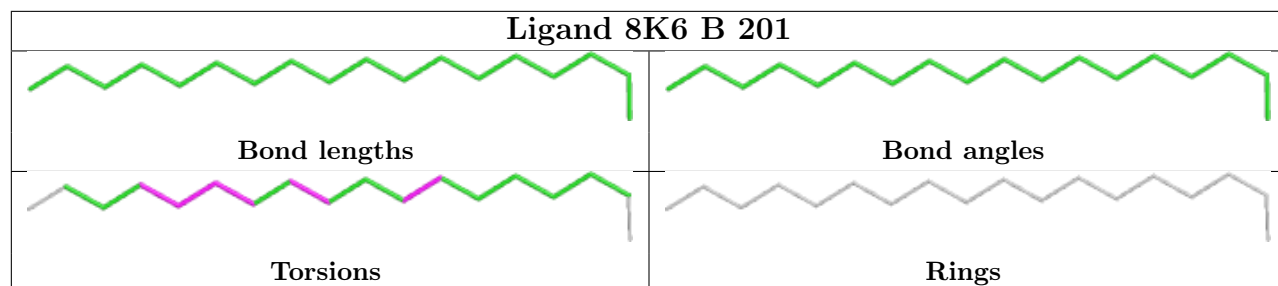


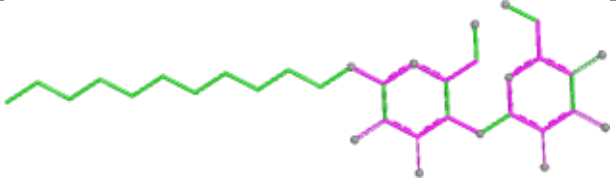
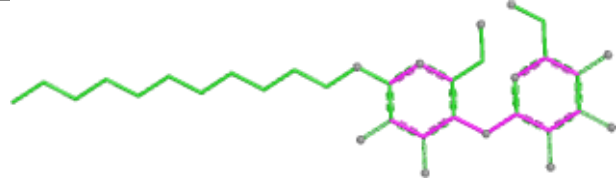
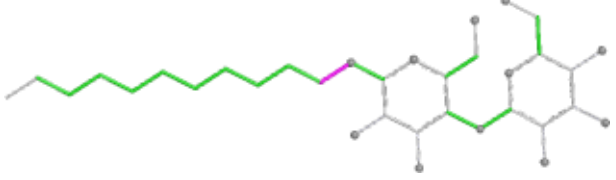
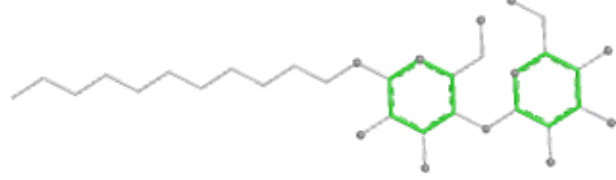
Ligand SMA A 308

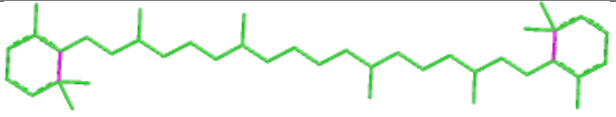
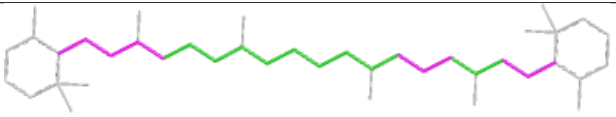
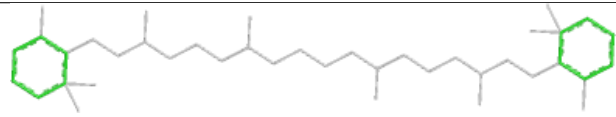


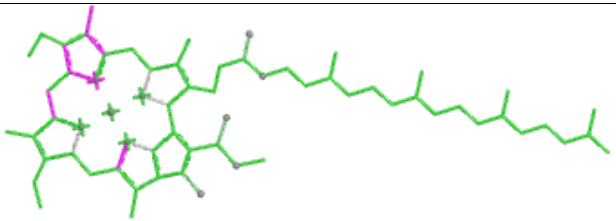
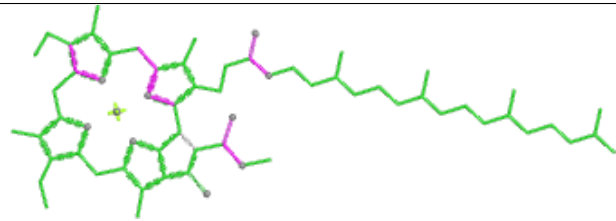
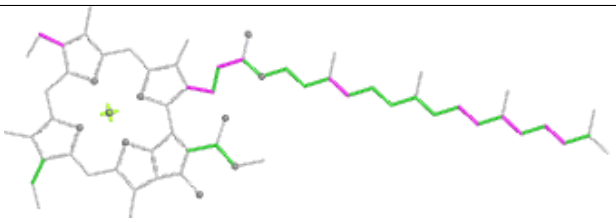
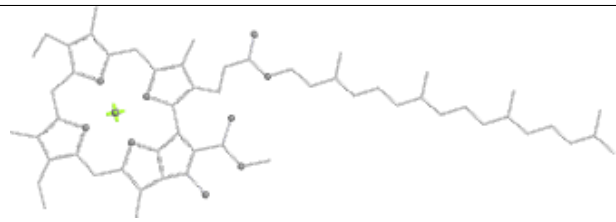


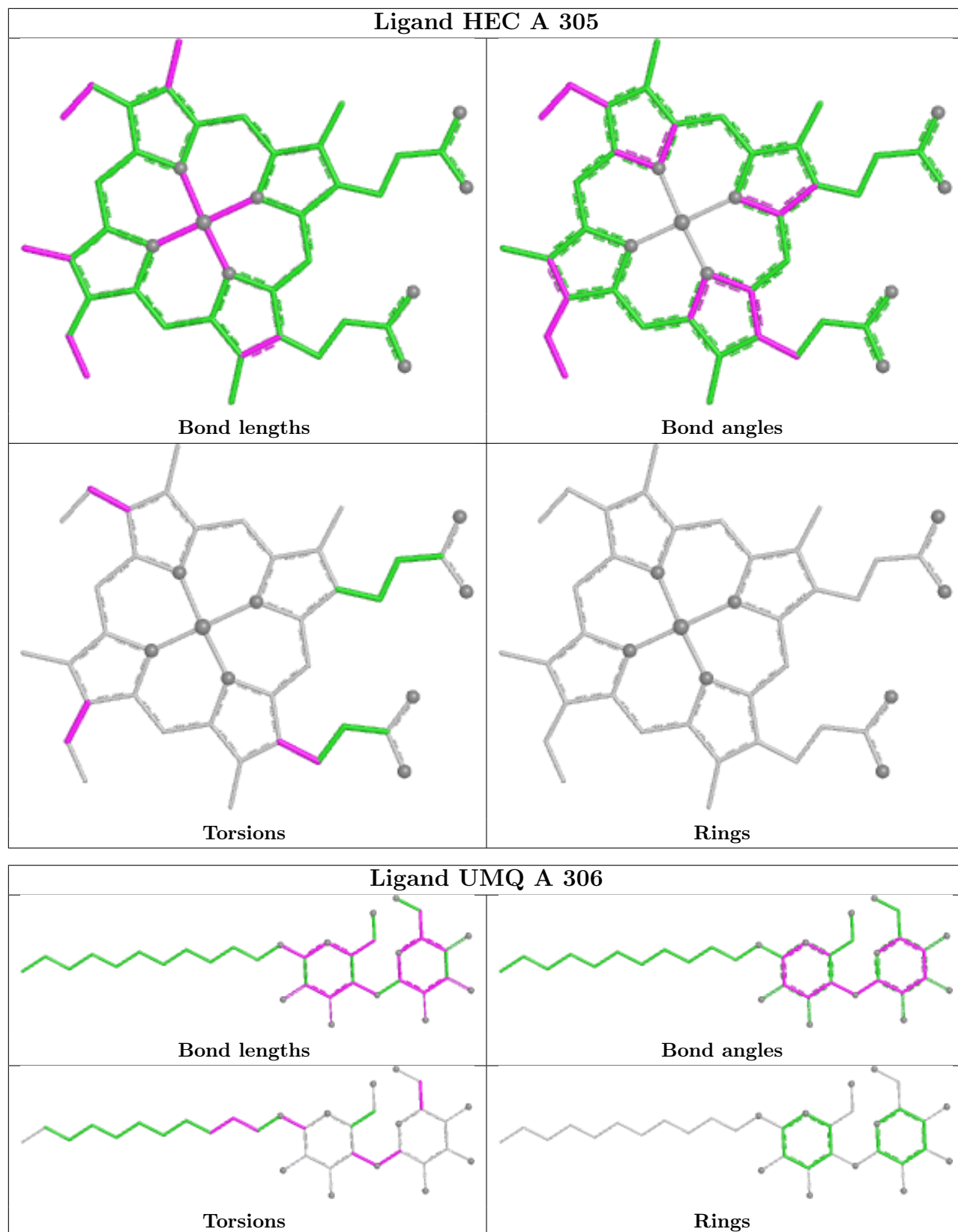


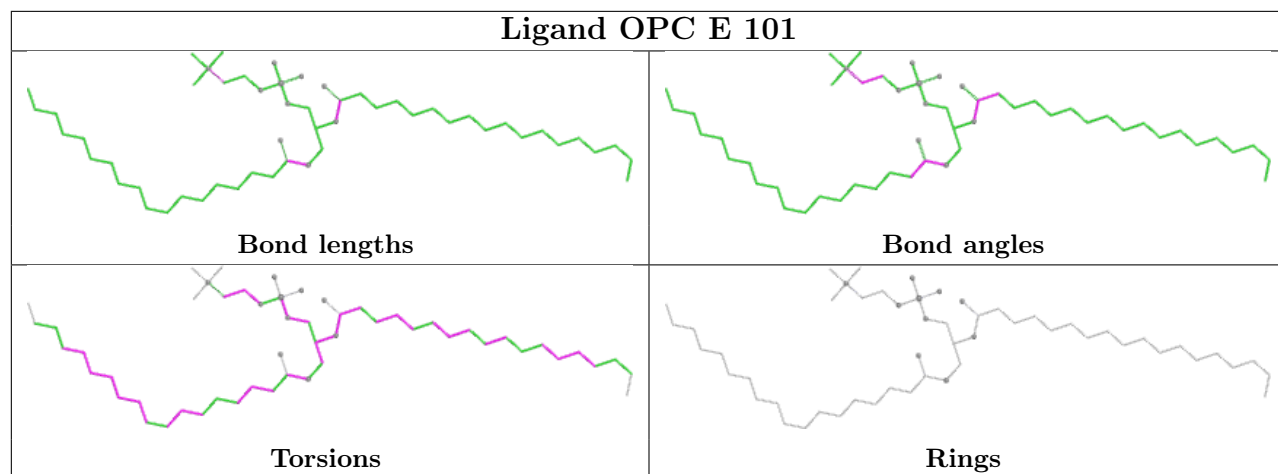


Ligand UMQ A 307	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand BCR G 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA B 204	
	
Bond lengths	Bond angles
	
Torsions	Rings





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	213/215 (99%)	-0.31	3 (1%) 73 51	49, 73, 114, 157	5 (2%)
2	B	159/160 (99%)	0.15	10 (6%) 26 13	60, 95, 139, 208	2 (1%)
3	C	288/289 (99%)	0.62	33 (11%) 9 6	63, 110, 237, 280	0
4	D	158/179 (88%)	1.15	32 (20%) 3 2	65, 170, 227, 287	0
5	E	28/32 (87%)	0.18	2 (7%) 22 11	92, 108, 131, 153	0
6	F	31/35 (88%)	0.38	3 (9%) 13 7	83, 100, 159, 177	0
7	G	37/37 (100%)	0.93	6 (16%) 4 3	70, 92, 202, 239	4 (10%)
8	H	28/29 (96%)	0.28	3 (10%) 11 6	77, 90, 128, 148	0
All	All	942/976 (96%)	0.40	92 (9%) 13 7	49, 99, 212, 287	11 (1%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	G	37	GLY	10.4
3	C	281	LYS	6.9
3	C	88	GLU	6.9
4	D	160	ILE	6.3
8	H	29	LEU	5.8
4	D	155	VAL	5.1
7	G	34	GLU	5.0
7	G	1	MET	4.9
6	F	31	GLY	4.9
4	D	110	HIS	4.8
4	D	91	ILE	4.6
3	C	214	GLY	4.4
4	D	92	VAL	4.3
4	D	119	ALA	4.1
2	B	74	GLU	4.1
2	B	2	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
3	C	181	THR	3.9
3	C	225	VAL	3.7
3	C	59	GLN	3.6
7	G	35	LEU	3.6
3	C	74	ALA	3.5
7	G	32	PRO	3.5
7	G	36	GLY	3.4
3	C	192	ASN	3.3
3	C	64	ASP	3.3
3	C	108	GLU	3.3
8	H	4	ASP	3.2
4	D	135	GLU	3.2
2	B	20	LYS	3.2
4	D	136	THR	3.2
4	D	65	LYS	3.1
6	F	32	ALA	3.1
3	C	222	GLY	3.1
5	E	26	ILE	3.1
2	B	116	ASN	3.0
4	D	75	ALA	3.0
2	B	160	PHE	3.0
3	C	86	PRO	3.0
4	D	170	PHE	3.0
3	C	176	ALA	3.0
3	C	218	ILE	2.9
4	D	150	LEU	2.9
4	D	145	PRO	2.8
3	C	279	VAL	2.8
4	D	179	VAL	2.8
4	D	85	LYS	2.8
4	D	154	THR	2.8
3	C	66	SER	2.8
4	D	161	VAL	2.8
4	D	130	GLY	2.8
6	F	30	GLN	2.7
2	B	75	ILE	2.7
4	D	101	ASP	2.7
4	D	80	LEU	2.7
3	C	100	ASP	2.7
3	C	47	LYS	2.6
3	C	87	GLU	2.6
3	C	229	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
3	C	242	GLN	2.5
3	C	89	ARG	2.5
4	D	175	LYS	2.5
4	D	120	ALA	2.5
4	D	73	HIS	2.5
2	B	3	THR	2.5
3	C	92	GLU	2.5
4	D	59	LYS	2.4
3	C	220	SER	2.4
4	D	156	GLN	2.4
3	C	230	ALA	2.4
1	A	10	GLU	2.4
3	C	57	LYS	2.3
3	C	197	VAL	2.3
4	D	122	ASN	2.3
2	B	153	LYS	2.3
2	B	24	HIS	2.3
5	E	28	SER	2.3
4	D	102	TYR	2.3
3	C	253	ASN	2.3
4	D	125	LYS	2.2
3	C	219	VAL	2.2
8	H	2	GLU	2.2
4	D	172	THR	2.2
1	A	159	PRO	2.2
3	C	182	LYS	2.2
3	C	178	GLY	2.1
4	D	82	GLN	2.1
4	D	68	LYS	2.1
1	A	136	TYR	2.1
3	C	280	GLU	2.1
4	D	177	TRP	2.1
2	B	27	TYR	2.1
3	C	231	LEU	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 ⓘ

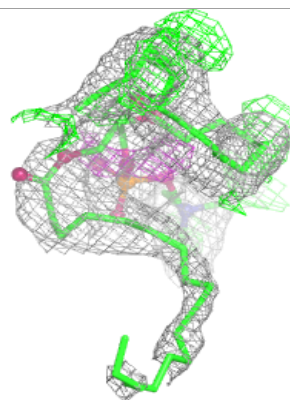
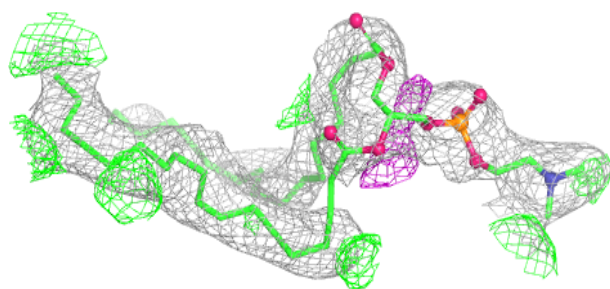
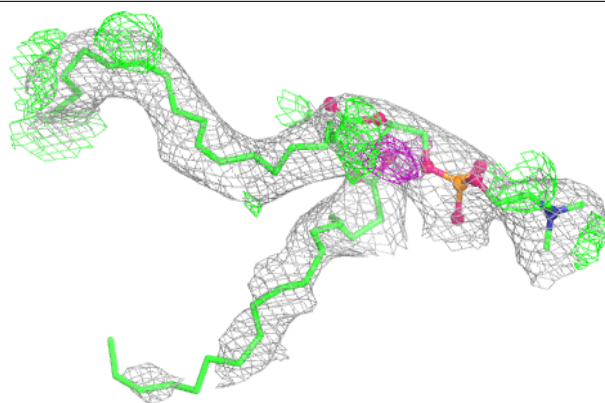
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
17	OPC	D	203	54/55	0.80	0.23	67,125,194,215	1
12	UMQ	B	203	34/34	0.81	0.18	107,167,218,223	0
19	SQD	D	202	54/54	0.82	0.16	104,125,149,154	30
12	UMQ	A	306	34/34	0.84	0.24	72,128,148,161	7
14	7PH	A	309	32/38	0.87	0.25	53,85,112,116	4
13	SMA	A	308	37/37	0.88	0.28	77,110,157,166	12
17	OPC	E	101	54/55	0.89	0.23	67,112,195,227	0
9	MYS	A	301	15/15	0.90	0.22	50,68,85,86	0
12	UMQ	A	307	34/34	0.90	0.15	100,139,156,232	3
17	OPC	B	205	54/55	0.91	0.20	80,118,150,151	0
15	8K6	B	201	18/18	0.91	0.23	74,93,107,115	0
20	BCR	G	101	40/40	0.93	0.16	57,80,98,107	14
10	CD	B	202	1/1	0.94	0.10	231,231,231,231	0
16	CLA	B	204	65/65	0.95	0.13	69,97,126,131	0
18	FES	D	201	4/4	0.96	0.07	151,161,163,260	0
11	HEC	C	301	43/43	0.98	0.10	60,87,128,141	0
11	HEC	A	305	43/43	0.98	0.09	71,96,110,126	0
10	CD	A	302	1/1	0.99	0.07	100,100,100,100	0
11	HEC	A	303	43/43	0.99	0.09	47,67,82,100	0
11	HEC	A	304	43/43	0.99	0.07	46,68,82,91	0

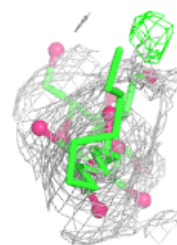
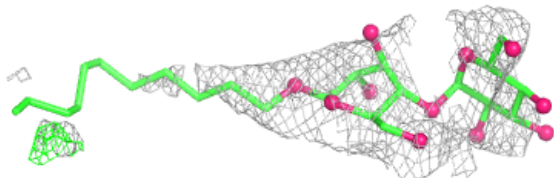
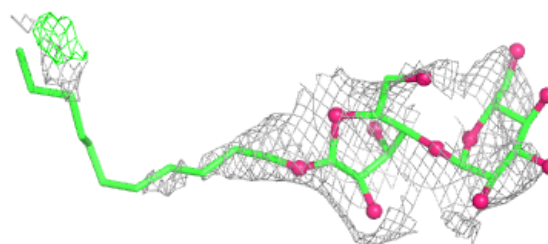
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OPC D 203:

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

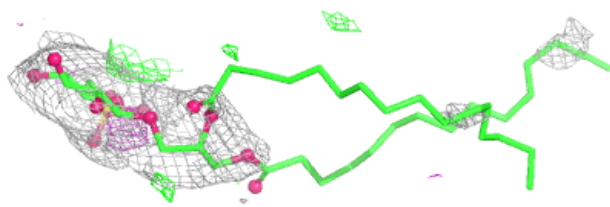
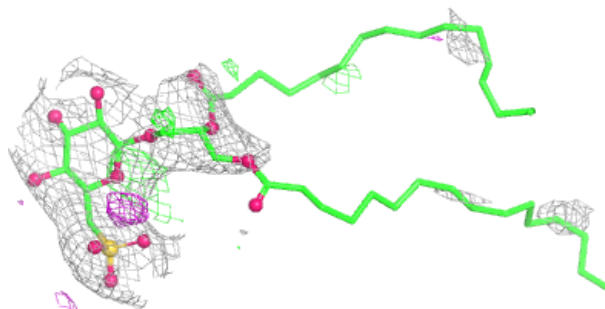
**Electron density around UMQ B 203:**

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

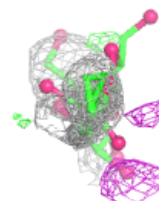
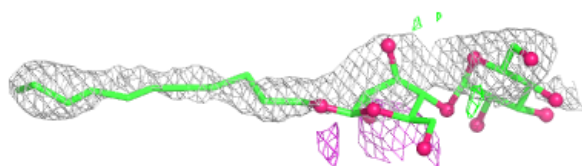
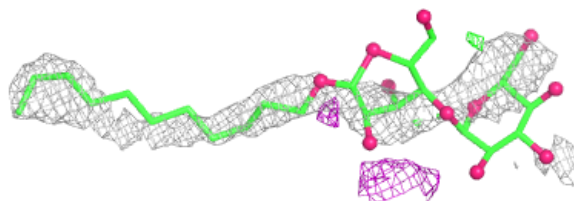


Electron density around SQD D 202:

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

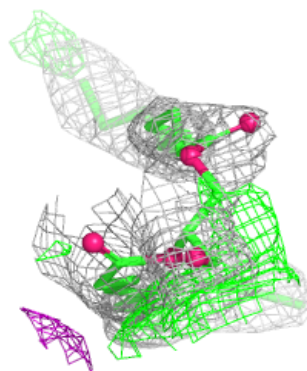
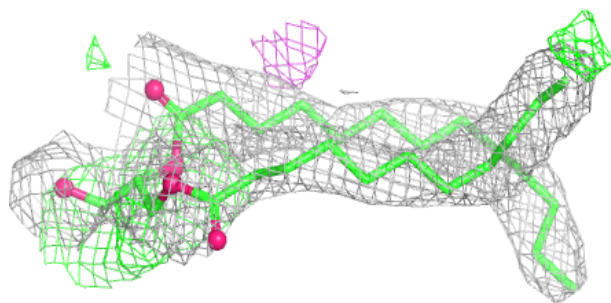
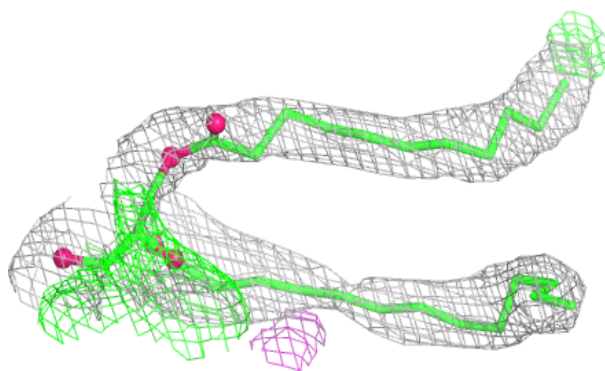
**Electron density around UMQ A 306:**

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

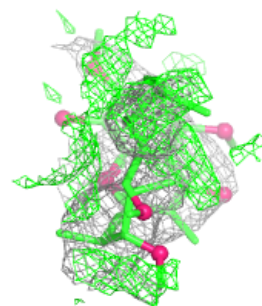
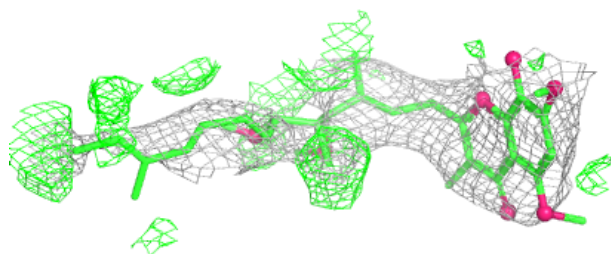
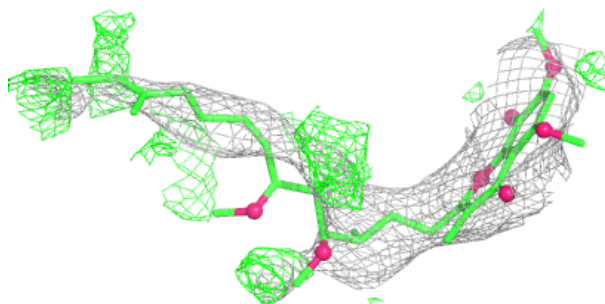


Electron density around 7PH A 309:

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

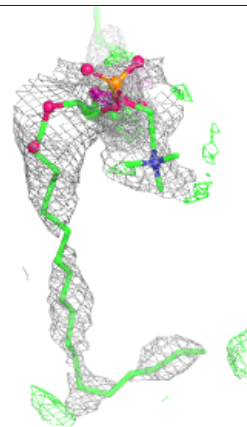
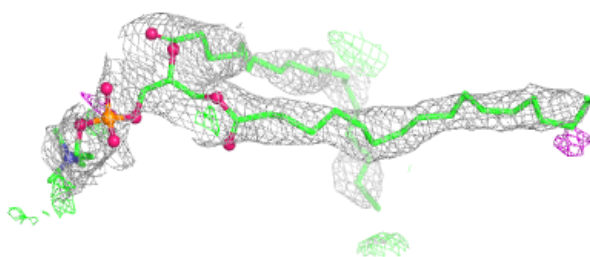
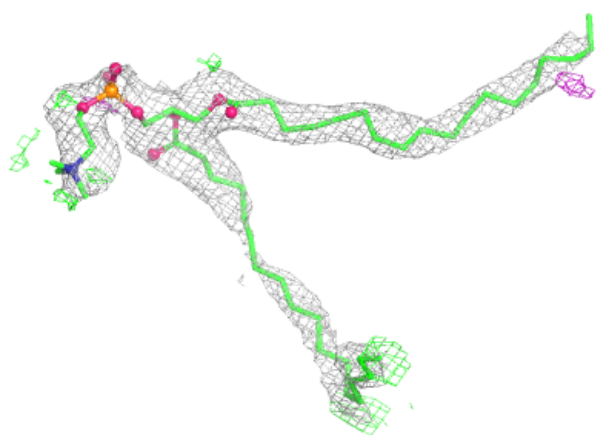
**Electron density around SMA A 308:**

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

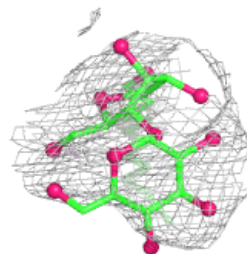
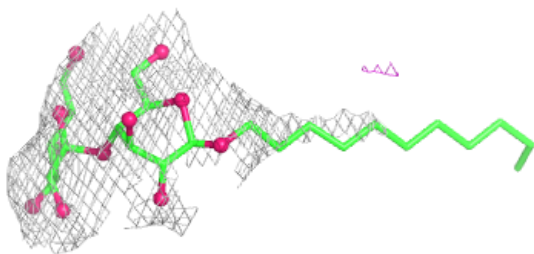
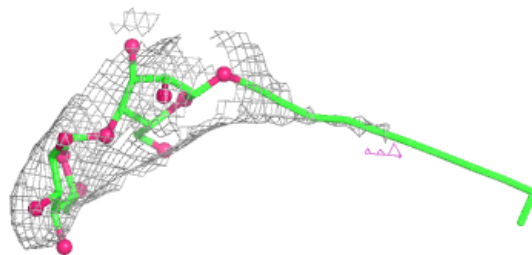


Electron density around OPC E 101:

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

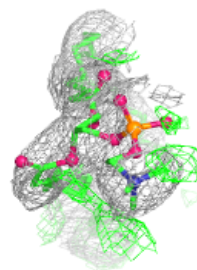
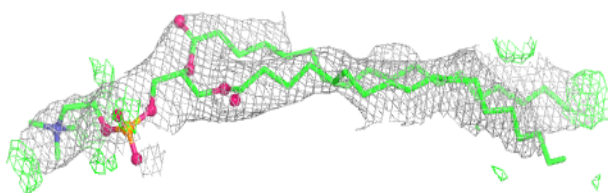
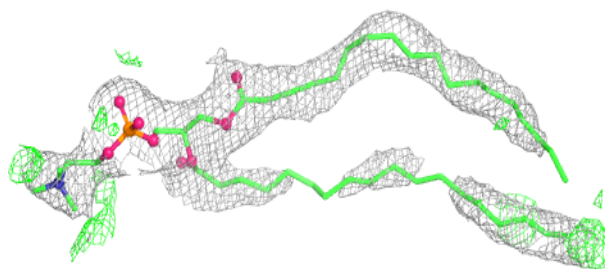
**Electron density around UMQ A 307:**

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

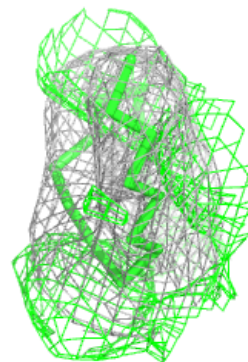
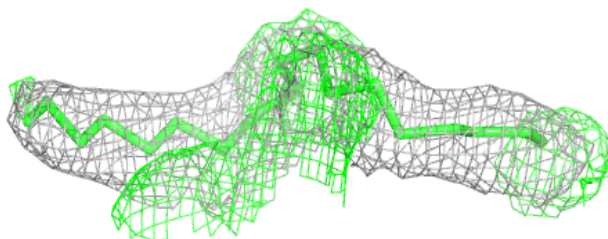
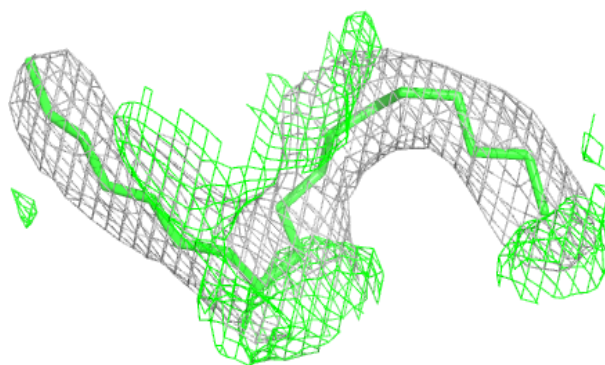


Electron density around OPC B 205:

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

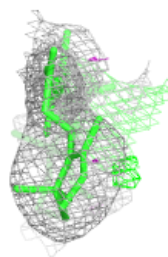
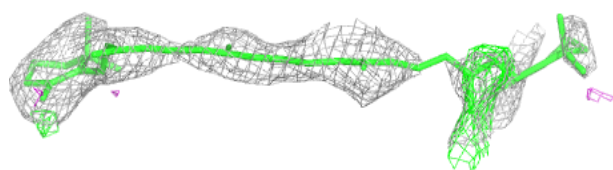
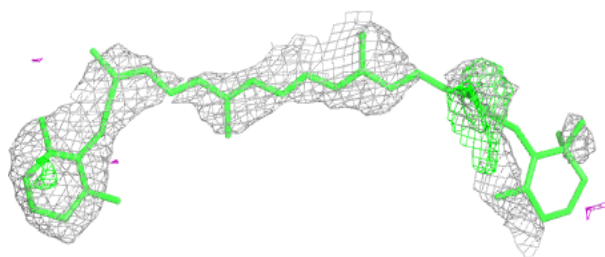
**Electron density around 8K6 B 201:**

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

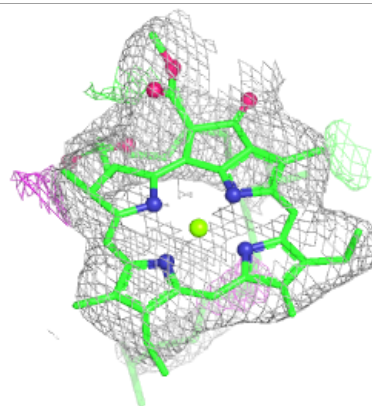
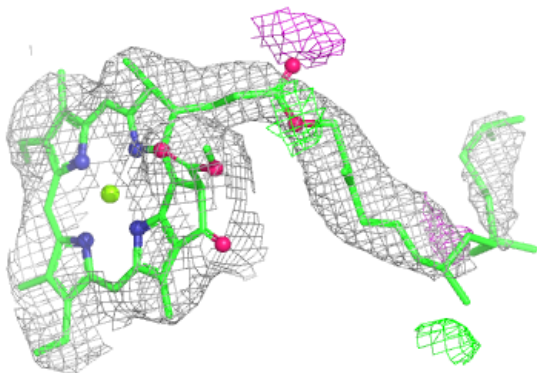
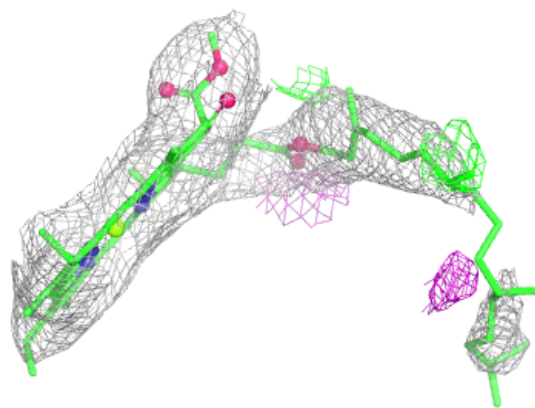


Electron density around BCR G 101:

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

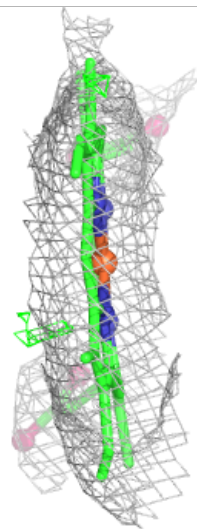
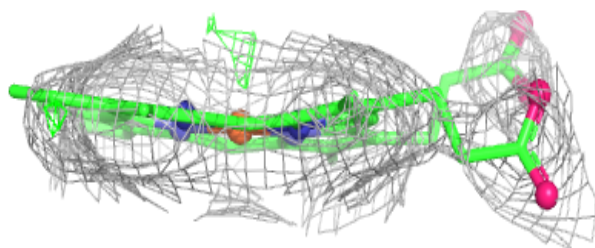
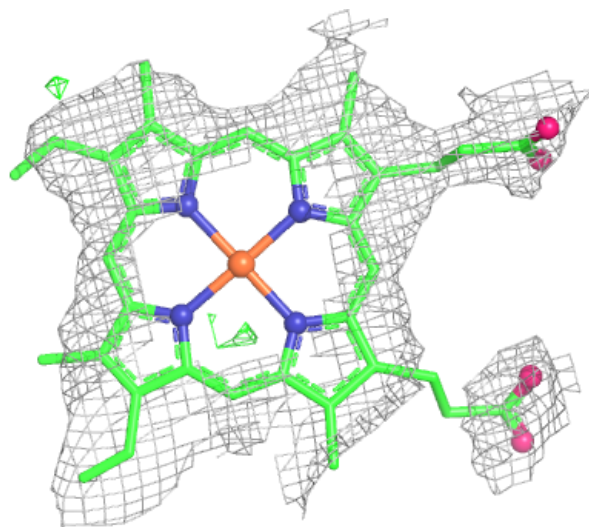
**Electron density around CLA B 204:**

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



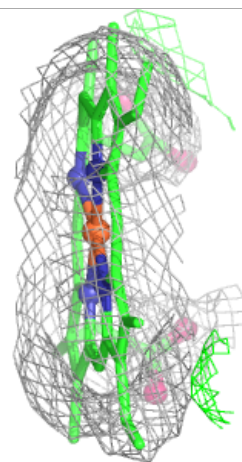
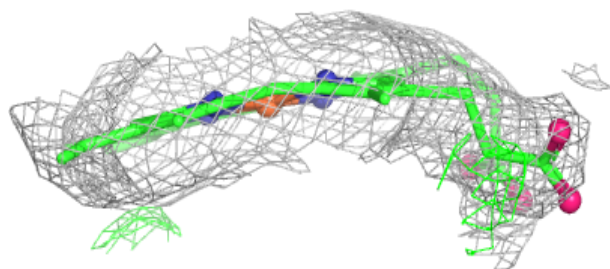
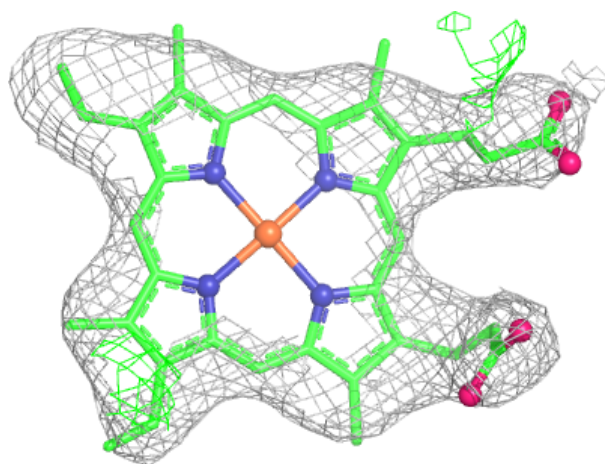
Electron density around HEC C 301:

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



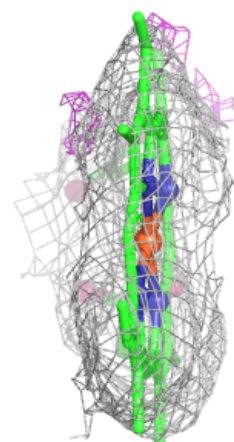
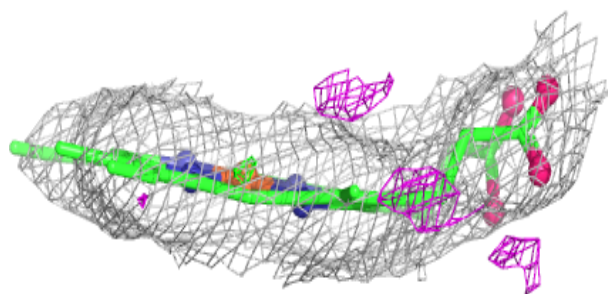
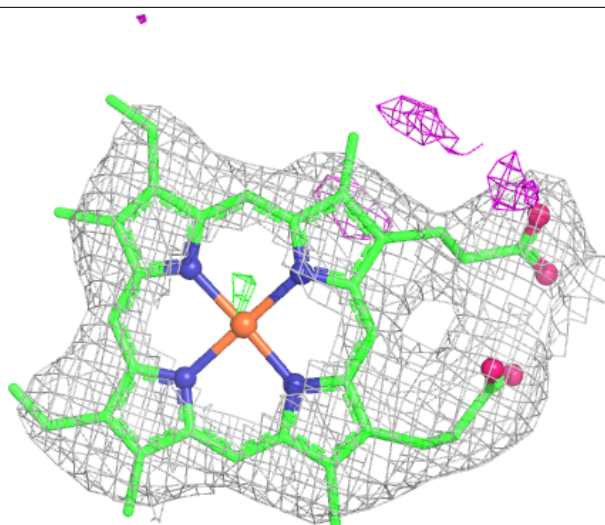
Electron density around HEC A 305:

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



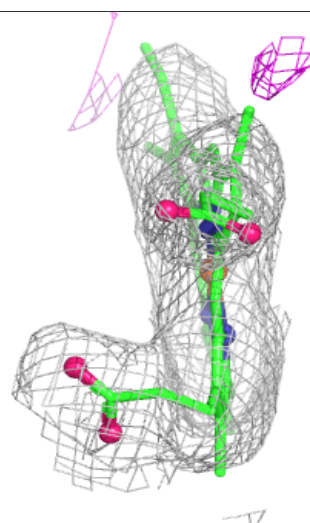
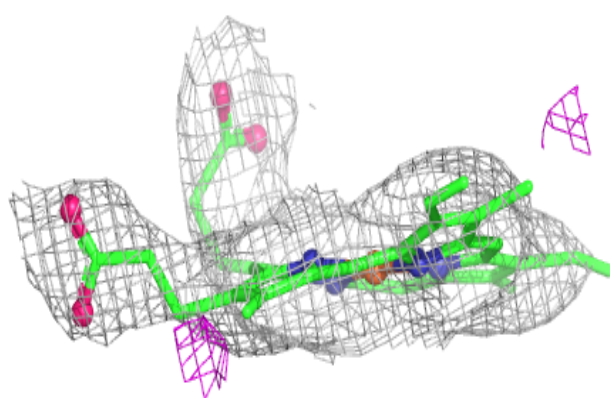
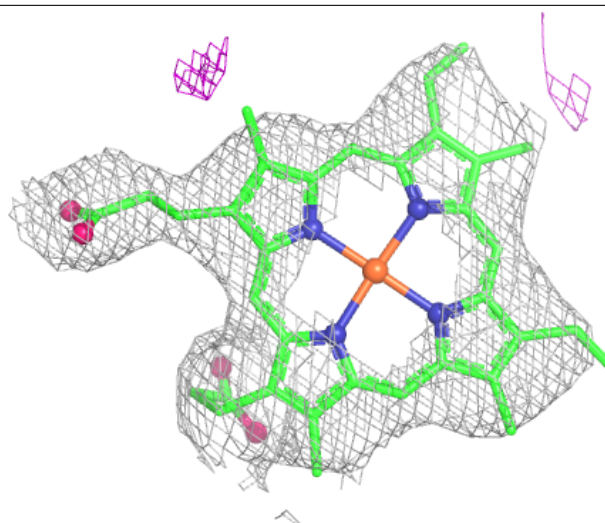
Electron density around HEC A 303:

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



Electron density around HEC A 304:

$2mF_o-DF_c$ (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.