



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:17 PM UTC

PDB ID : 4CAS / pdb_00004cas

Title : Serial femtosecond crystallography structure of a photosynthetic reaction center

Authors : Johansson, L.C.; Arnlund, D.; Katona, G.; White, T.A.; Barty, A.; DePonte, D.P.; Shoeman, R.L.; Wickstrand, C.; Sharma, A.; Williams, G.J.; Aquila, A.; Bogan, M.J.; Caleman, C.; Davidsson, J.; Doak, R.B.; Frank, M.; Fromme, R.; Galli, L.; Grotjohann, I.; Hunter, M.S.; Kassemeyer, S.; Kirian, R.A.; Kupitz, C.; Liang, M.; Lomb, L.; Malmerberg, E.; Martin, A.V.; Messerschmidt, M.; Nass, K.; Redecke, L.; Seibert, M.M.; Sjöhamn, J.; Steinbrener, J.; Stellato, F.; Wang, D.; Wahlgren, W.Y.; Weierstall, U.; Westenhoff, S.; Zatsepin, N.A.; Boutet, S.; Spence, J.C.H.; Schlichting, I.; Chapman, H.N.; Fromme, P.; Neutze, R.

Deposited on : 2013-10-09

Resolution : 3.50 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

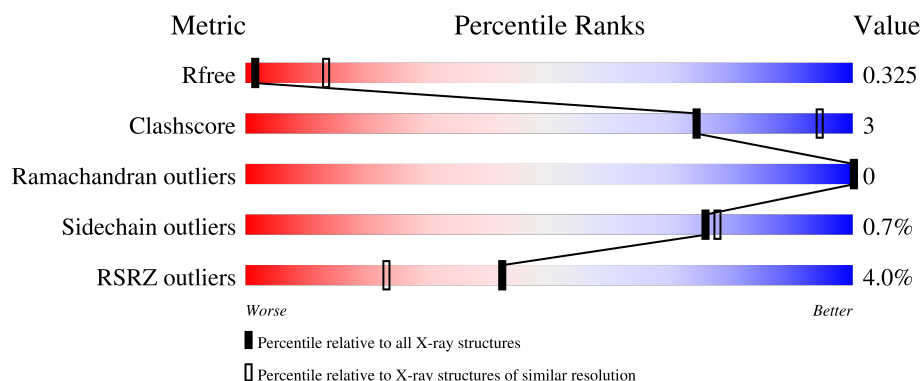
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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.

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

Mol	Chain	Length	Quality of chain
1	A	356	% 91% 7%
2	B	274	2% 92% 7%
3	C	324	3% 94% 6%
4	D	258	11% 90% 6%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 9890 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 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	0	0
			2598	1637	465	478	18			

- Molecule 2 is a protein called REACTION CENTER PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	273	Total	C	N	O	S	0	2	0
			2170	1458	350	355	7			

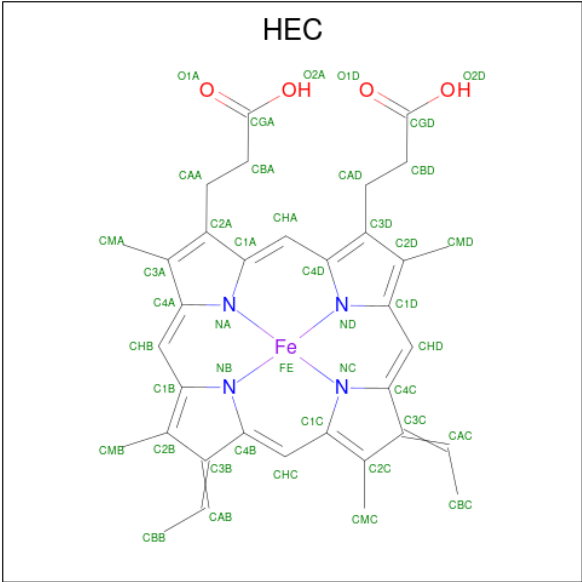
- Molecule 3 is a protein called REACTION CENTER PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	323	Total	C	N	O	S	0	0	0
			2546	1696	417	422	11			

- Molecule 4 is a protein called REACTION CENTER PROTEIN H CHAIN.

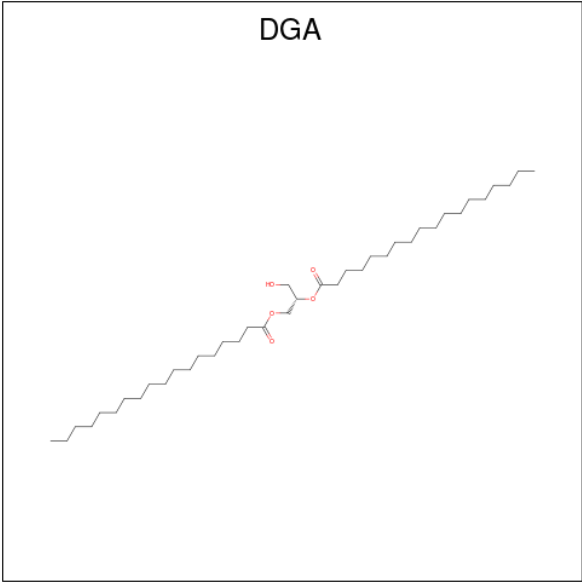
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	243	Total	C	N	O	S	0	0	0
			1771	1140	297	332	2			

- Molecule 5 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



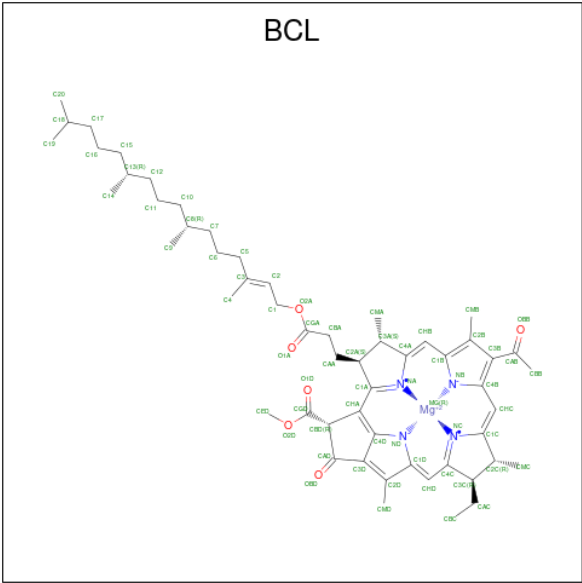
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is DIACYL GLYCEROL (CCD ID: DGA) (formula: C₃₉H₇₆O₅).



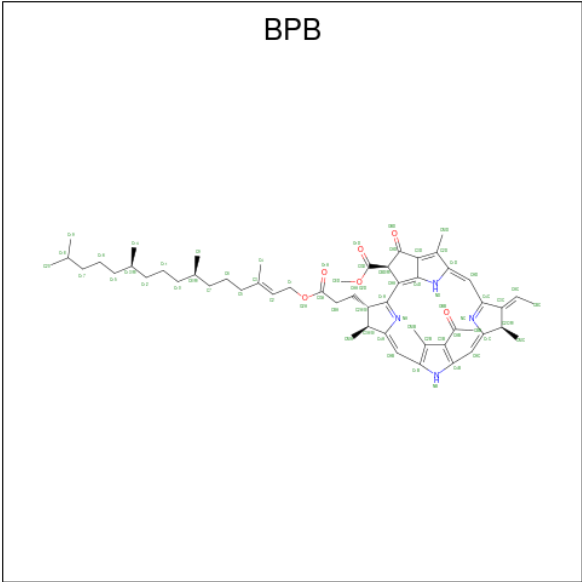
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			37	33	4		

- Molecule 7 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



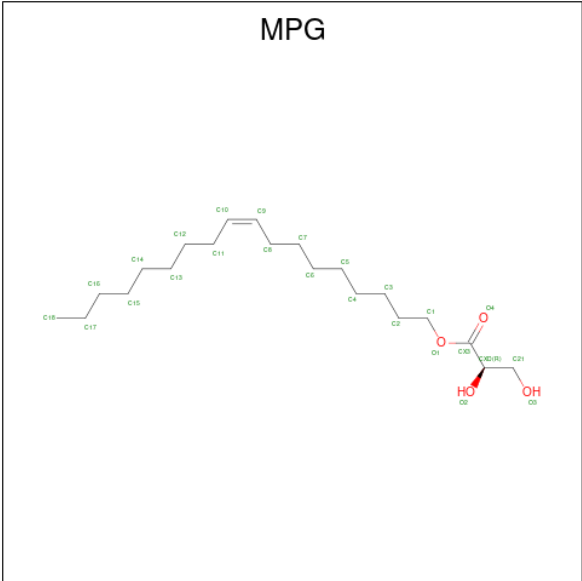
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	Mg	N	O	0	0
			65	54	1	4	6		
7	B	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	B	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
7	C	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 8 is BACTERIOPHEOPHYTIN B (CCD ID: BPB) (formula: $C_{55}H_{74}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	N	O	0	0
			65	55	4	6		
8	C	1	Total	C	N	O	0	0
			61	51	4	6		

- Molecule 9 is [(Z)-octadec-9-enyl] (2R)-2,3-bis(oxidanyl)propanoate (CCD ID: MPG) (formula: C₂₁H₄₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			25	21	4		

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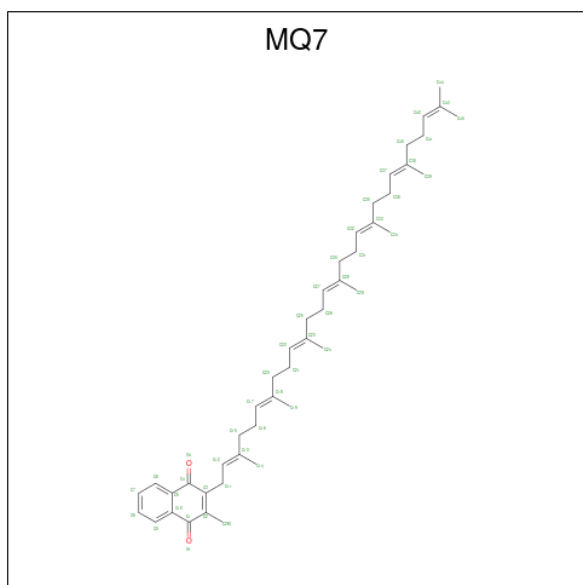
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 25 21 4	0	0
9	C	1	Total C 17 17	0	0

- Molecule 10 is FE (II) ION (CCD ID: FE2) (formula: Fe).

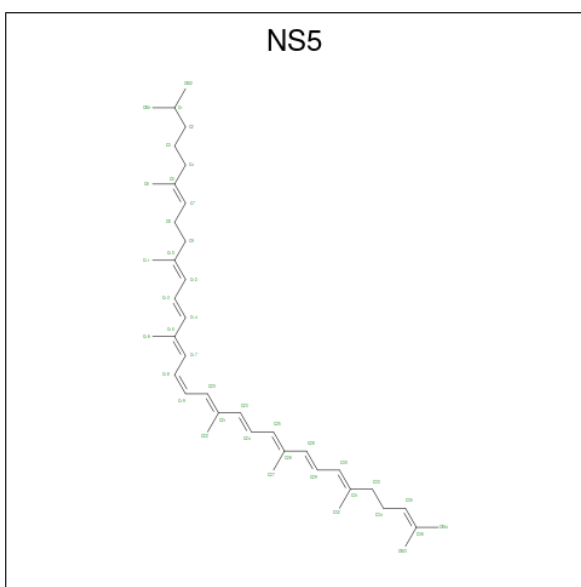
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	C	1	Total Fe 1 1	0	0

- Molecule 11 is MENAQUINONE-7 (CCD ID: MQ7) (formula: C₄₆H₆₄O₂).



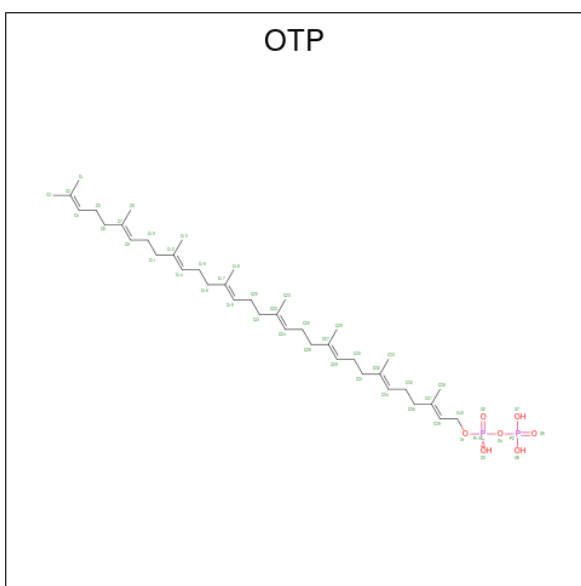
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	C	1	Total C O 48 46 2	0	0

- Molecule 12 is 15-cis-1,2-dihydroneurosporene (CCD ID: NS5) (formula: C₄₀H₆₀).



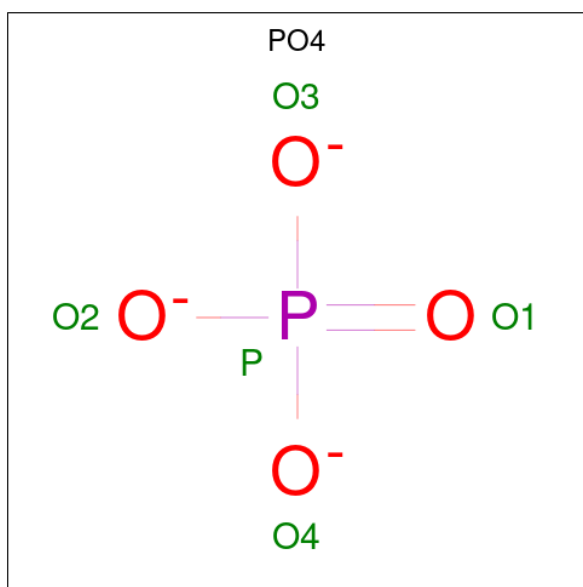
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	C	1	Total	C	0	0
			40	40		

- Molecule 13 is (2E,6E,10E,14E,18E,22E,26E)-3,7,11,15,19,23,27,31-OCTAMETHYLDOT RIACONTA-2,6,10,14,18,22,26,30-OCTAENYL TRIHYDROGEN DIPHOSPHATE (CCD ID: OTP) (formula: $C_{40}H_{68}O_7P_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O	0	0
			41	40	1		

- Molecule 14 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

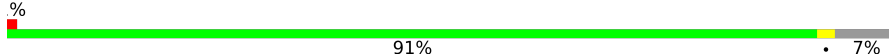


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	C	1	Total	O	P	0	0
			5	4	1		
14	C	1	Total	O	P	0	0
			5	4	1		

3 Residue-property plots [i](#)

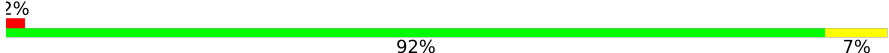
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT

Chain A: 

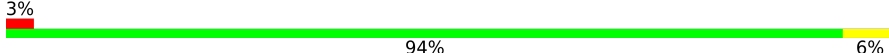


- Molecule 2: REACTION CENTER PROTEIN L CHAIN

Chain B: 



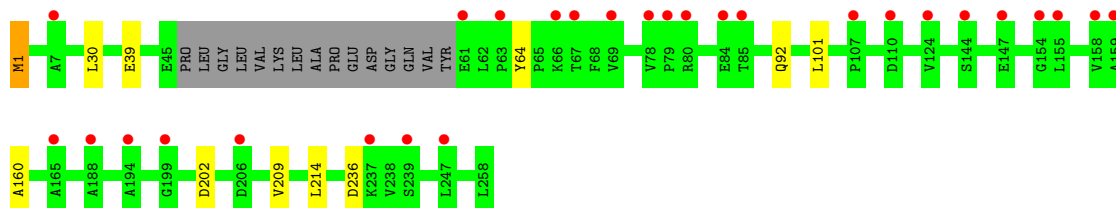
- Molecule 3: REACTION CENTER PROTEIN M CHAIN

Chain C: 



- Molecule 4: REACTION CENTER PROTEIN H CHAIN

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.90Å 84.80Å 384.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.64 – 3.50 49.64 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.64-3.50) 99.1 (49.64-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.295 , 0.329 0.296 , 0.325	Depositor DCC
R_{free} test set	1262 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	73.5	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 107.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.72	EDS
Total number of atoms	9890	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BPB, PO4, BCL, FE2, DGA, FME, OTP, MQ7, HEC, MPG, NS5

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	0.74	1/2665 (0.0%)	0.86	0/3633
2	B	0.65	0/2263	0.81	0/3089
3	C	0.66	0/2650	0.80	0/3629
4	D	0.61	0/1804	0.74	2/2485 (0.1%)
All	All	0.67	1/9382 (0.0%)	0.81	2/12836 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	50	PRO	CA-C	5.16	1.54	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	64	TYR	CA-C-N	6.40	126.43	119.90
4	D	64	TYR	C-N-CA	6.40	126.43	119.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2598	0	2567	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2170	0	2100	21	0
3	C	2546	0	2430	19	0
4	D	1771	0	1656	6	0
5	A	172	0	120	3	0
6	A	37	0	58	0	0
7	B	197	0	217	9	0
7	C	66	0	74	5	0
8	B	65	0	74	8	0
8	C	61	0	63	5	0
9	B	50	0	80	2	0
9	C	17	0	31	1	0
10	C	1	0	0	0	0
11	C	48	0	64	2	0
12	C	40	0	60	5	0
13	C	41	0	65	7	0
14	C	10	0	0	0	0
All	All	9890	0	9659	61	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 (61) 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)
8:C:403:BPB:HHC	8:C:403:BPB:HBBB	1.62	0.81
8:B:304:BPB:HHC	8:B:304:BPB:HBBB	1.61	0.81
7:B:301:BCL:HHC	7:B:301:BCL:HBB2	1.75	0.68
2:B:181:PHE:HB3	8:C:403:BPB:HBBA	1.80	0.63
13:C:406:OTP:C29	13:C:406:OTP:H331	2.29	0.62
2:B:3:LEU:HG	3:C:251:ARG:NE	2.16	0.61
1:A:212:VAL:HG11	4:D:1:FME:HE3	1.83	0.60
3:C:159:GLY:HA3	12:C:405:NS5:C11	2.34	0.58
2:B:39:ILE:HD12	11:C:404:MQ7:H452	1.86	0.58
2:B:124:PRO:HD3	8:B:304:BPB:HAC	1.86	0.58
3:C:159:GLY:HA3	12:C:405:NS5:H113	1.86	0.58
1:A:56:TYR:HB3	5:A:401:HEC:O2A	2.04	0.57
1:A:240:LEU:HD11	5:A:404:HEC:CHB	2.36	0.56
2:B:244:GLY:O	7:B:302:BCL:HED3	2.06	0.55
9:B:305:MPG:H21C	3:C:1:ALA:HA	1.87	0.55
3:C:195:TYR:CE2	7:C:402:BCL:HMC2	2.42	0.54
2:B:62:PHE:CZ	13:C:406:OTP:H333	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3:LEU:HD11	3:C:251:ARG:HD2	1.89	0.53
4:D:92:GLN:HA	4:D:101:LEU:HD23	1.93	0.51
2:B:177:VAL:HG11	7:B:301:BCL:HMD3	1.93	0.50
8:C:403:BPB:HHC	8:C:403:BPB:CBB	2.38	0.50
13:C:406:OTP:C29	13:C:406:OTP:C33	2.89	0.50
8:B:304:BPB:HBB	3:C:208:TYR:CD2	2.46	0.50
2:B:16:LEU:HD13	2:B:106:GLU:HG2	1.93	0.50
2:B:148:TYR:CE1	8:B:304:BPB:H14B	2.47	0.49
2:B:181:PHE:CD2	8:C:403:BPB:HBB	2.48	0.48
2:B:39:ILE:CD1	11:C:404:MQ7:H452	2.44	0.48
2:B:42:ILE:CD1	8:B:304:BPB:H4A	2.45	0.47
7:B:303:BCL:HED3	13:C:406:OTP:H282	1.95	0.47
1:A:233:MET:HE3	5:A:403:HEC:CHA	2.45	0.46
3:C:195:TYR:OH	7:C:402:BCL:OBB	2.16	0.46
7:B:302:BCL:H2C	7:C:402:BCL:H2C	1.98	0.46
7:B:301:BCL:HHC	7:B:301:BCL:CBB	2.43	0.46
2:B:259:TRP:N	2:B:260:PRO:CD	2.79	0.46
7:B:303:BCL:H142	7:B:303:BCL:HMA1	1.98	0.46
4:D:160:ALA:HB3	4:D:214:LEU:HD23	1.97	0.46
9:B:306:MPG:H52C	9:C:407:MPG:H182	1.98	0.46
1:A:212:VAL:HG11	4:D:1:FME:CE	2.45	0.46
3:C:120:MET:SD	7:C:402:BCL:H172	2.56	0.45
3:C:33:PHE:CE2	3:C:46:ILE:HD12	2.52	0.45
8:B:304:BPB:HHC	8:B:304:BPB:CBB	2.38	0.45
2:B:179:PHE:HA	2:B:182:VAL:HG12	1.99	0.44
3:C:200:HIS:CE1	3:C:204:ILE:HD11	2.53	0.43
2:B:42:ILE:HD11	8:B:304:BPB:H4A	2.00	0.42
2:B:195:LEU:HD21	3:C:265:ARG:HG3	2.00	0.42
2:B:151:LEU:HD21	13:C:406:OTP:H301	2.02	0.42
12:C:405:NS5:H18	12:C:405:NS5:H161	1.81	0.42
13:C:406:OTP:C33	13:C:406:OTP:H29	2.50	0.42
2:B:177:VAL:HG11	7:B:301:BCL:CMD	2.50	0.42
3:C:195:TYR:CZ	7:C:402:BCL:HMC2	2.55	0.41
3:C:70:LEU:HD21	12:C:405:NS5:H323	2.02	0.41
3:C:239:ARG:NH1	4:D:39:GLU:OE1	2.50	0.41
2:B:233:GLY:HA3	3:C:214:PHE:CE1	2.56	0.41
2:B:151:LEU:HD23	2:B:151:LEU:HA	1.90	0.41
7:B:303:BCL:HED3	13:C:406:OTP:C28	2.51	0.41
1:A:80:TRP:CD1	1:A:133:TYR:HB2	2.56	0.41
4:D:202:ASP:HB3	4:D:209:VAL:HB	2.01	0.41
8:B:304:BPB:HBBA	3:C:208:TYR:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:98:ALA:HB3	3:C:100:TYR:CZ	2.56	0.40
3:C:181:ILE:HD13	3:C:181:ILE:HA	1.96	0.40
8:C:403:BPB:C9	12:C:405:NS5:HM32	2.51	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	330/356 (93%)	323 (98%)	7 (2%)	0	100	100
2	B	273/274 (100%)	266 (97%)	7 (3%)	0	100	100
3	C	321/324 (99%)	312 (97%)	9 (3%)	0	100	100
4	D	239/258 (93%)	233 (98%)	6 (2%)	0	100	100
All	All	1163/1212 (96%)	1134 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	280/297 (94%)	279 (100%)	1 (0%)	84	81
2	B	218/219 (100%)	216 (99%)	2 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	247/250 (99%)	246 (100%)	1 (0%)	84	81
4	D	167/212 (79%)	165 (99%)	2 (1%)	63	73
All	All	912/978 (93%)	906 (99%)	6 (1%)	76	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	LEU
2	B	17	ILE
2	B	249	ILE
3	C	194	PHE
4	D	30	LEU
4	D	236	ASP

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

Mol	Chain	Res	Type
1	A	37	GLN
1	A	302	GLN
2	B	183	ASN
2	B	190	HIS
2	B	214	GLN
2	B	239	ASN
3	C	45	GLN
3	C	200	HIS
4	D	8	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
4	FME	D	1	4	8,9,10	0.83	0	8,9,11	2.99	4 (50%)

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
4	FME	D	1	4	-	4/7/9/11	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	FME	CA-N-CN	-6.92	112.18	122.82
4	D	1	FME	CE-SD-CG	2.93	115.49	100.32
4	D	1	FME	O-C-CA	-2.16	119.22	124.77
4	D	1	FME	CB-CA-N	-2.01	106.86	110.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	FME	O1-CN-N-CA
4	D	1	FME	C-CA-CB-CG
4	D	1	FME	N-CA-CB-CG
4	D	1	FME	CB-CG-SD-CE

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1	FME	2	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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$
5	HEC	A	404	1	46,50,50	1.75	9 (19%)	58,82,82	1.46	10 (17%)
12	NS5	C	405	-	39,39,39	2.14	6 (15%)	46,46,46	2.19	14 (30%)
11	MQ7	C	404	-	49,49,49	1.65	3 (6%)	61,63,63	1.32	8 (13%)
7	BCL	B	303	-	69,74,74	1.99	18 (26%)	79,115,115	2.77	21 (26%)
7	BCL	C	402	-	69,74,74	2.00	17 (24%)	79,115,115	2.73	28 (35%)
7	BCL	B	302	-	69,74,74	1.93	17 (24%)	79,115,115	2.89	31 (39%)
9	MPG	C	407	-	16,16,24	0.43	0	15,15,25	0.65	0
13	OTP	C	406	-	40,40,48	1.59	1 (2%)	47,47,61	2.21	14 (29%)
9	MPG	B	306	-	24,24,24	1.55	1 (4%)	24,25,25	1.20	3 (12%)
7	BCL	B	301	-	68,73,74	1.95	17 (25%)	77,113,115	2.88	24 (31%)
5	HEC	A	403	1	46,50,50	1.82	8 (17%)	58,82,82	1.46	10 (17%)
6	DGA	A	405	1	36,36,43	1.24	2 (5%)	38,38,45	1.24	4 (10%)
14	PO4	C	408	-	4,4,4	0.89	0	6,6,6	0.64	0
5	HEC	A	402	1	46,50,50	1.75	8 (17%)	58,82,82	1.45	11 (18%)
8	BPB	C	403	-	53,66,70	2.66	12 (22%)	50,96,101	2.36	14 (28%)
5	HEC	A	401	1	46,50,50	1.85	12 (26%)	58,82,82	1.31	8 (13%)
14	PO4	C	409	-	4,4,4	0.75	0	6,6,6	0.69	0
8	BPB	B	304	-	57,70,70	2.60	13 (22%)	55,101,101	2.36	17 (30%)
9	MPG	B	305	-	24,24,24	1.30	1 (4%)	24,25,25	1.55	3 (12%)

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
5	HEC	A	402	1	-	8/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HEC	A	404	1	-	3/14/54/54	-
12	NS5	C	405	-	-	14/43/43/43	-
11	MQ7	C	404	-	-	4/41/61/61	0/2/2/2
7	BCL	B	303	-	-	8/41/137/137	-
7	BCL	B	301	-	-	8/40/136/137	-
7	BCL	C	402	-	-	7/41/137/137	-
9	MPG	B	306	-	-	8/25/25/25	-
8	BPB	C	403	-	-	16/33/101/105	0/5/6/6
5	HEC	A	403	1	-	2/14/54/54	-
5	HEC	A	401	1	-	2/14/54/54	-
6	DGA	A	405	1	-	17/37/37/45	-
8	BPB	B	304	-	-	12/37/105/105	0/5/6/6
7	BCL	B	302	-	-	3/41/137/137	-
9	MPG	C	407	-	-	4/14/14/25	-
9	MPG	B	305	-	-	15/25/25/25	-
13	OTP	C	406	-	-	16/45/45/55	-

All (145) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	304	BPB	C1B-C2B	9.42	1.49	1.39
13	C	406	OTP	C39-C37	9.11	1.54	1.33
8	C	403	BPB	C1B-C2B	8.89	1.49	1.39
8	B	304	BPB	C1D-C2D	8.30	1.48	1.39
11	C	404	MQ7	C3-C2	8.23	1.50	1.35
8	C	403	BPB	C1D-C2D	7.92	1.48	1.39
12	C	405	NS5	C35-C36	7.38	1.54	1.32
12	C	405	NS5	C29-C28	7.26	1.53	1.34
9	B	306	MPG	O1-CX3	7.08	1.48	1.33
9	B	305	MPG	O1-CX3	5.98	1.45	1.33
11	C	404	MQ7	C10-C5	5.91	1.50	1.40
8	C	403	BPB	C3D-C2D	5.80	1.49	1.39
7	B	301	BCL	O2D-CGD	5.69	1.47	1.33
8	B	304	BPB	C3D-C2D	5.67	1.49	1.39
8	C	403	BPB	C4D-CHA	5.54	1.47	1.39
12	C	405	NS5	C9-C8	-5.51	1.35	1.53
8	C	403	BPB	OBD-CAD	5.36	1.29	1.22
7	B	303	BCL	O2D-CGD	5.33	1.46	1.33
7	C	402	BCL	O2D-CGD	5.32	1.46	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	302	BCL	CHD-C1D	5.17	1.48	1.38
8	B	304	BPB	OBD-CAD	5.13	1.29	1.22
8	B	304	BPB	O2D-CGD	5.05	1.45	1.33
5	A	402	HEC	CAC-C3C	5.00	1.51	1.35
6	A	405	DGA	OG1-CA1	5.00	1.47	1.33
7	C	402	BCL	OBD-CAD	4.99	1.31	1.22
8	B	304	BPB	C4D-CHA	4.98	1.47	1.39
5	A	403	HEC	CAC-C3C	4.88	1.50	1.35
7	B	303	BCL	CHD-C1D	4.80	1.47	1.38
7	B	301	BCL	C3B-C4B	4.71	1.50	1.41
7	B	303	BCL	CHC-C4B	4.67	1.49	1.39
6	A	405	DGA	OG2-CB1	4.65	1.47	1.34
5	A	403	HEC	CAB-C3B	4.64	1.50	1.35
7	B	302	BCL	C3B-C4B	4.62	1.50	1.41
8	C	403	BPB	O2D-CGD	4.62	1.44	1.33
8	C	403	BPB	O2A-CGA	4.59	1.46	1.33
8	B	304	BPB	C3B-C2B	4.58	1.47	1.39
5	A	402	HEC	CBC-CAC	-4.58	1.32	1.49
5	A	401	HEC	CAC-C3C	4.56	1.49	1.35
8	C	403	BPB	C3B-C2B	4.54	1.47	1.39
5	A	404	HEC	CBB-CAB	-4.54	1.32	1.49
7	C	402	BCL	C3B-C4B	4.54	1.50	1.41
7	C	402	BCL	CHC-C4B	4.53	1.49	1.39
5	A	404	HEC	CBC-CAC	-4.50	1.32	1.49
8	C	403	BPB	C3B-C4B	4.50	1.48	1.41
7	B	302	BCL	O2A-CGA	4.49	1.46	1.33
7	B	302	BCL	CHC-C4B	4.46	1.49	1.39
7	B	303	BCL	CHC-C1C	4.45	1.48	1.37
5	A	401	HEC	CBC-CAC	-4.38	1.33	1.49
5	A	401	HEC	CBB-CAB	-4.35	1.33	1.49
7	B	303	BCL	O2A-CGA	4.32	1.45	1.33
8	B	304	BPB	O2A-CGA	4.31	1.45	1.33
7	C	402	BCL	CHD-C1D	4.31	1.46	1.38
7	B	303	BCL	C3B-C4B	4.31	1.49	1.41
7	B	302	BCL	O2D-CGD	4.27	1.43	1.33
7	B	301	BCL	O2A-CGA	4.21	1.45	1.33
5	A	401	HEC	CAB-C3B	4.19	1.48	1.35
7	C	402	BCL	CHC-C1C	4.17	1.48	1.37
7	B	301	BCL	CHC-C1C	4.16	1.48	1.37
7	B	302	BCL	CHC-C1C	4.15	1.48	1.37
5	A	402	HEC	CAB-C3B	4.15	1.48	1.35
7	B	301	BCL	CHB-C1B	4.13	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	301	BCL	CHD-C1D	4.12	1.46	1.38
5	A	404	HEC	CAC-C3C	4.11	1.48	1.35
5	A	403	HEC	CBC-CAC	-4.10	1.34	1.49
7	B	301	BCL	CHC-C4B	4.09	1.48	1.39
7	C	402	BCL	C3C-C4C	-4.09	1.46	1.51
7	B	303	BCL	CHB-C1B	4.09	1.48	1.39
8	B	304	BPB	C3B-C4B	3.98	1.47	1.41
7	C	402	BCL	O2A-CGA	3.96	1.44	1.33
5	A	404	HEC	CAB-C3B	3.95	1.47	1.35
7	B	302	BCL	OBD-CAD	3.84	1.29	1.22
5	A	403	HEC	CBB-CAB	-3.79	1.35	1.49
5	A	403	HEC	C4B-NB	-3.71	1.32	1.39
5	A	402	HEC	CBB-CAB	-3.69	1.35	1.49
5	A	403	HEC	C1B-NB	-3.65	1.32	1.39
7	B	303	BCL	OBD-CAD	3.61	1.28	1.22
7	B	303	BCL	C2C-C3C	-3.58	1.44	1.54
7	B	301	BCL	C3D-C2D	3.53	1.48	1.39
7	C	402	BCL	CHB-C1B	3.52	1.47	1.39
8	B	304	BPB	C4C-NC	-3.37	1.27	1.37
7	B	302	BCL	CHB-C1B	3.31	1.46	1.39
7	B	301	BCL	C2C-C3C	-3.30	1.45	1.54
7	B	303	BCL	C3D-C2D	3.29	1.48	1.39
7	C	402	BCL	C3D-C2D	3.27	1.47	1.39
7	B	301	BCL	CAC-C3C	-3.24	1.47	1.54
8	C	403	BPB	C4C-NC	-3.22	1.27	1.37
8	B	304	BPB	CHA-CBD	-3.21	1.47	1.51
8	C	403	BPB	CHA-CBD	-3.18	1.47	1.51
5	A	404	HEC	C1B-NB	-3.15	1.33	1.39
7	B	301	BCL	C1B-C2B	3.14	1.50	1.43
7	B	302	BCL	CHD-C4C	3.13	1.48	1.39
7	B	301	BCL	OBD-CAD	3.12	1.27	1.22
7	B	303	BCL	CHD-C4C	3.08	1.47	1.39
7	C	402	BCL	C2C-C3C	-3.05	1.46	1.54
12	C	405	NS5	C29-C30	3.02	1.52	1.43
7	B	302	BCL	C3D-C2D	2.96	1.47	1.39
7	B	302	BCL	C2C-C3C	-2.96	1.46	1.54
7	B	301	BCL	CHD-C4C	2.95	1.47	1.39
5	A	403	HEC	C1D-C2D	2.92	1.50	1.43
7	C	402	BCL	C1D-ND	-2.88	1.34	1.37
5	A	401	HEC	C3B-C4B	2.86	1.51	1.46
5	A	402	HEC	C1D-ND	-2.85	1.34	1.39
7	B	303	BCL	CAC-C3C	-2.83	1.48	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	302	BCL	C1D-ND	-2.81	1.34	1.37
7	B	303	BCL	C3C-C4C	-2.80	1.48	1.51
7	B	302	BCL	C3C-C4C	-2.78	1.48	1.51
7	C	402	BCL	CHD-C4C	2.76	1.47	1.39
8	B	304	BPB	C1D-ND	-2.76	1.33	1.38
7	B	303	BCL	C1B-C2B	2.75	1.49	1.43
7	B	301	BCL	C1D-ND	-2.73	1.34	1.37
7	B	303	BCL	C3D-C4D	-2.73	1.38	1.44
7	C	402	BCL	C1B-NB	-2.72	1.34	1.37
8	C	403	BPB	C3A-C2A	-2.71	1.52	1.54
7	B	302	BCL	CAC-C3C	-2.68	1.48	1.54
7	B	302	BCL	C1B-C2B	2.64	1.49	1.43
5	A	401	HEC	C4B-NB	-2.63	1.34	1.39
7	C	402	BCL	C1B-C2B	2.61	1.49	1.43
7	B	302	BCL	C3D-C4D	-2.60	1.38	1.44
7	B	303	BCL	C1D-ND	-2.55	1.34	1.37
5	A	402	HEC	C4B-NB	-2.52	1.34	1.39
7	C	402	BCL	CAC-C3C	-2.50	1.49	1.54
7	B	301	BCL	C3D-C4D	-2.43	1.38	1.44
7	B	301	BCL	C3C-C4C	-2.36	1.48	1.51
5	A	402	HEC	C4A-C3A	-2.35	1.40	1.45
5	A	401	HEC	C1D-C2D	2.34	1.48	1.43
7	B	303	BCL	C1B-NB	-2.34	1.34	1.37
7	B	302	BCL	C4D-CHA	2.32	1.46	1.38
12	C	405	NS5	C14-C15	2.31	1.50	1.46
5	A	401	HEC	C1C-NC	-2.31	1.35	1.39
8	B	304	BPB	CBD-CGD	-2.29	1.49	1.52
5	A	401	HEC	C1D-ND	-2.29	1.35	1.39
7	C	402	BCL	C3D-C4D	-2.27	1.39	1.44
7	B	301	BCL	C4D-CHA	2.26	1.46	1.38
12	C	405	NS5	C28-C26	2.26	1.50	1.46
5	A	403	HEC	O2A-CGA	-2.20	1.23	1.30
5	A	404	HEC	C1A-C2A	-2.16	1.41	1.45
5	A	402	HEC	C1B-NB	-2.10	1.35	1.39
5	A	401	HEC	O2A-CGA	-2.10	1.23	1.30
5	A	404	HEC	C1D-ND	-2.06	1.35	1.39
5	A	401	HEC	C1A-C2A	-2.05	1.41	1.45
5	A	404	HEC	C4B-NB	-2.01	1.35	1.39
5	A	404	HEC	C3C-C4C	-2.01	1.42	1.46
11	C	404	MQ7	C12-C13	2.01	1.37	1.33
5	A	401	HEC	C4A-C3A	-2.01	1.41	1.45
7	B	303	BCL	CBD-CAD	-2.01	1.47	1.56

All (220) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	302	BCL	C1C-NC-C4C	-14.00	100.29	106.68
7	B	301	BCL	C1C-NC-C4C	-13.85	100.36	106.68
7	B	303	BCL	C1C-NC-C4C	-13.53	100.50	106.68
7	C	402	BCL	C1C-NC-C4C	-12.65	100.91	106.68
8	C	403	BPB	O2D-CGD-CBD	9.31	121.18	110.95
8	B	304	BPB	O2D-CGD-CBD	8.66	120.47	110.95
7	B	301	BCL	C4D-C3D-CAD	-7.47	99.99	108.11
8	B	304	BPB	C3D-C4D-ND	7.46	117.28	107.71
7	B	302	BCL	C2B-C1B-NB	7.17	117.76	110.33
7	B	301	BCL	C2C-C3C-C4C	7.00	111.82	101.34
8	C	403	BPB	C3D-C4D-ND	6.73	116.33	107.71
7	C	402	BCL	C2B-C1B-NB	6.67	117.24	110.33
7	B	303	BCL	C4D-C3D-CAD	-6.57	100.97	108.11
7	C	402	BCL	C4D-C3D-CAD	-6.43	101.12	108.11
7	B	303	BCL	CMD-C2D-C1D	6.41	136.01	124.73
7	B	303	BCL	C2B-C1B-NB	6.34	116.90	110.33
7	B	303	BCL	C2C-C3C-C4C	6.29	110.76	101.34
12	C	405	NS5	C29-C28-C26	-6.08	109.70	126.36
7	B	301	BCL	C3C-C2C-C1C	-6.06	92.09	101.87
7	C	402	BCL	CMD-C2D-C1D	6.03	135.35	124.73
8	C	403	BPB	C2B-C1B-NB	6.02	113.78	109.43
7	B	302	BCL	CMD-C2D-C1D	5.98	135.26	124.73
7	B	302	BCL	C4D-C3D-CAD	-5.97	101.62	108.11
7	B	303	BCL	C3D-C4D-ND	5.84	119.48	109.99
7	B	302	BCL	C2C-C3C-C4C	5.74	109.94	101.34
7	B	301	BCL	C2B-C1B-NB	5.71	116.25	110.33
7	C	402	BCL	O2D-CGD-CBD	5.66	121.13	111.23
7	B	301	BCL	CAC-C3C-C4C	5.58	124.97	112.58
8	B	304	BPB	C2B-C1B-NB	5.39	113.33	109.43
7	B	302	BCL	C3D-C4D-ND	5.31	118.62	109.99
7	B	301	BCL	CMD-C2D-C1D	5.31	134.07	124.73
7	B	301	BCL	C3D-C4D-ND	5.29	118.58	109.99
7	C	402	BCL	C3D-C4D-ND	5.03	118.17	109.99
5	A	404	HEC	CHC-C4B-NB	4.95	129.85	124.45
9	B	305	MPG	O1-CX3-CXD	4.91	123.14	111.78
13	C	406	OTP	C38-C37-C39	-4.78	111.36	123.63
7	B	303	BCL	C1D-ND-C4D	-4.74	102.98	106.31
7	B	301	BCL	O2D-CGD-CBD	4.68	119.41	111.23
12	C	405	NS5	C34-C35-C36	-4.67	112.08	127.64
5	A	403	HEC	CHC-C4B-NB	4.66	129.53	124.45
7	B	302	BCL	C3C-C2C-C1C	-4.63	94.39	101.87
13	C	406	OTP	C38-C37-C36	-4.62	107.21	115.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	304	BPB	OBD-CAD-C3D	-4.62	120.69	127.89
13	C	406	OTP	C8-C7-C6	4.60	123.22	115.23
7	B	303	BCL	C3C-C2C-C1C	-4.59	94.46	101.87
13	C	406	OTP	C23-C22-C21	4.56	123.14	115.23
7	B	303	BCL	O2D-CGD-CBD	4.43	118.98	111.23
6	A	405	DGA	OG2-CB1-CB2	4.43	121.06	111.48
7	B	302	BCL	CMD-C2D-C3D	-4.39	117.62	127.69
7	C	402	BCL	C2C-C3C-C4C	4.38	107.90	101.34
9	B	305	MPG	O1-CX3-O4	-4.34	116.20	124.14
7	B	303	BCL	CMD-C2D-C3D	-4.20	118.07	127.69
5	A	402	HEC	CHC-C4B-NB	4.17	129.00	124.45
13	C	406	OTP	C40-C39-C37	-4.11	112.70	126.38
7	B	301	BCL	C1D-ND-C4D	-4.07	103.45	106.31
7	C	402	BCL	C1D-ND-C4D	-4.03	103.48	106.31
7	B	303	BCL	CAC-C3C-C4C	4.02	121.51	112.58
12	C	405	NS5	C8-C9-C10	4.00	126.43	113.19
7	B	302	BCL	C1D-ND-C4D	-3.99	103.51	106.31
12	C	405	NS5	C19-C20-C21	-3.95	121.74	127.28
11	C	404	MQ7	C21-C22-C23	-3.90	118.70	127.62
7	C	402	BCL	C3C-C2C-C1C	-3.86	95.64	101.87
13	C	406	OTP	C36-C37-C39	-3.84	112.54	121.17
9	B	306	MPG	O1-CX3-CXD	3.83	120.65	111.78
12	C	405	NS5	C24-C25-C26	-3.78	121.98	127.28
12	C	405	NS5	C18-C17-C15	-3.77	121.98	127.28
8	B	304	BPB	C4D-CHA-CBD	-3.76	106.65	108.45
7	B	302	BCL	CAC-C3C-C4C	3.76	120.93	112.58
12	C	405	NS5	CM3-C36-C35	-3.74	111.43	122.66
13	C	406	OTP	C33-C32-C31	3.73	121.71	115.23
13	C	406	OTP	C18-C17-C19	-3.71	114.10	123.63
7	B	302	BCL	O2A-CGA-CBA	3.70	123.12	111.83
7	C	402	BCL	O2D-CGD-O1D	-3.67	116.70	123.85
7	B	302	BCL	O2D-CGD-CBD	3.62	117.55	111.23
7	B	301	BCL	CBC-CAC-C3C	3.60	121.04	113.41
7	C	402	BCL	CMD-C2D-C3D	-3.59	119.47	127.69
7	B	302	BCL	OBD-CAD-C3D	-3.59	120.04	128.42
7	C	402	BCL	CBC-CAC-C3C	3.57	120.98	113.41
7	B	302	BCL	CHB-C4A-NA	3.55	129.53	124.40
7	B	302	BCL	C1-C2-C3	-3.53	120.41	126.20
8	B	304	BPB	O2A-CGA-CBA	3.53	122.60	111.83
12	C	405	NS5	CM4-C36-C35	-3.51	112.11	122.66
5	A	403	HEC	C4B-NB-C1B	3.49	111.50	105.82
7	B	303	BCL	CBC-CAC-C3C	3.45	120.73	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	C	405	NS5	C29-C30-C31	-3.44	122.85	127.69
7	B	301	BCL	CMD-C2D-C3D	-3.44	119.81	127.69
7	C	402	BCL	OBD-CAD-C3D	-3.40	120.47	128.42
8	B	304	BPB	O1D-CGD-CBD	-3.39	119.59	124.72
8	B	304	BPB	C1-C2-C3	-3.36	120.69	126.20
8	C	403	BPB	CMD-C2D-C3D	-3.35	117.98	124.68
13	C	406	OTP	C18-C17-C16	3.30	120.95	115.23
7	C	402	BCL	C3B-C4B-NB	3.28	114.09	109.76
7	B	301	BCL	OBD-CAD-C3D	-3.28	120.76	128.42
5	A	404	HEC	CHD-C1D-ND	3.27	129.79	123.86
8	C	403	BPB	C1-O2A-CGA	3.22	124.45	116.65
12	C	405	NS5	C6-C5-C4	3.20	120.78	115.23
7	B	302	BCL	O2D-CGD-O1D	-3.19	117.64	123.85
7	B	302	BCL	C3B-C4B-NB	3.18	113.96	109.76
11	C	404	MQ7	C11-C3-C2	-3.17	119.45	124.89
8	B	304	BPB	CMD-C2D-C3D	-3.16	118.38	124.68
8	C	403	BPB	O2D-CGD-O1D	-3.13	117.76	123.85
7	C	402	BCL	CHA-C4D-ND	-3.08	126.18	132.55
7	B	302	BCL	C4-C3-C5	3.07	120.56	115.23
7	B	303	BCL	OBD-CAD-C3D	-3.05	121.30	128.42
7	B	302	BCL	CBC-CAC-C3C	3.05	119.87	113.41
5	A	402	HEC	C4B-NB-C1B	3.04	110.78	105.82
7	C	402	BCL	CED-O2D-CGD	3.02	122.77	115.92
7	B	303	BCL	CED-O2D-CGD	3.00	122.73	115.92
13	C	406	OTP	C28-C27-C26	2.99	120.43	115.23
8	C	403	BPB	C4-C3-C5	2.98	120.39	115.23
6	A	405	DGA	OG1-CA1-CA2	2.96	120.85	111.83
13	C	406	OTP	C21-C22-C24	-2.95	114.55	121.17
7	B	302	BCL	C4A-NA-C1A	2.94	108.02	106.68
7	B	301	BCL	C3B-C4B-NB	2.94	113.63	109.76
8	C	403	BPB	OBD-CAD-C3D	-2.89	123.39	127.89
5	A	402	HEC	CHA-C4D-ND	2.88	129.08	123.86
9	B	305	MPG	C1-O1-CX3	2.87	122.86	116.53
7	B	303	BCL	CHA-C4D-ND	-2.87	126.64	132.55
9	B	306	MPG	C1-O1-CX3	2.86	122.84	116.53
5	A	404	HEC	CHD-C1D-C2D	-2.86	119.12	127.43
5	A	402	HEC	CBA-CAA-C2A	-2.85	104.64	112.53
13	C	406	OTP	C30-C29-C27	-2.84	121.11	127.62
7	B	301	BCL	CHA-C4D-ND	-2.84	126.68	132.55
7	B	301	BCL	CHB-C4A-NA	2.83	128.49	124.40
8	B	304	BPB	C4D-ND-C1D	-2.82	105.49	108.87
11	C	404	MQ7	C2M-C2-C3	-2.82	119.81	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	402	BCL	CAC-C3C-C4C	2.82	118.84	112.58
8	B	304	BPB	C4A-C3A-C2A	-2.80	100.17	102.84
5	A	402	HEC	CHD-C1D-ND	2.80	128.94	123.86
7	C	402	BCL	CAA-C2A-C1A	2.76	121.00	111.97
5	A	401	HEC	CHC-C4B-NB	2.75	127.45	124.45
5	A	401	HEC	CBA-CAA-C2A	-2.74	104.95	112.53
11	C	404	MQ7	C19-C18-C20	2.73	119.97	115.23
5	A	401	HEC	CHA-C4D-ND	2.70	128.76	123.86
7	B	301	BCL	C2A-C1A-CHA	-2.69	119.20	123.87
7	B	303	BCL	C4A-NA-C1A	-2.69	105.45	106.68
7	B	302	BCL	CHA-C4D-ND	-2.67	127.03	132.55
7	B	301	BCL	O1D-CGD-CBD	-2.63	119.33	124.52
7	B	303	BCL	C3B-C4B-NB	2.61	113.20	109.76
5	A	401	HEC	CHA-C4D-C3D	-2.58	119.64	125.30
5	A	403	HEC	O2A-CGA-O1A	-2.57	116.71	123.33
8	C	403	BPB	C3D-CAD-CBD	2.56	110.97	107.61
13	C	406	OTP	C13-C12-C11	2.56	119.66	115.23
7	B	302	BCL	CAA-C2A-C1A	2.54	120.31	111.97
7	C	402	BCL	CHB-C4A-NA	2.54	128.07	124.40
5	A	403	HEC	O2D-CGD-CBD	2.54	122.02	114.00
5	A	404	HEC	CHA-C4D-ND	2.53	128.46	123.86
8	B	304	BPB	O2A-CGA-O1A	-2.53	117.30	123.63
5	A	401	HEC	CHB-C4A-NA	2.52	127.20	124.45
11	C	404	MQ7	C11-C12-C13	-2.47	122.57	126.83
12	C	405	NS5	C13-C12-C10	-2.47	124.21	127.69
13	C	406	OTP	C10-C9-C7	-2.44	122.04	127.62
7	B	302	BCL	C2A-C1A-CHA	-2.43	119.64	123.87
8	C	403	BPB	O2A-CGA-CBA	2.43	119.25	111.83
7	B	303	BCL	C2A-C1A-CHA	-2.43	119.66	123.87
8	C	403	BPB	O1D-CGD-CBD	-2.42	121.05	124.72
5	A	404	HEC	CHB-C4A-NA	2.41	127.08	124.45
7	C	402	BCL	O2A-CGA-O1A	-2.41	117.59	123.63
12	C	405	NS5	C32-C31-C33	2.41	119.42	115.23
12	C	405	NS5	C30-C29-C28	-2.41	116.21	123.20
5	A	401	HEC	CHD-C1D-ND	2.41	128.22	123.86
5	A	402	HEC	CHD-C1D-C2D	-2.40	120.47	127.43
5	A	401	HEC	C4B-NB-C1B	2.40	109.73	105.82
5	A	404	HEC	CBC-CAC-C3C	-2.39	122.65	127.43
7	B	301	BCL	C4-C3-C5	2.37	119.34	115.23
5	A	403	HEC	CHD-C1D-ND	2.35	128.12	123.86
5	A	402	HEC	O2D-CGD-CBD	2.33	121.35	114.00
5	A	403	HEC	CMA-C3A-C4A	2.32	128.81	124.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	402	HEC	CHA-C4D-C3D	-2.32	120.23	125.30
8	B	304	BPB	C4-C3-C5	2.31	119.24	115.23
7	B	302	BCL	CED-O2D-CGD	2.29	121.11	115.92
7	C	402	BCL	C4-C3-C5	2.28	119.19	115.23
7	B	302	BCL	CHC-C4B-C3B	-2.27	122.71	131.72
7	B	303	BCL	CHC-C4B-C3B	-2.27	122.72	131.72
5	A	401	HEC	O2D-CGD-O1D	-2.26	117.52	123.33
5	A	403	HEC	CBB-CAB-C3B	-2.26	122.92	127.43
7	B	301	BCL	C1-O2A-CGA	2.25	122.10	116.65
11	C	404	MQ7	C34-C33-C35	2.24	119.11	115.23
5	A	404	HEC	CHA-C4D-C3D	-2.23	120.41	125.30
5	A	403	HEC	C2A-C1A-NA	-2.22	108.18	110.32
11	C	404	MQ7	C20-C18-C17	-2.22	116.17	121.17
7	B	303	BCL	C1-O2A-CGA	2.22	122.02	116.65
5	A	404	HEC	C4B-NB-C1B	2.21	109.43	105.82
9	B	306	MPG	O4-CX3-CXD	-2.20	118.23	123.56
7	B	302	BCL	C7-C6-C5	-2.20	107.40	113.26
8	C	403	BPB	C4D-CHA-CBD	-2.20	107.40	108.45
7	B	302	BCL	CHB-C1B-NB	-2.19	120.76	124.05
7	C	402	BCL	CMB-C2B-C3B	2.19	132.58	125.67
5	A	402	HEC	CHB-C1B-NB	2.19	127.83	123.86
5	A	404	HEC	CBB-CAB-C3B	-2.19	123.06	127.43
5	A	402	HEC	O2A-CGA-O1A	-2.19	117.70	123.33
7	C	402	BCL	C4D-CHA-C1A	2.17	123.83	121.24
7	C	402	BCL	C4A-NA-C1A	2.15	107.66	106.68
7	C	402	BCL	O2A-CGA-CBA	2.15	118.40	111.83
7	B	301	BCL	C1D-CHD-C4C	-2.15	121.43	126.62
7	C	402	BCL	C1D-CHD-C4C	-2.13	121.49	126.62
5	A	404	HEC	CHC-C4B-C3B	-2.12	121.63	125.21
5	A	403	HEC	CHD-C1D-C2D	-2.11	121.30	127.43
8	B	304	BPB	CED-O2D-CGD	2.11	120.70	115.92
8	B	304	BPB	C3D-CAD-CBD	2.11	110.38	107.61
7	C	402	BCL	CHB-C1B-NB	-2.09	120.91	124.05
7	B	301	BCL	CHC-C4B-C3B	-2.09	123.44	131.72
11	C	404	MQ7	C26-C27-C28	-2.08	122.87	127.62
8	C	403	BPB	C3B-C4B-NB	2.06	111.05	108.05
7	B	302	BCL	C1D-CHD-C4C	-2.06	121.65	126.62
12	C	405	NS5	C13-C14-C15	-2.06	120.73	126.36
6	A	405	DGA	CG1-OG1-CA1	2.05	124.63	117.12
7	B	302	BCL	CHB-C1B-C2B	-2.05	121.47	127.43
8	C	403	BPB	C1-C2-C3	-2.04	122.85	126.20
7	B	302	BCL	CMB-C2B-C3B	2.04	132.11	125.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	301	BCL	CMB-C2B-C1B	2.04	128.52	125.42
7	B	302	BCL	O2A-CGA-O1A	-2.03	118.55	123.63
8	B	304	BPB	CMB-C2B-C3B	2.03	128.74	124.68
5	A	402	HEC	C2A-C1A-NA	-2.02	108.37	110.32
7	B	301	BCL	CED-O2D-CGD	2.02	120.49	115.92
7	B	303	BCL	CHB-C4A-NA	2.02	127.31	124.40
5	A	403	HEC	CHA-C4D-ND	2.01	127.50	123.86
7	C	402	BCL	CHC-C4B-C3B	-2.01	123.74	131.72
8	B	304	BPB	O2D-CGD-O1D	-2.01	119.94	123.85
6	A	405	DGA	OG1-CA1-OA1	-2.00	118.61	123.63

There are no chirality outliers.

All (147) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	402	HEC	C4B-C3B-CAB-CBB
5	A	402	HEC	C2C-C3C-CAC-CBC
5	A	402	HEC	C4C-C3C-CAC-CBC
5	A	403	HEC	C2B-C3B-CAB-CBB
5	A	403	HEC	C4B-C3B-CAB-CBB
5	A	404	HEC	C2C-C3C-CAC-CBC
5	A	404	HEC	C4C-C3C-CAC-CBC
6	A	405	DGA	CA2-CA1-OG1-CG1
6	A	405	DGA	OA1-CA1-OG1-CG1
6	A	405	DGA	OG1-CG1-CG2-OG2
6	A	405	DGA	OG1-CG1-CG2-CG3
7	C	402	BCL	CAD-CBD-CGD-O1D
7	C	402	BCL	CAD-CBD-CGD-O2D
8	B	304	BPB	C2C-C3C-CAC-CBC
8	C	403	BPB	C2C-C3C-CAC-CBC
9	B	305	MPG	CXD-CX3-O1-C1
9	B	305	MPG	O4-CX3-O1-C1
9	B	305	MPG	O3-C21-CXD-O2
9	B	305	MPG	O1-CX3-CXD-C21
9	B	305	MPG	O4-CX3-CXD-C21
9	B	306	MPG	O3-C21-CXD-O2
12	C	405	NS5	C25-C26-C28-C29
12	C	405	NS5	C27-C26-C28-C29
12	C	405	NS5	C26-C28-C29-C30
12	C	405	NS5	C28-C29-C30-C31
13	C	406	OTP	C38-C37-C39-C40
12	C	405	NS5	C34-C35-C36-CM4

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Mol	Chain	Res	Type	Atoms
12	C	405	NS5	C2-C3-C4-C5
8	B	304	BPB	CBD-CGD-O2D-CED
7	B	302	BCL	C4-C3-C5-C6
12	C	405	NS5	C3-C4-C5-C6
13	C	406	OTP	C30-C31-C32-C33
13	C	406	OTP	C20-C21-C22-C23
13	C	406	OTP	C5-C6-C7-C8
12	C	405	NS5	C3-C4-C5-C7
13	C	406	OTP	C20-C21-C22-C24
13	C	406	OTP	C5-C6-C7-C9
12	C	405	NS5	C11-C10-C9-C8
12	C	405	NS5	C12-C10-C9-C8
13	C	406	OTP	C34-C35-C36-C37
13	C	406	OTP	C24-C25-C26-C27
13	C	406	OTP	C14-C15-C16-C17
7	C	402	BCL	C2A-CAA-CBA-CGA
8	C	403	BPB	CBD-CGD-O2D-CED
7	B	302	BCL	C2-C3-C5-C6
13	C	406	OTP	C30-C31-C32-C34
7	B	301	BCL	C14-C13-C15-C16
8	C	403	BPB	C11-C10-C8-C9
8	C	403	BPB	C4-C3-C5-C6
7	B	302	BCL	C15-C16-C17-C18
7	B	303	BCL	CBD-CGD-O2D-CED
8	B	304	BPB	O1D-CGD-O2D-CED
8	B	304	BPB	C8-C10-C11-C12
9	B	305	MPG	O3-C21-CXD-CX3
8	C	403	BPB	C2-C3-C5-C6
7	B	303	BCL	C16-C17-C18-C19
9	B	305	MPG	C5-C6-C7-C8
9	B	306	MPG	C11-C12-C13-C14
6	A	405	DGA	CBB-CAB-CB9-CB8
9	B	305	MPG	C2-C3-C4-C5
8	C	403	BPB	O1D-CGD-O2D-CED
7	B	303	BCL	C16-C17-C18-C20
6	A	405	DGA	CCB-CDB-CEB-CFB
6	A	405	DGA	CA5-CA6-CA7-CA8
7	B	301	BCL	C15-C16-C17-C18
11	C	404	MQ7	C23-C25-C26-C27
6	A	405	DGA	CEB-CFB-CGB-CHB
9	B	306	MPG	C12-C13-C14-C15
9	C	407	MPG	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
9	B	305	MPG	C10-C11-C12-C13
9	B	306	MPG	O1-C1-C2-C3
8	C	403	BPB	C11-C12-C13-C14
13	C	406	OTP	C9-C10-C11-C12
9	C	407	MPG	C10-C11-C12-C13
6	A	405	DGA	CA7-CA8-CA9-CAA
9	B	306	MPG	O3-C21-CXD-CX3
12	C	405	NS5	C1-C2-C3-C4
8	C	403	BPB	C10-C11-C12-C13
9	B	305	MPG	C12-C13-C14-C15
6	A	405	DGA	CB6-CB7-CB8-CB9
6	A	405	DGA	CB9-CAB-CBB-CCB
8	B	304	BPB	C4-C3-C5-C6
9	B	306	MPG	C2-C1-O1-CX3
7	B	303	BCL	C11-C12-C13-C14
6	A	405	DGA	CA8-CA9-CAA-CBA
6	A	405	DGA	CB4-CB5-CB6-CB7
7	B	303	BCL	C11-C12-C13-C15
8	C	403	BPB	C11-C12-C13-C15
9	B	305	MPG	C15-C16-C17-C18
13	C	406	OTP	C35-C36-C37-C39
7	B	303	BCL	O1D-CGD-O2D-CED
9	B	305	MPG	O4-CX3-CXD-O2
8	B	304	BPB	C2-C3-C5-C6
9	B	306	MPG	C3-C4-C5-C6
8	C	403	BPB	C8-C10-C11-C12
9	B	305	MPG	C13-C14-C15-C16
6	A	405	DGA	CA3-CA4-CA5-CA6
8	C	403	BPB	C11-C10-C8-C7
8	C	403	BPB	O2A-C1-C2-C3
8	B	304	BPB	C16-C17-C18-C19
7	B	301	BCL	C10-C11-C12-C13
7	B	301	BCL	C4-C3-C5-C6
13	C	406	OTP	C15-C16-C17-C18
6	A	405	DGA	CBB-CCB-CDB-CEB
7	B	301	BCL	CHA-CBD-CGD-O1D
7	B	301	BCL	CHA-CBD-CGD-O2D
7	B	303	BCL	CHA-CBD-CGD-O1D
7	B	303	BCL	CHA-CBD-CGD-O2D
12	C	405	NS5	C32-C31-C33-C34
7	C	402	BCL	C11-C12-C13-C14
7	B	301	BCL	C2-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
7	C	402	BCL	C11-C12-C13-C15
5	A	402	HEC	C3D-CAD-CBD-CGD
8	C	403	BPB	C6-C7-C8-C9
9	C	407	MPG	C2-C3-C4-C5
5	A	402	HEC	CAD-CBD-CGD-O1D
13	C	406	OTP	C36-C37-C39-C40
5	A	401	HEC	CAA-CBA-CGA-O2A
11	C	404	MQ7	C39-C38-C40-C41
5	A	401	HEC	CAA-CBA-CGA-O1A
11	C	404	MQ7	C37-C38-C40-C41
13	C	406	OTP	C15-C16-C17-C19
13	C	406	OTP	C37-C39-C40-O1
9	B	305	MPG	C6-C7-C8-C9
8	B	304	BPB	O1A-CGA-O2A-C1
5	A	402	HEC	CAD-CBD-CGD-O2D
8	B	304	BPB	CBA-CGA-O2A-C1
9	B	306	MPG	C7-C8-C9-C10
5	A	402	HEC	CAA-CBA-CGA-O1A
5	A	402	HEC	CAA-CBA-CGA-O2A
8	B	304	BPB	C5-C6-C7-C8
5	A	404	HEC	C3D-CAD-CBD-CGD
8	B	304	BPB	O2A-C1-C2-C3
11	C	404	MQ7	C38-C40-C41-C42
12	C	405	NS5	C30-C31-C33-C34
9	B	305	MPG	C7-C8-C9-C10
9	C	407	MPG	C7-C8-C9-C10
6	A	405	DGA	OG2-CB1-CB2-CB3
8	C	403	BPB	C6-C7-C8-C10
8	C	403	BPB	C5-C6-C7-C8
7	C	402	BCL	CBA-CGA-O2A-C1
7	B	301	BCL	C6-C7-C8-C10
7	C	402	BCL	O1A-CGA-O2A-C1
6	A	405	DGA	OB1-CB1-CB2-CB3
12	C	405	NS5	C5-C7-C8-C9
8	C	403	BPB	C14-C13-C15-C16
8	B	304	BPB	C16-C17-C18-C20

There are no ring outliers.

15 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	404	HEC	1	0

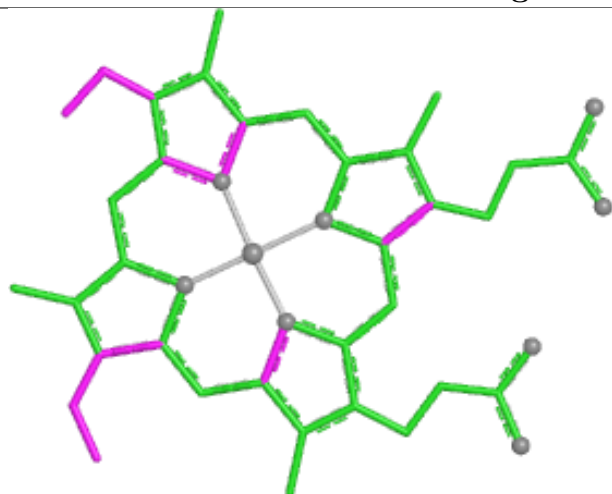
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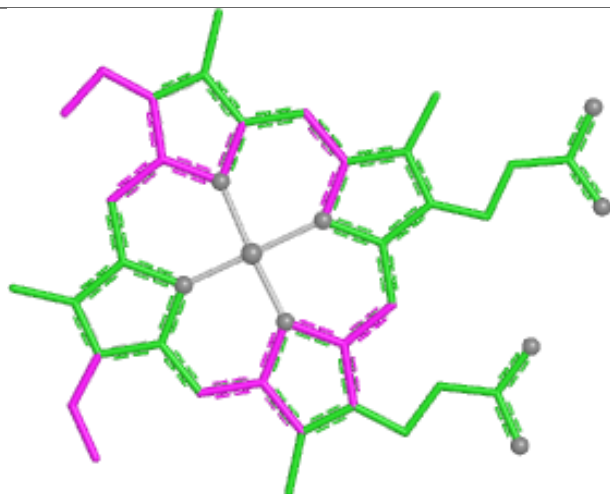
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	405	NS5	5	0
11	C	404	MQ7	2	0
7	B	303	BCL	3	0
7	C	402	BCL	5	0
7	B	302	BCL	2	0
9	C	407	MPG	1	0
13	C	406	OTP	7	0
9	B	306	MPG	1	0
7	B	301	BCL	4	0
5	A	403	HEC	1	0
8	C	403	BPB	5	0
5	A	401	HEC	1	0
8	B	304	BPB	8	0
9	B	305	MPG	1	0

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.

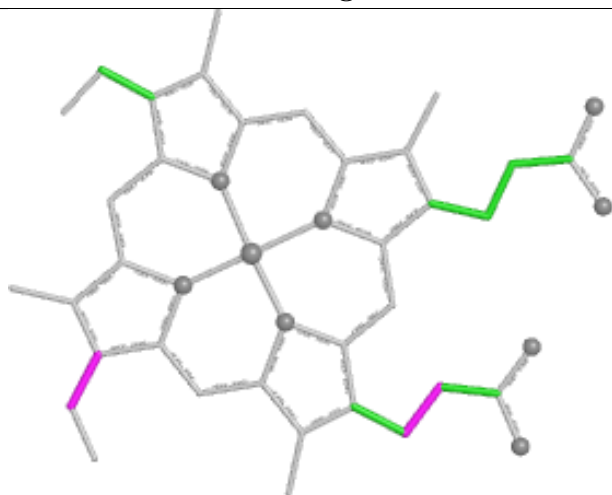
Ligand HEC A 404



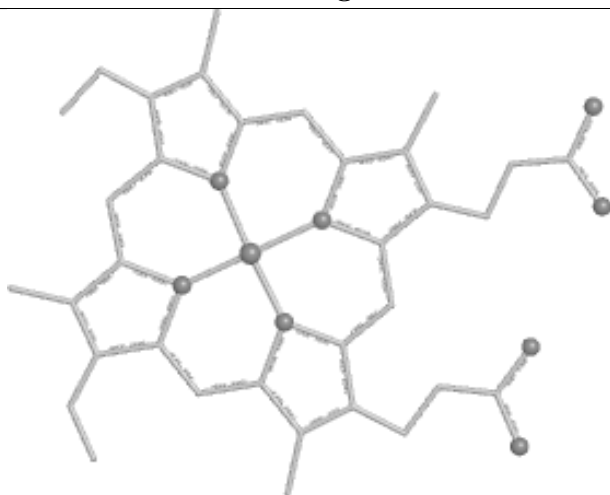
Bond lengths



Bond angles

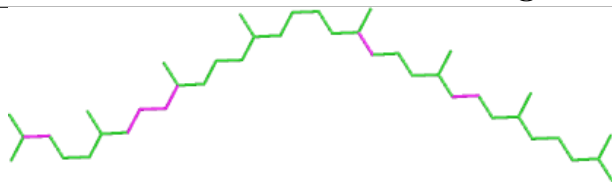


Torsions

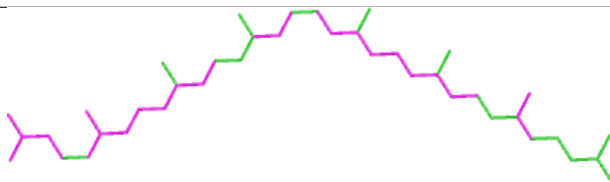


Rings

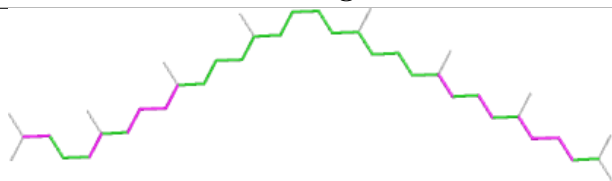
Ligand NS5 C 405



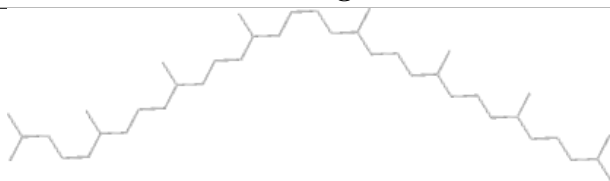
Bond lengths



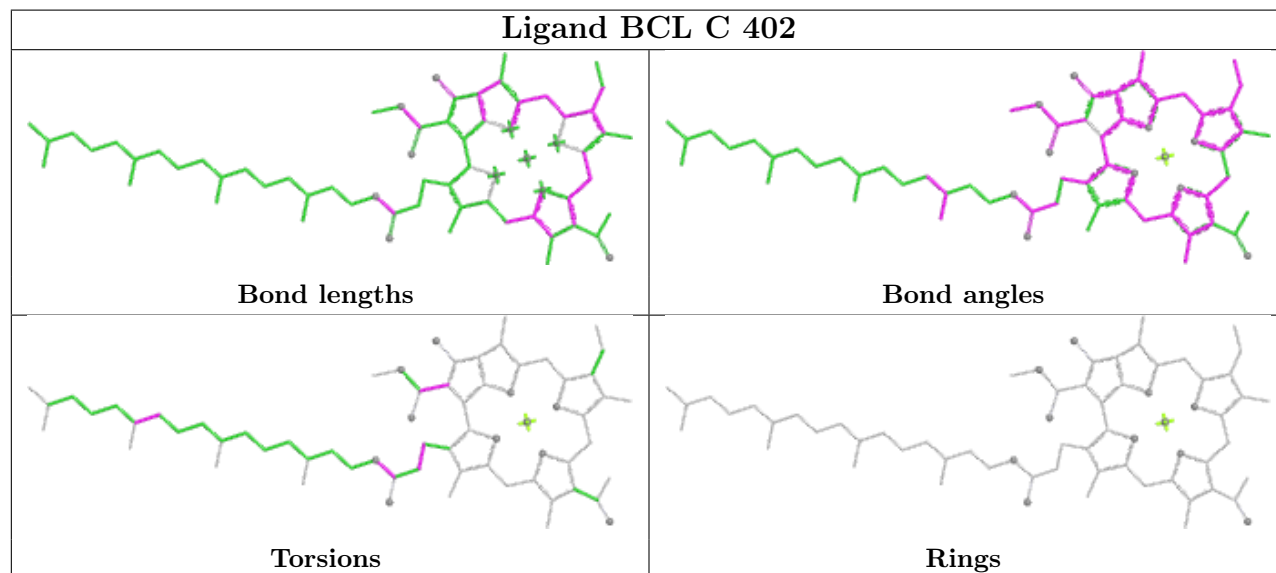
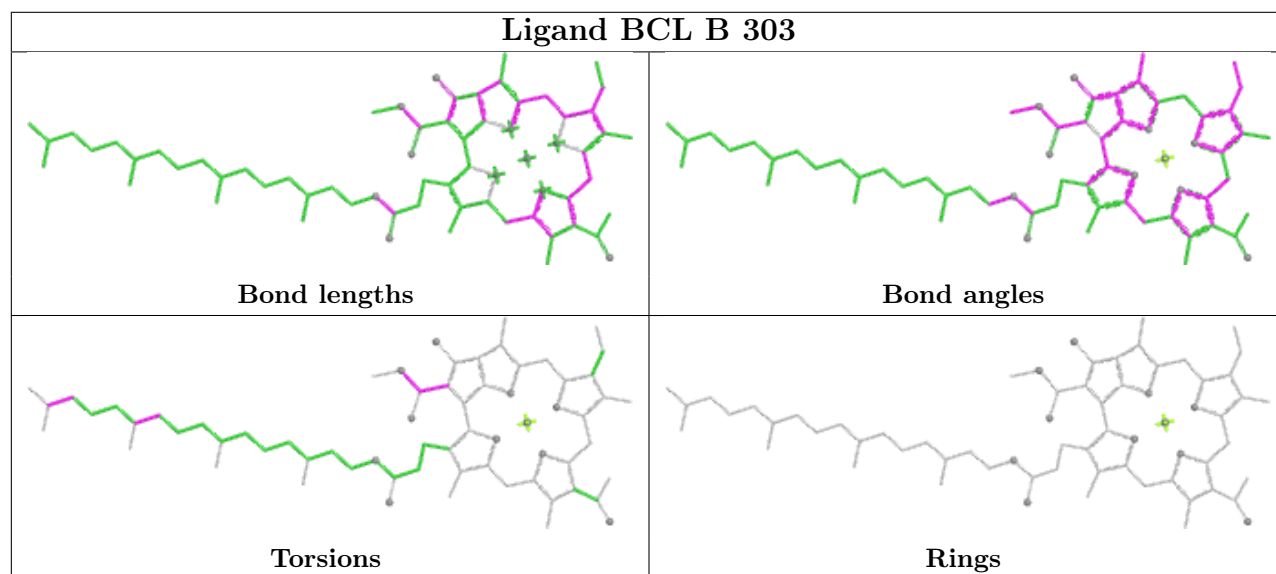
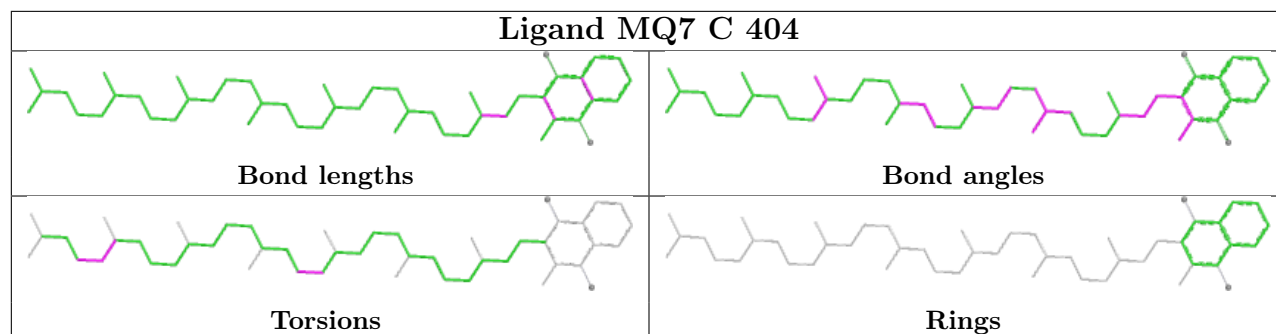
Bond angles

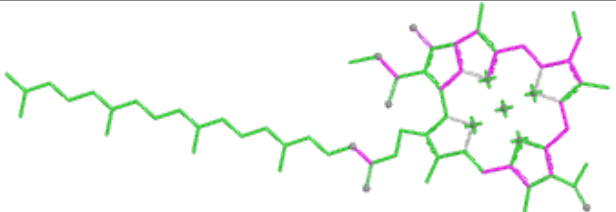
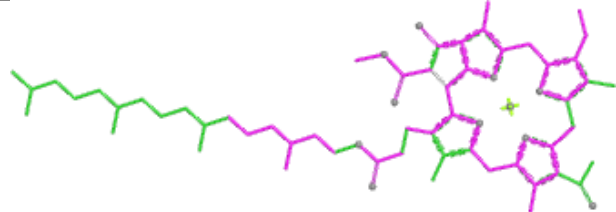
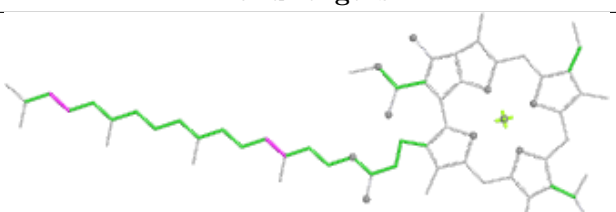
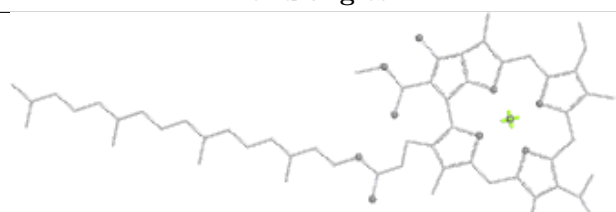


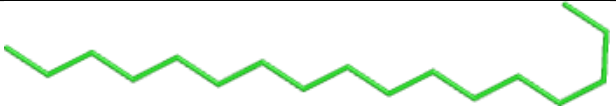
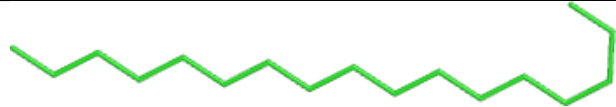
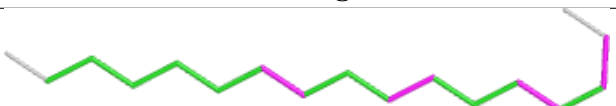
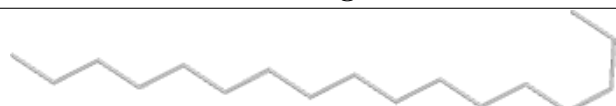
Torsions

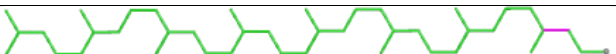
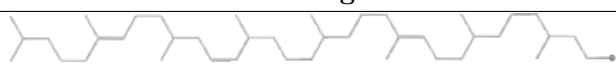


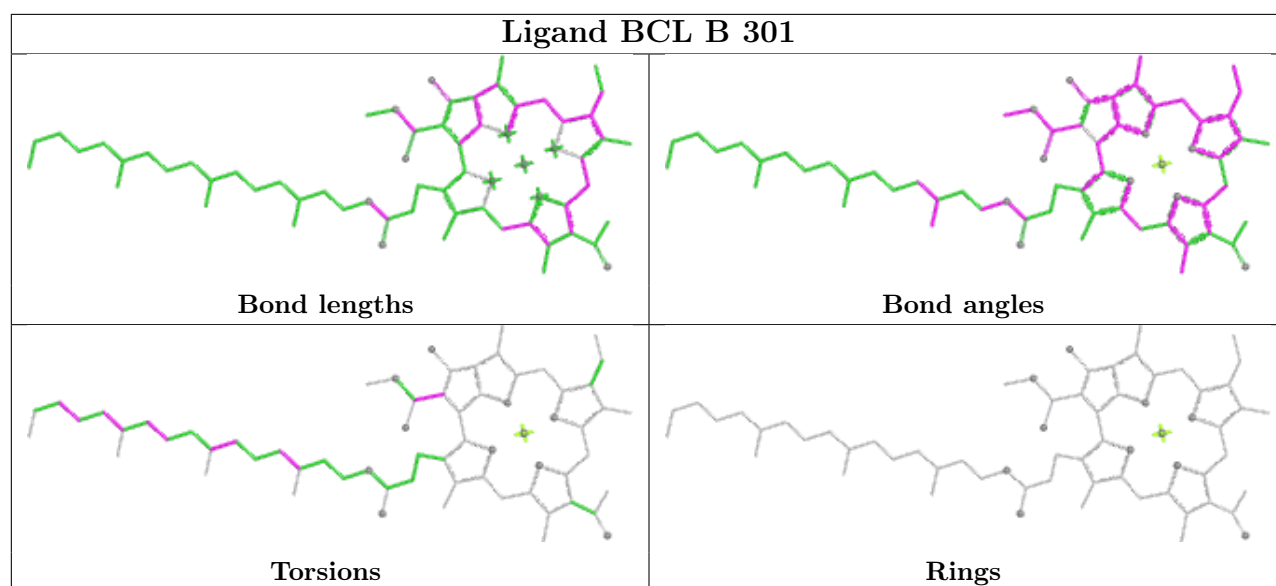
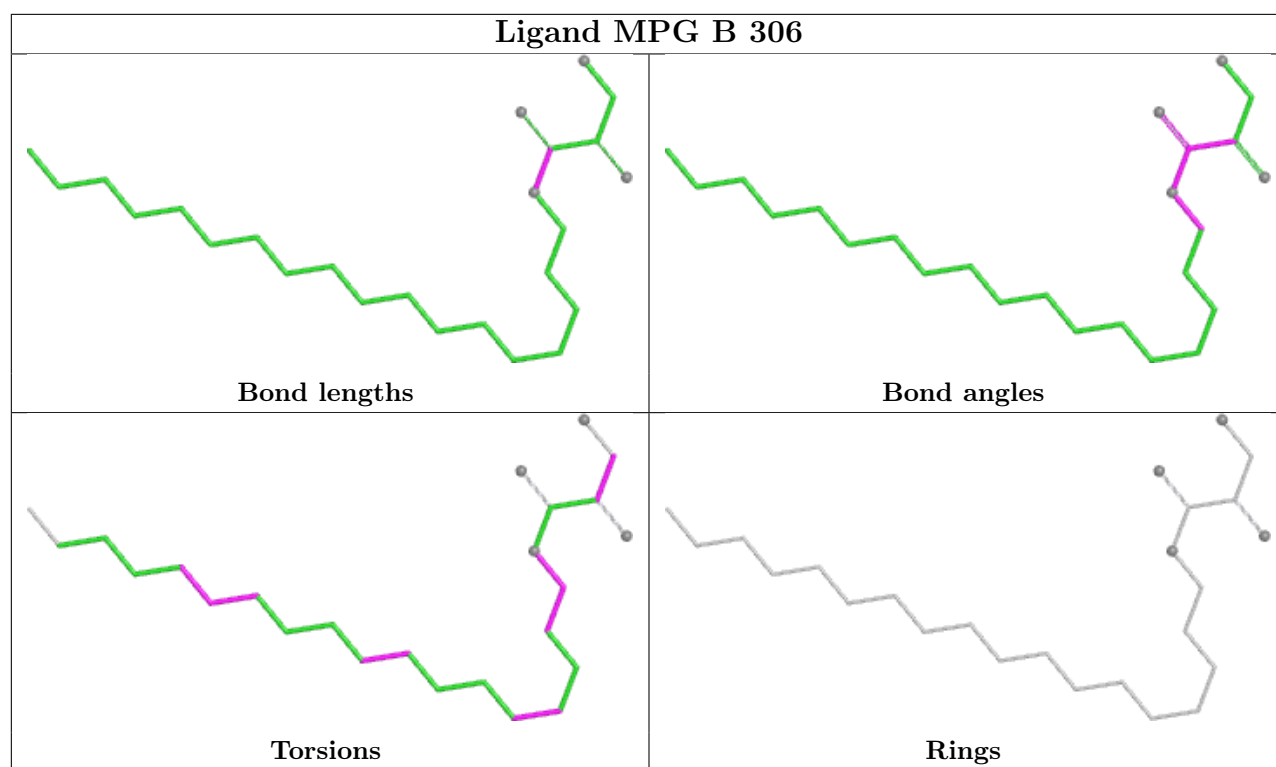
Rings



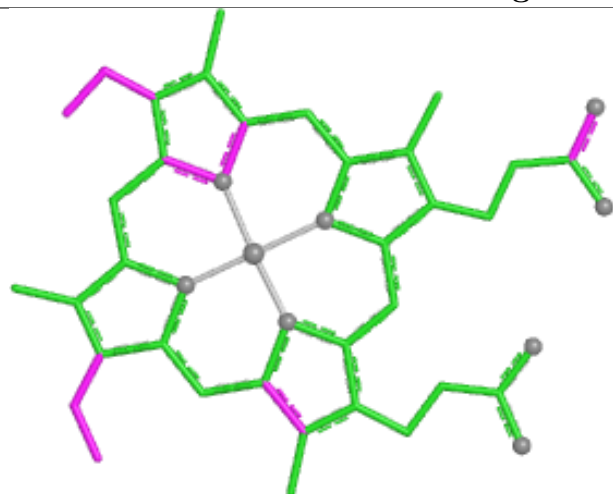
Ligand BCL B 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand MPG C 407	
	
Bond lengths	Bond angles
	
Torsions	Rings

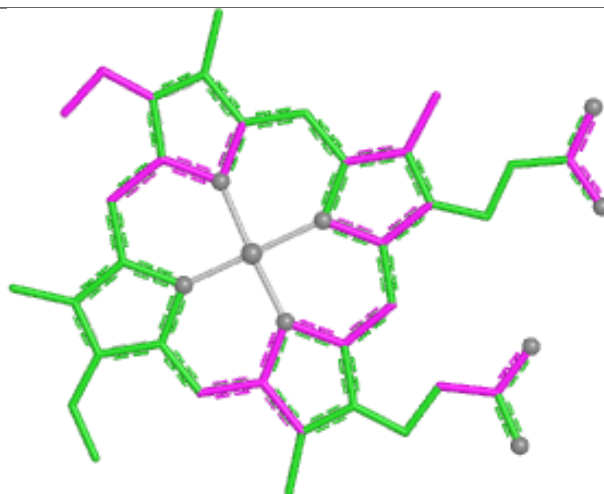
Ligand OTP C 406	
	
Bond lengths	Bond angles
	
Torsions	Rings



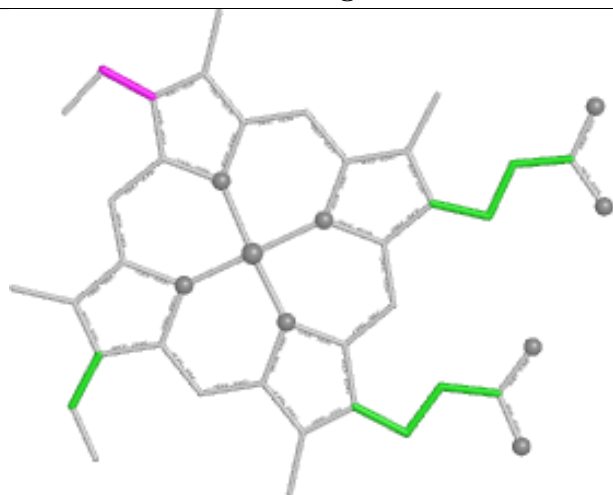
Ligand HEC A 403



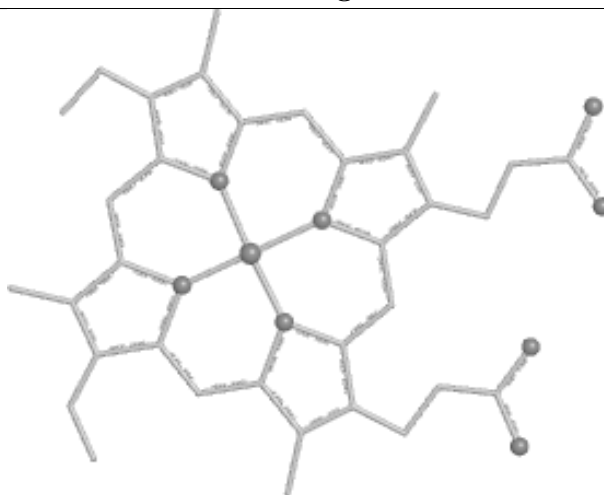
Bond lengths



Bond angles

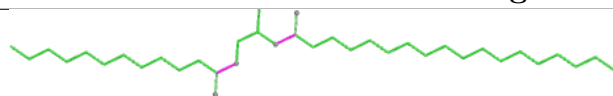


Torsions

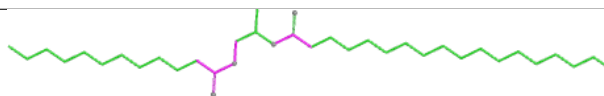


Rings

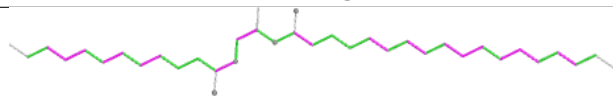
Ligand DGA A 405



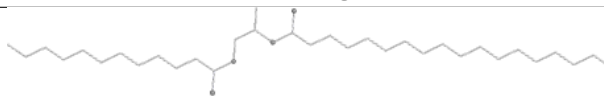
Bond lengths



Bond angles

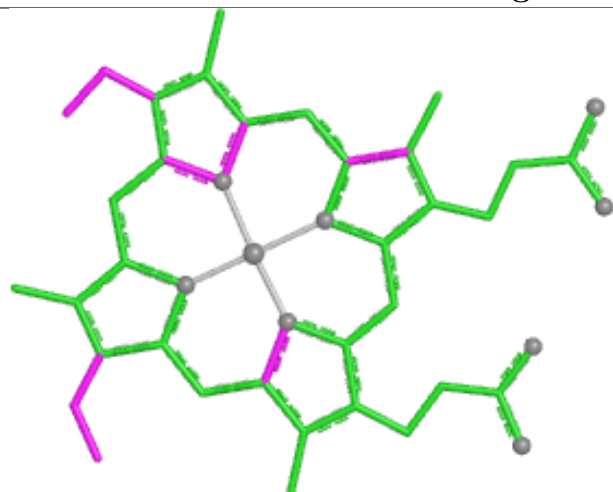


Torsions

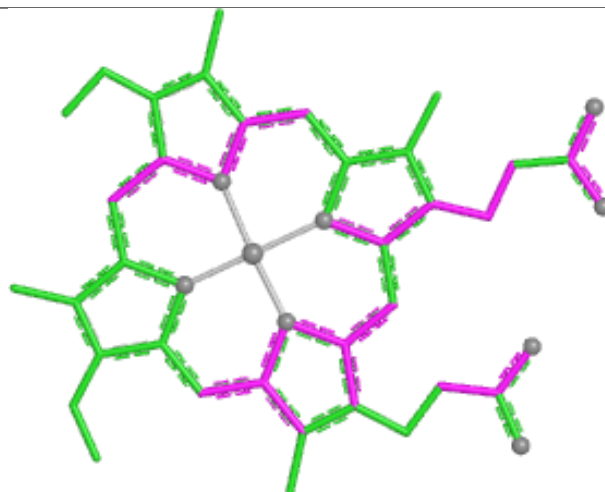


Rings

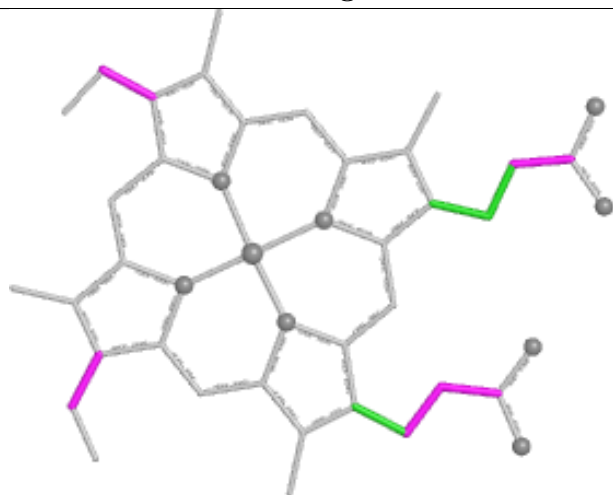
Ligand HEC A 402



Bond lengths



Bond angles

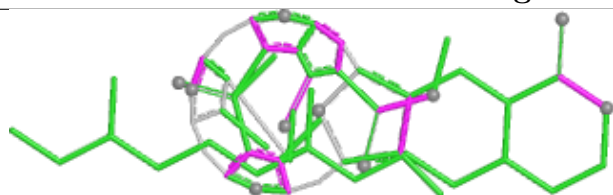


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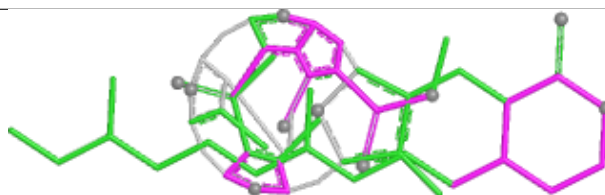


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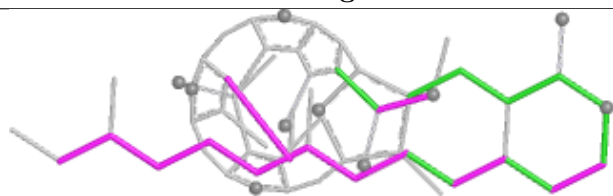
Ligand BPB C 403



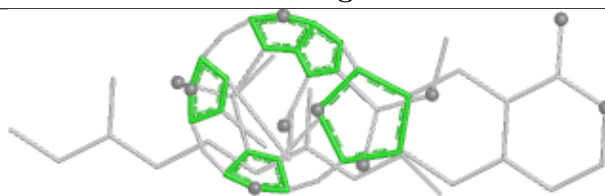
Bond lengths



Bond angles

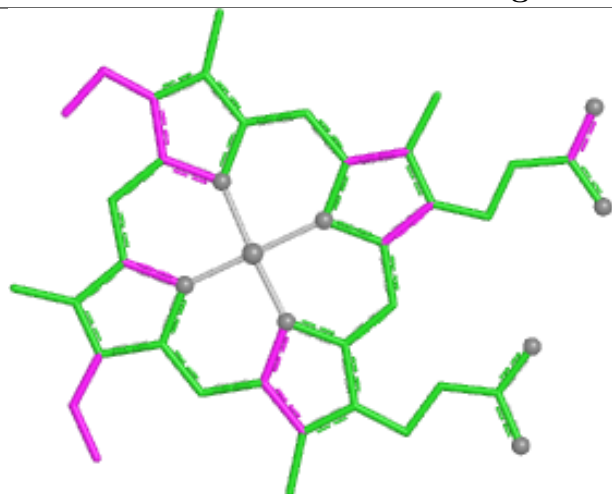


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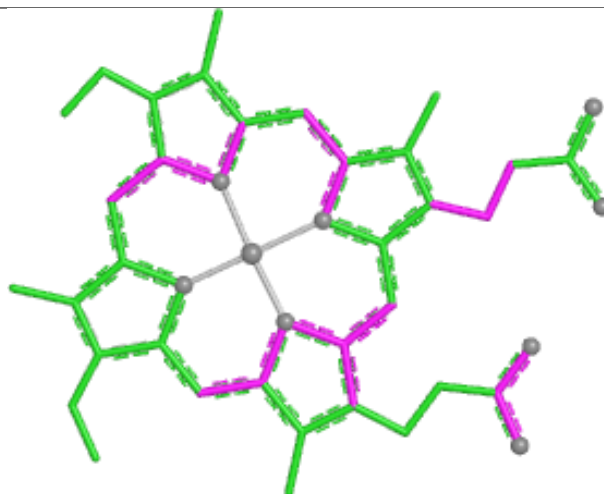


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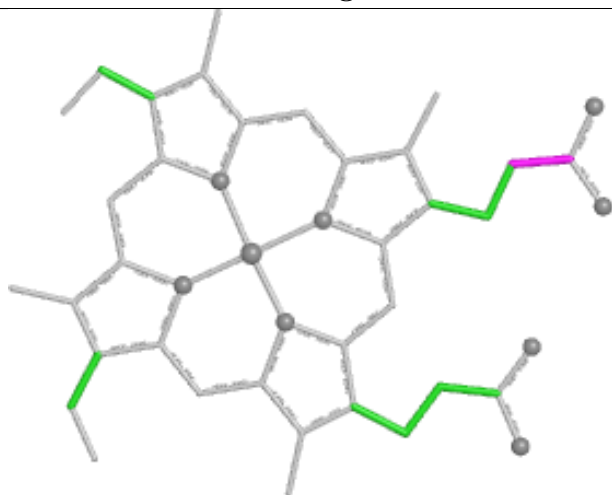
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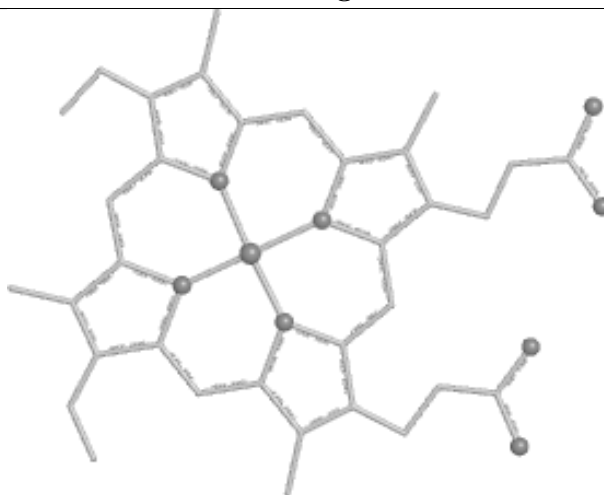
Bond lengths



Bond angles

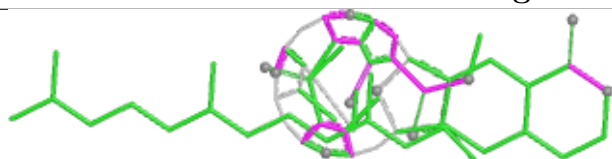


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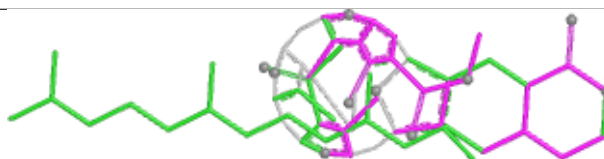


Rings

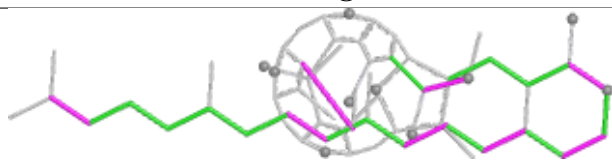
Ligand BPB B 304



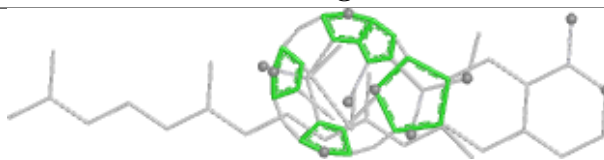
Bond lengths



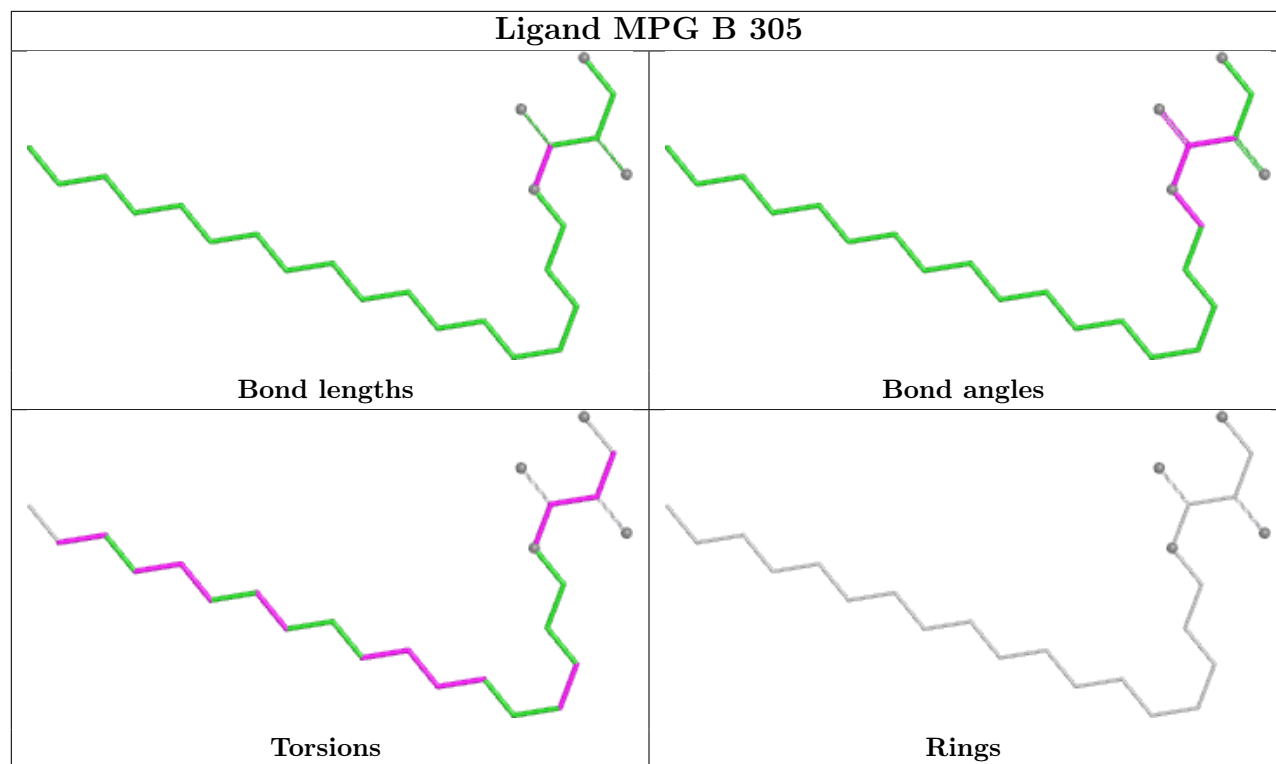
Bond angles



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	332/356 (93%)	0.12	3 (0%) 81 58	21, 38, 56, 78	0
2	B	273/274 (99%)	0.45	6 (2%) 62 37	22, 55, 89, 113	2 (0%)
3	C	323/324 (99%)	0.47	10 (3%) 51 29	28, 56, 88, 109	0
4	D	242/258 (93%)	1.08	28 (11%) 9 6	63, 92, 115, 136	0
All	All	1170/1212 (96%)	0.49	47 (4%) 42 23	21, 54, 101, 136	2 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	85	THR	4.1
4	D	84	GLU	4.1
3	C	246	ALA	4.0
3	C	29	VAL	4.0
4	D	66	LYS	3.5
3	C	242	ALA	3.4
4	D	79	PRO	3.4
4	D	188	ALA	3.2
4	D	7	ALA	3.1
3	C	323	LYS	3.0
2	B	61	PRO	3.0
4	D	67	THR	3.0
4	D	78	VAL	2.9
4	D	199	GLY	2.9
3	C	229	GLY	2.8
4	D	154	GLY	2.7
4	D	194	ALA	2.7
4	D	61	GLU	2.6
3	C	226	ARG	2.5
4	D	155	LEU	2.5
2	B	203	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	49	ILE	2.5
1	A	270	GLY	2.4
4	D	144	SER	2.4
4	D	158	VAL	2.4
2	B	221	GLY	2.3
4	D	237	LYS	2.3
2	B	202	ASP	2.3
4	D	247	LEU	2.3
4	D	206	ASP	2.3
4	D	165	ALA	2.2
2	B	4	SER	2.2
4	D	124	VAL	2.2
4	D	159	ALA	2.2
3	C	110	GLY	2.2
4	D	107	PRO	2.2
2	B	116	HIS	2.1
4	D	80	ARG	2.1
4	D	69	VAL	2.1
1	A	168	THR	2.1
3	C	44	ALA	2.1
3	C	12	ALA	2.1
4	D	239	SER	2.1
4	D	147	GLU	2.1
1	A	95	ASN	2.1
4	D	110	ASP	2.0
4	D	63	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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
4	FME	D	1	10/11	0.87	0.20	64,69,72,73	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

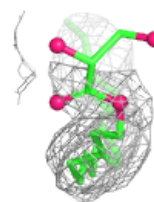
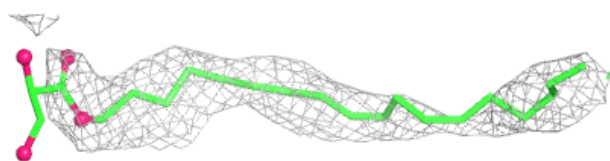
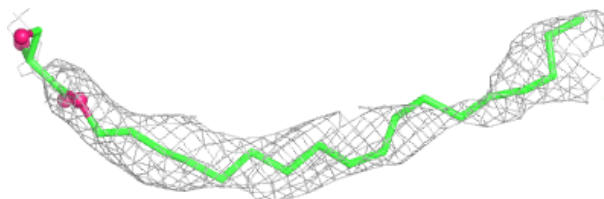
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	MPG	B	306	25/25	0.76	0.25	67,77,97,98	0
9	MPG	B	305	25/25	0.81	0.28	80,101,116,120	0
6	DGA	A	405	37/44	0.81	0.18	53,77,94,103	0
9	MPG	C	407	17/25	0.81	0.28	60,84,100,103	0
12	NS5	C	405	40/40	0.84	0.27	50,79,103,106	0
11	MQ7	C	404	48/48	0.87	0.17	32,42,66,70	0
14	PO4	C	409	5/5	0.88	0.16	66,68,71,71	0
13	OTP	C	406	41/49	0.90	0.18	48,60,78,84	0
7	BCL	B	301	65/66	0.90	0.17	32,43,164,175	0
8	BPB	C	403	61/65	0.91	0.16	51,68,83,88	0
14	PO4	C	408	5/5	0.93	0.12	93,95,102,104	0
7	BCL	B	302	66/66	0.93	0.12	27,33,42,50	0
7	BCL	B	303	66/66	0.94	0.12	18,27,47,48	0
7	BCL	C	402	66/66	0.94	0.12	29,37,54,66	0
8	BPB	B	304	65/65	0.94	0.12	27,35,47,60	0
5	HEC	A	401	43/43	0.95	0.09	23,31,34,35	0
5	HEC	A	404	43/43	0.96	0.10	32,37,53,58	0
5	HEC	A	403	43/43	0.96	0.10	22,25,27,30	0
5	HEC	A	402	43/43	0.97	0.09	23,25,29,35	0
10	FE2	C	401	1/1	0.99	0.04	48,48,48,48	0

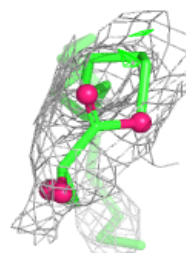
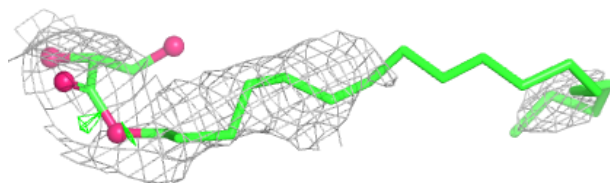
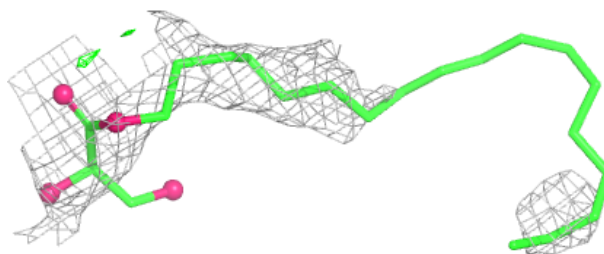
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MPG B 306:

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

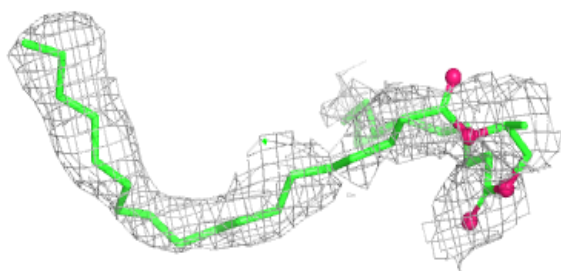
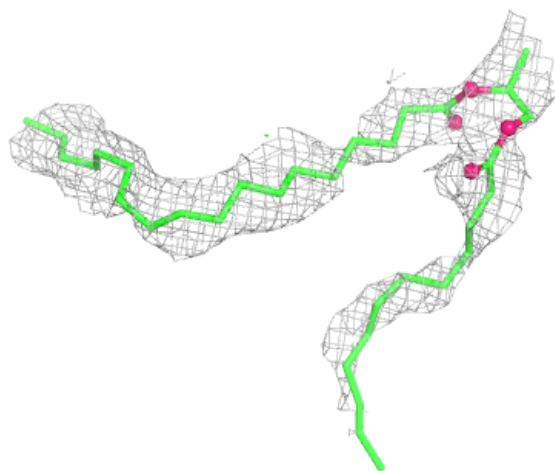
**Electron density around MPG B 305:**

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



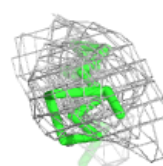
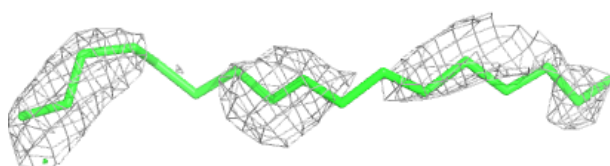
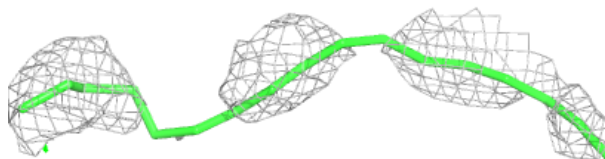
Electron density around DGA A 405:

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

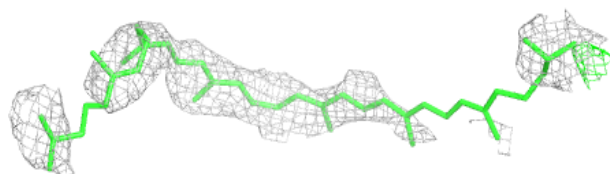
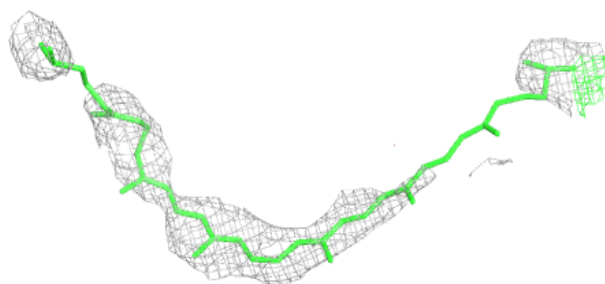


Electron density around MPG C 407:

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

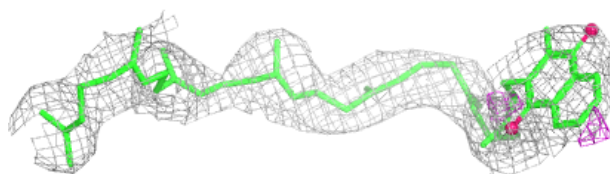
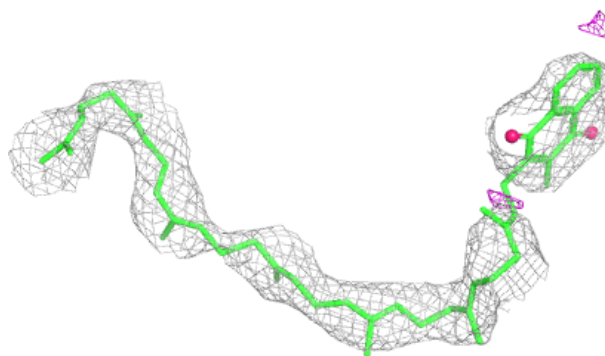
**Electron density around NS5 C 405:**

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

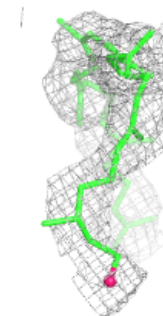
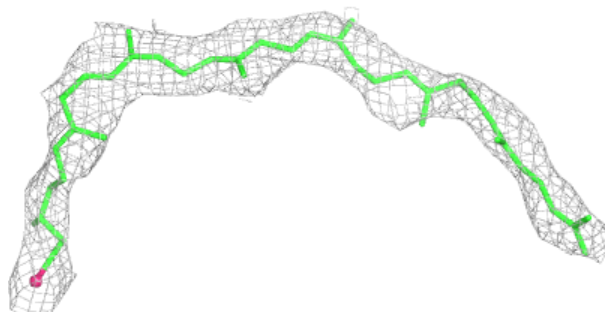


Electron density around MQ7 C 404:

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

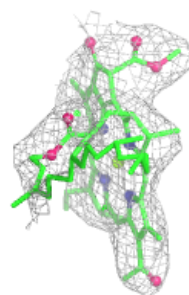
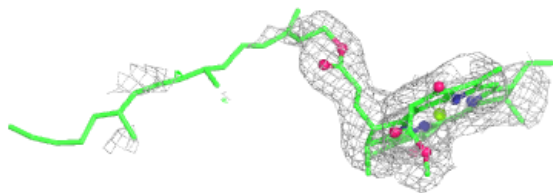
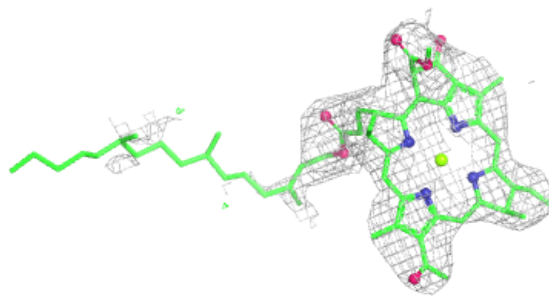
**Electron density around OTP C 406:**

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

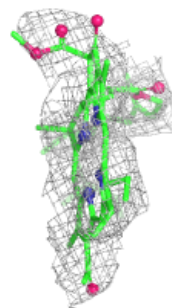
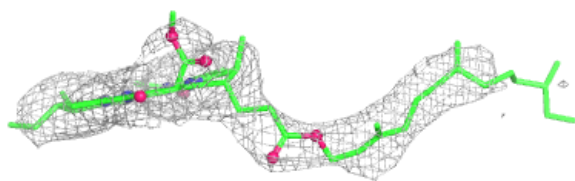
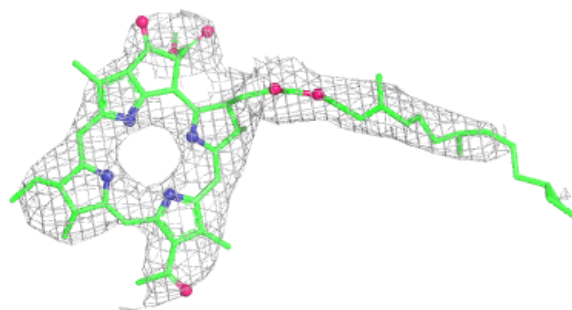


Electron density around BCL B 301:

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

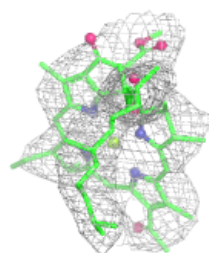
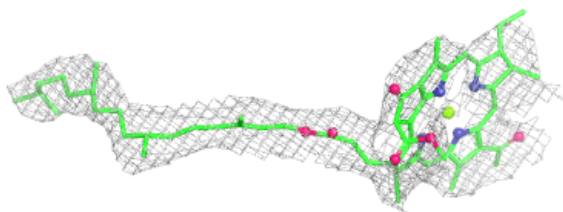
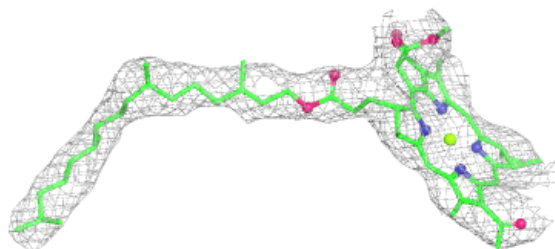
**Electron density around BPB C 403:**

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

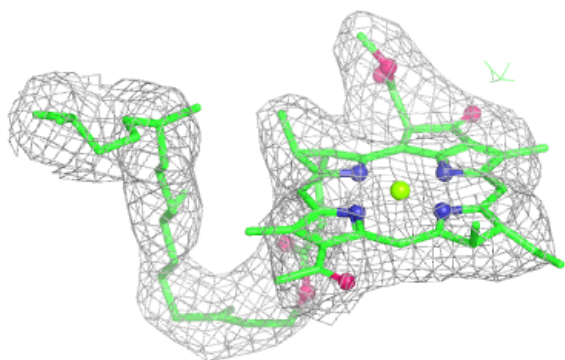
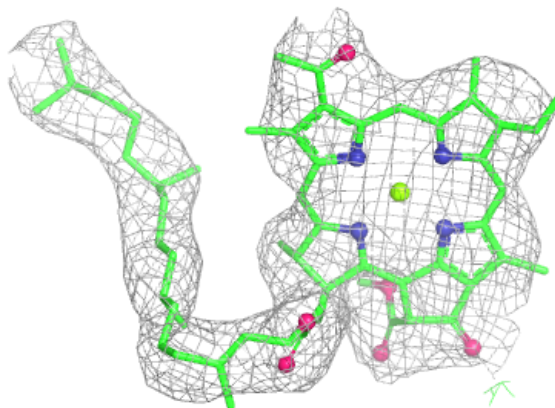


Electron density around BCL B 302:

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

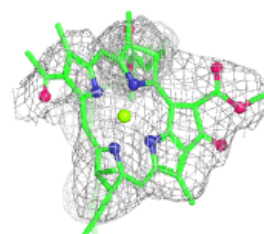
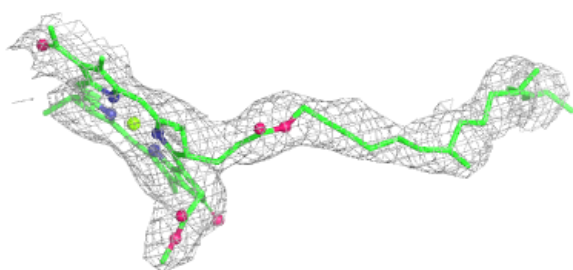
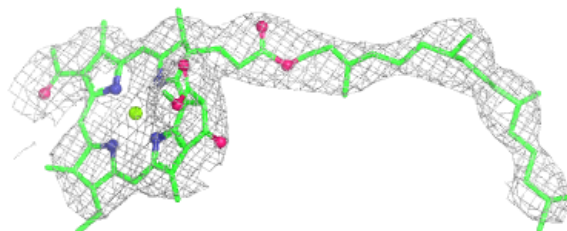
**Electron density around BCL B 303:**

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



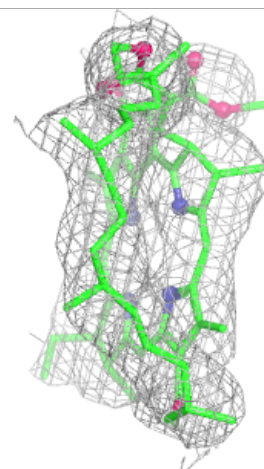
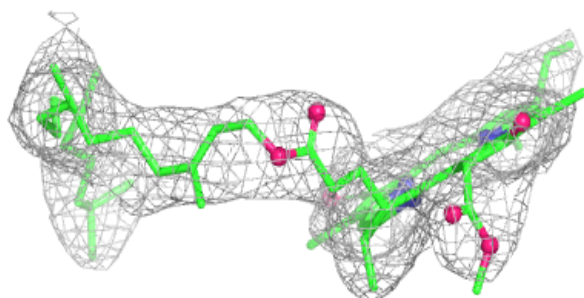
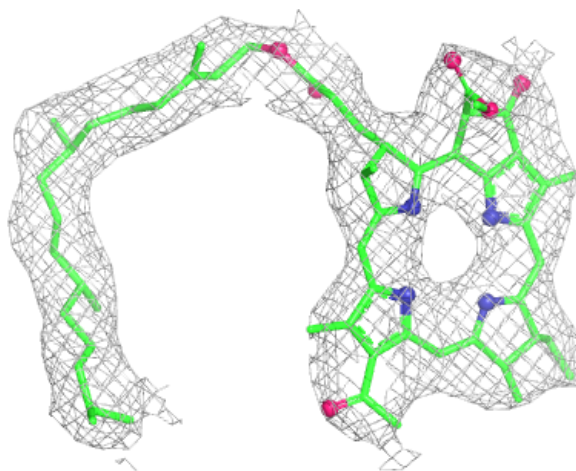
Electron density around BCL C 402:

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



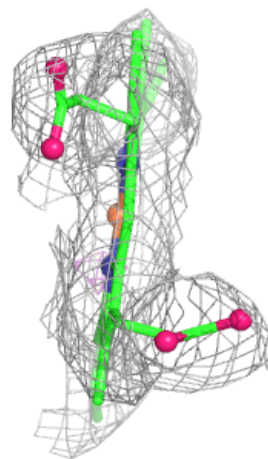
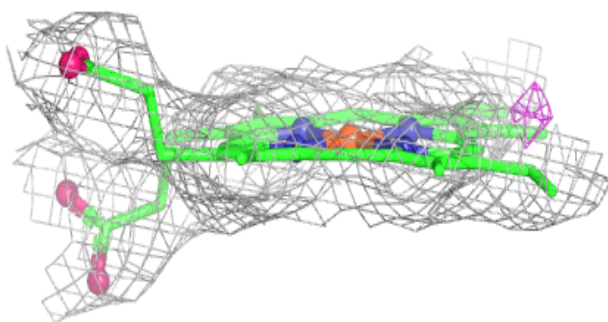
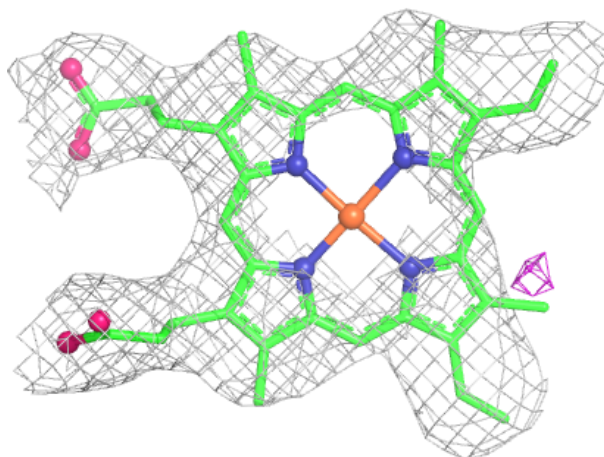
Electron density around BPB B 304:

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



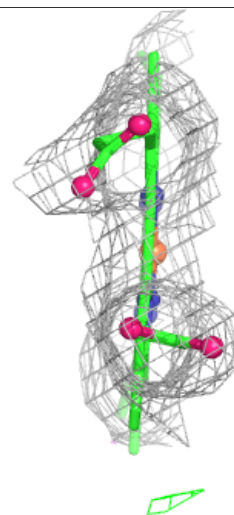
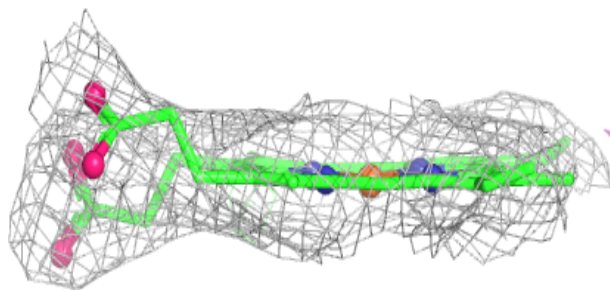
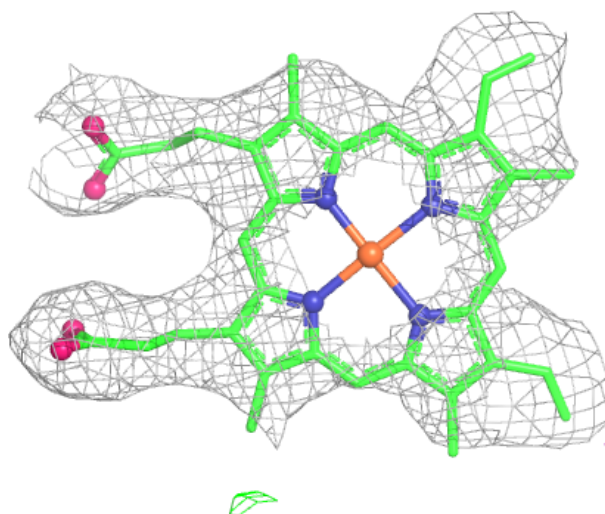
Electron density around HEC A 401:

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



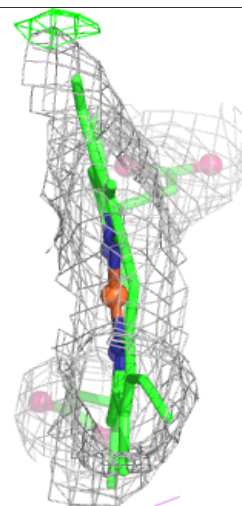
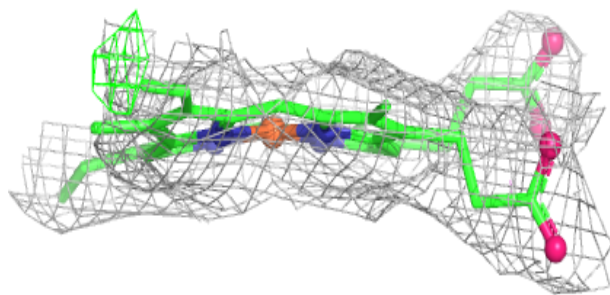
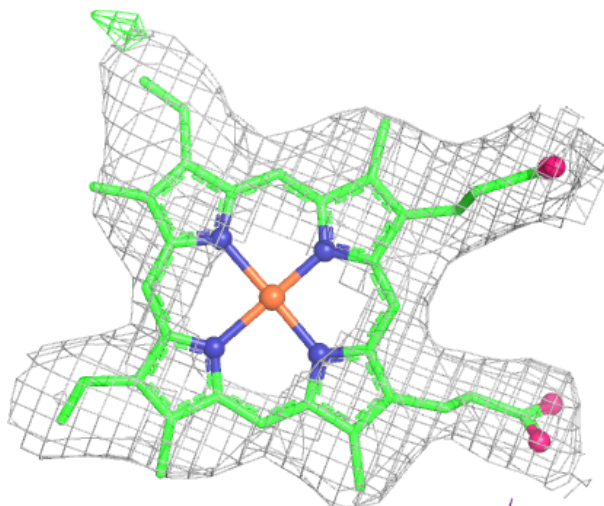
Electron density around HEC A 404:

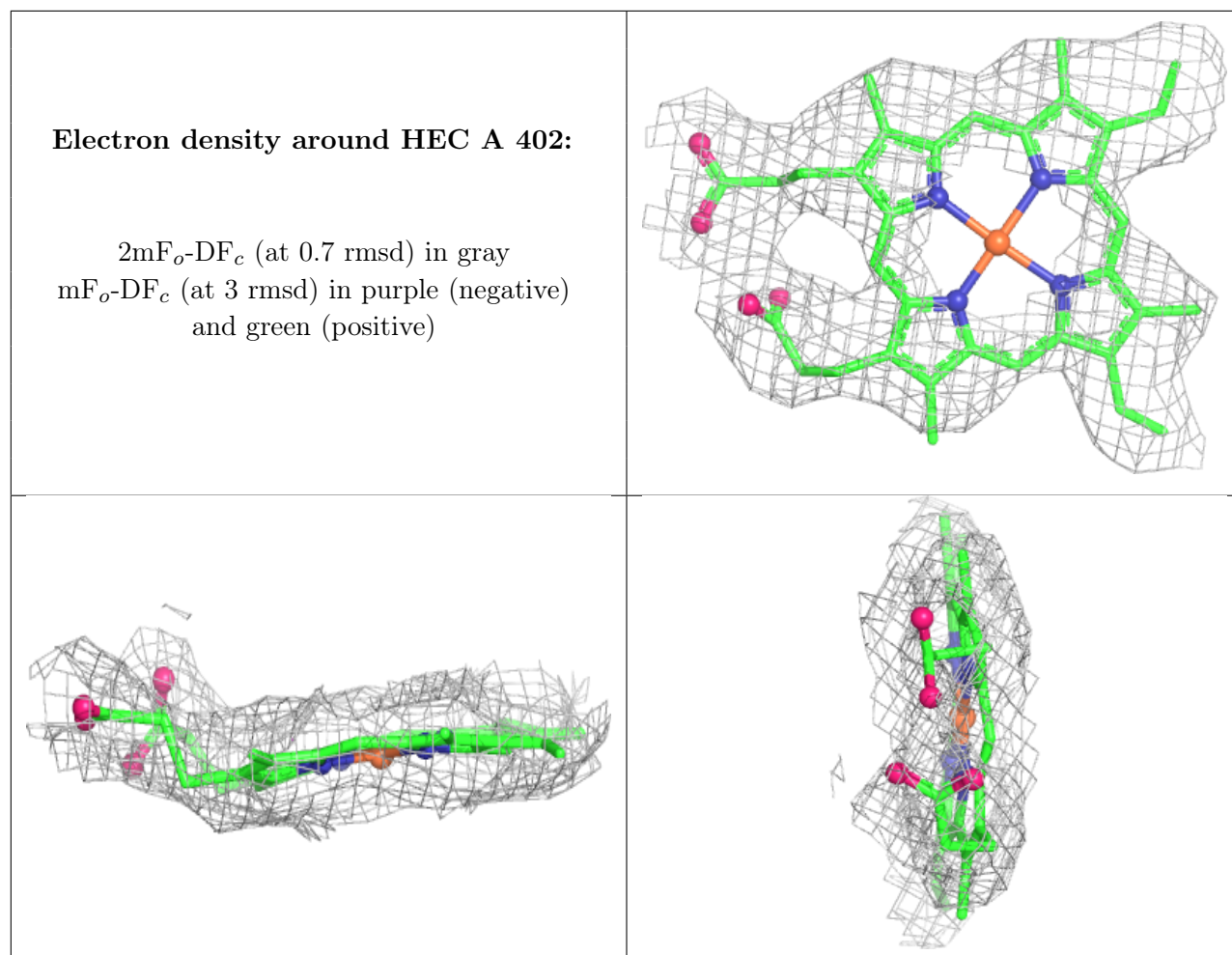
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 403:

$2mF_o-DF_c$ (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.