



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 10:31 PM EDT

PDB ID : 3PXW / pdb_00003pxw
Title : Crystal Structure of Ferrous NO Adduct of MauG in Complex with Pre-Methylamine Dehydrogenase
Authors : Yukl, E.T.; Goblirsch, B.R.; Wilmot, C.M.
Deposited on : 2010-12-10
Resolution : 2.11 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

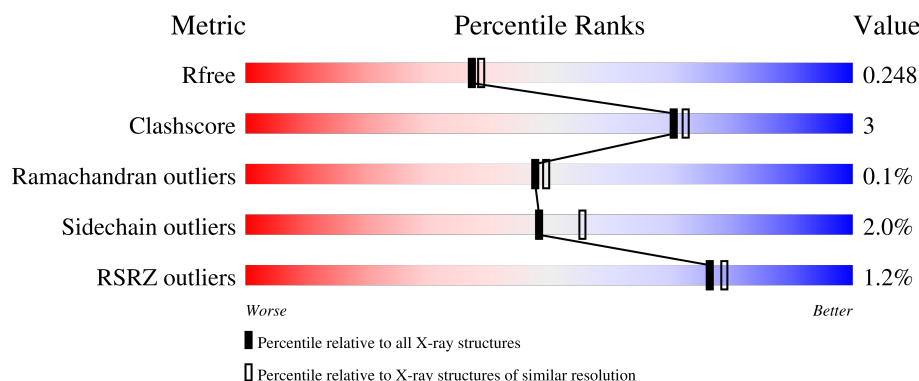
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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	373	86% 9% 5%
1	B	373	87% 9% 5%
2	C	137	85% 5% 9%
2	E	137	81% 9% 9%
3	D	385	89% 9%

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Mol	Chain	Length	Quality of chain
3	F	385	% 87% 10%

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
2	0AF	E	57	-	-	X	-
6	HEC	A	500	X	-	-	-
6	HEC	A	600	X	-	-	-
6	HEC	B	500	X	-	-	-
6	HEC	B	600	X	-	-	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 14700 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 Methylamine utilization protein MauG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	1	0
			2740	1711	491	527	11			
1	B	355	Total	C	N	O	S	0	1	0
			2754	1718	495	530	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	368	HIS	-	expression tag	UNP Q51658
A	369	HIS	-	expression tag	UNP Q51658
A	370	HIS	-	expression tag	UNP Q51658
A	371	HIS	-	expression tag	UNP Q51658
A	372	HIS	-	expression tag	UNP Q51658
A	373	HIS	-	expression tag	UNP Q51658
B	368	HIS	-	expression tag	UNP Q51658
B	369	HIS	-	expression tag	UNP Q51658
B	370	HIS	-	expression tag	UNP Q51658
B	371	HIS	-	expression tag	UNP Q51658
B	372	HIS	-	expression tag	UNP Q51658
B	373	HIS	-	expression tag	UNP Q51658

- Molecule 2 is a protein called Methylamine dehydrogenase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	125	Total	C	N	O	S	0	0	0
			954	590	161	190	13			
2	E	125	Total	C	N	O	S	0	1	0
			957	592	161	190	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	132	HIS	-	expression tag	UNP P22619
C	133	HIS	-	expression tag	UNP P22619
C	134	HIS	-	expression tag	UNP P22619
C	135	HIS	-	expression tag	UNP P22619
C	136	HIS	-	expression tag	UNP P22619
C	137	HIS	-	expression tag	UNP P22619
E	132	HIS	-	expression tag	UNP P22619
E	133	HIS	-	expression tag	UNP P22619
E	134	HIS	-	expression tag	UNP P22619
E	135	HIS	-	expression tag	UNP P22619
E	136	HIS	-	expression tag	UNP P22619
E	137	HIS	-	expression tag	UNP P22619

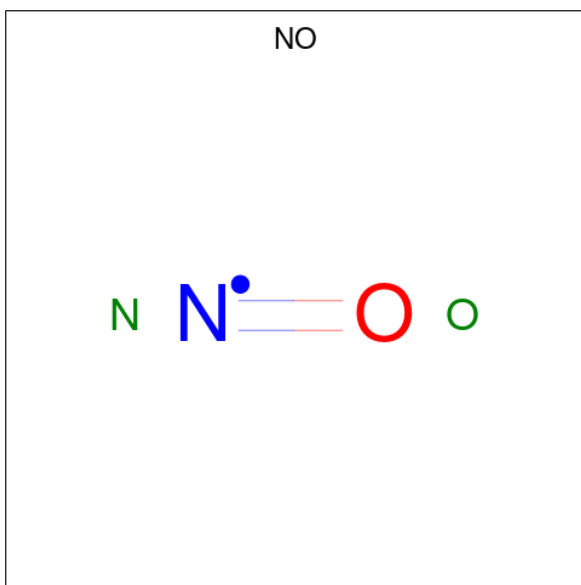
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	1	0
			2934	1859	506	561	8			
3	F	376	Total	C	N	O	S	0	0	0
			2923	1853	502	560	8			

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

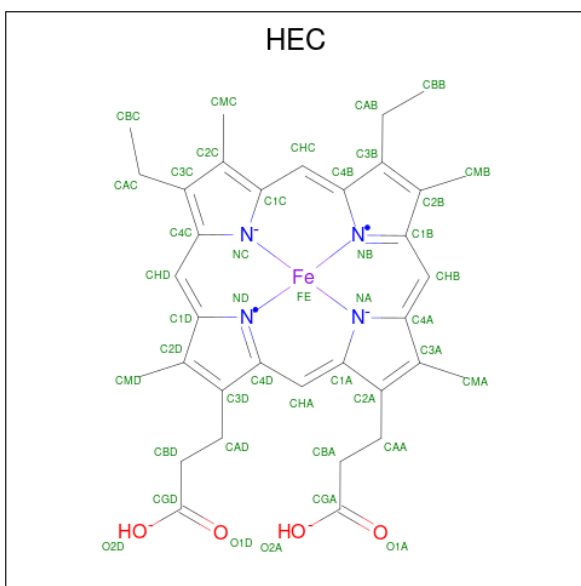
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		
4	B	1	Total	Na	0	0
			1	1		

- Molecule 5 is NITRIC OXIDE (CCD ID: NO) (formula: NO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 2	N 1	O 1	0	0
5	B	1	Total 2	N 1	O 1	0	0

- Molecule 6 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{36}\text{FeN}_4\text{O}_4$).



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

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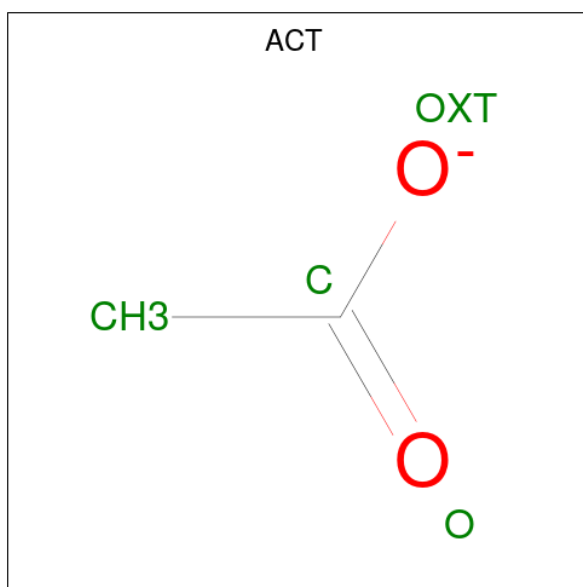
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	
6	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

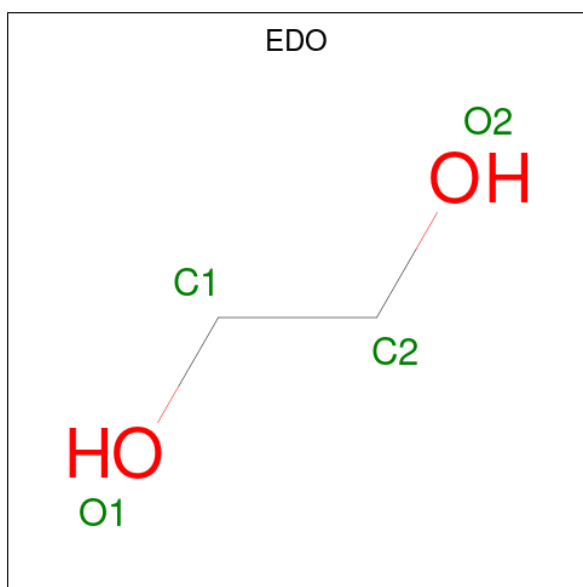
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca		
			1	1	0	0
7	B	1	Total	Ca		
			1	1	0	0

- Molecule 8 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



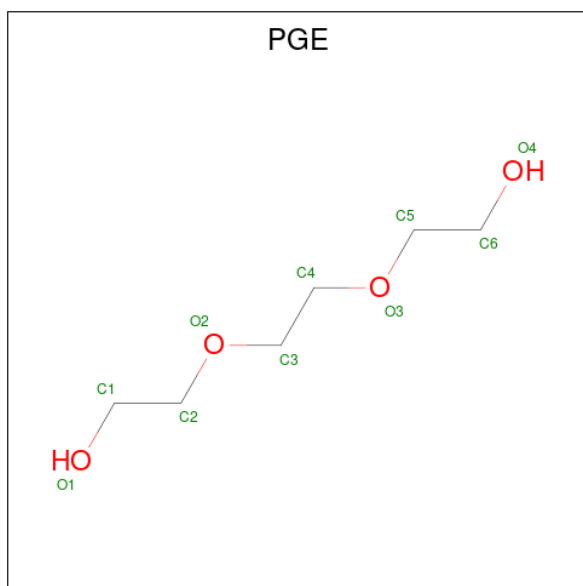
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O		
			4	2	2	0	0

- Molecule 9 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



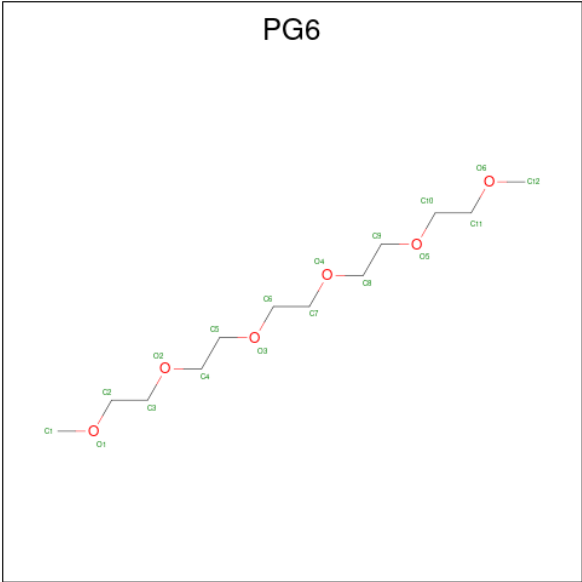
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 11 is 1-(2-METHOXY-ETHOXY)-2-{2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHANE (CCD ID: PG6) (formula: $C_{12}H_{26}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	F	1	Total	C	O	0	0
			18	12	6		

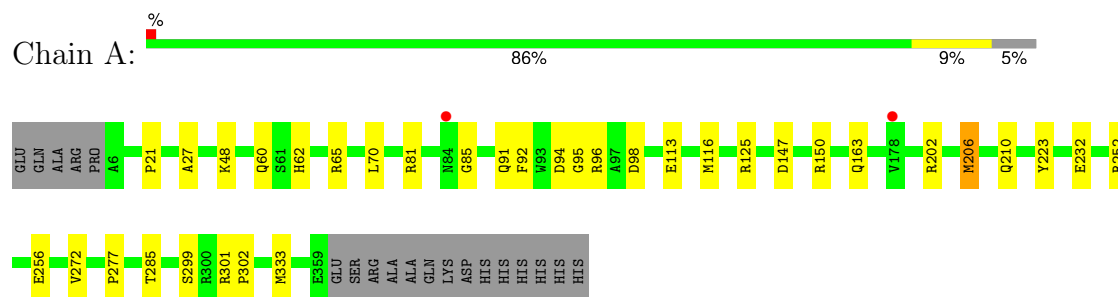
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	227	Total	O	0	0
			227	227		
12	B	247	Total	O	0	0
			247	247		
12	C	82	Total	O	0	0
			82	82		
12	D	272	Total	O	0	0
			272	272		
12	E	79	Total	O	0	0
			79	79		
12	F	315	Total	O	0	0
			315	315		

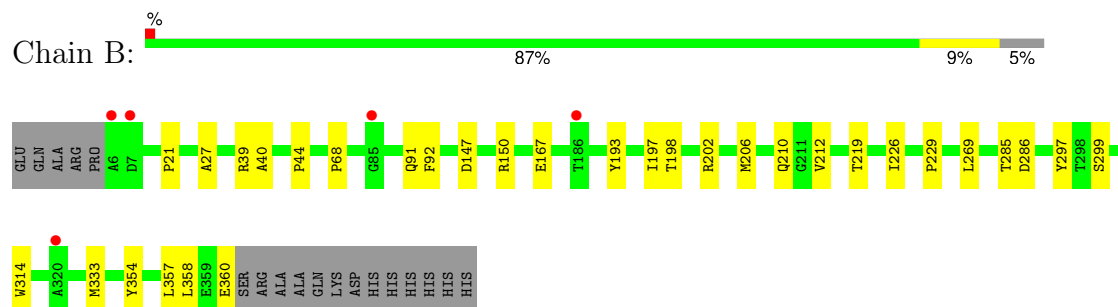
3 Residue-property plots [i](#)

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.

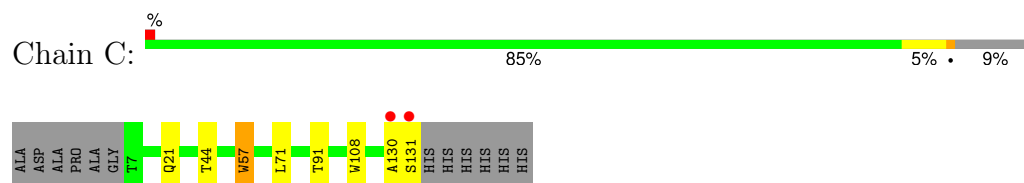
- Molecule 1: Methylamine utilization protein MauG



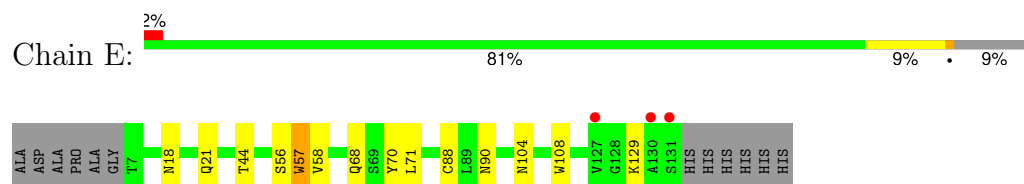
- Molecule 1: Methylamine utilization protein MauG



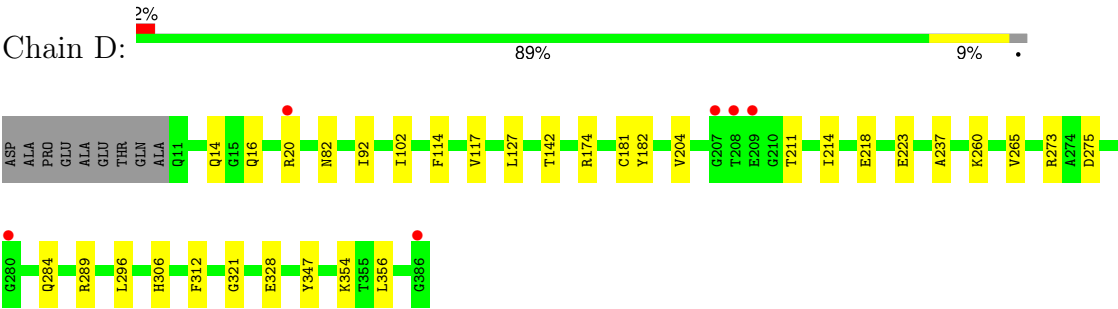
- Molecule 2: Methylamine dehydrogenase light chain



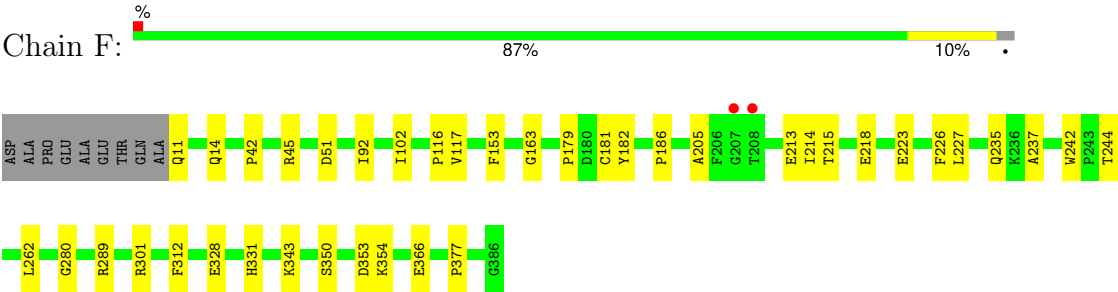
- Molecule 2: Methylamine dehydrogenase light chain



- Molecule 3: Methylamine dehydrogenase heavy chain



• Molecule 3: Methylamine dehydrogenase heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.53Å 83.52Å 107.78Å 109.94° 91.54° 105.78°	Depositor
Resolution (Å)	44.49 – 2.11 44.49 – 2.11	Depositor EDS
% Data completeness (in resolution range)	95.3 (44.49-2.11) 95.3 (44.49-2.11)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.189 , 0.242 0.194 , 0.248	Depositor DCC
R_{free} test set	4810 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14700	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PG6, HEC, EDO, 0AF, PGE, ACT, CA, NA, NO

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	0.51	0/2807	0.81	0/3809
1	B	0.51	0/2818	0.81	0/3823
2	C	0.54	0/963	0.76	0/1315
2	E	0.55	0/969	0.74	1/1323 (0.1%)
3	D	0.49	0/3011	0.73	0/4102
3	F	0.51	0/3000	0.73	0/4088
All	All	0.51	0/13568	0.77	1/18460 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	104	ASN	N-CA-C	5.14	119.51	112.88

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	2740	0	2615	20	0
1	B	2754	0	2625	21	0
2	C	954	0	858	9	0
2	E	957	0	864	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	2934	0	2820	17	0
3	F	2923	0	2808	17	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	86	0	60	2	0
6	B	86	0	60	1	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	C	4	0	3	0	0
9	F	4	0	6	0	0
10	F	10	0	14	0	0
11	F	18	0	26	0	0
12	A	227	0	0	0	0
12	B	247	0	0	0	0
12	C	82	0	0	0	0
12	D	272	0	0	2	0
12	E	79	0	0	0	0
12	F	315	0	0	0	0
All	All	14700	0	12759	89	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 (89) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:57:0AF:HE3	2:E:108:TRP:CD1	1.82	1.14
2:E:57:0AF:CE3	2:E:108:TRP:CD1	2.42	1.03
2:C:57:0AF:HE3	2:C:108:TRP:CD1	2.01	0.95
2:C:57:0AF:CE3	2:C:108:TRP:CD1	2.50	0.94
2:E:57:0AF:CE3	2:E:108:TRP:HD1	1.88	0.82
1:B:299:SER:HB2	1:B:333:MET:HG3	1.62	0.80
3:D:265:VAL:HG21	3:D:321:GLY:HA3	1.67	0.77
2:C:57:0AF:CE3	2:C:108:TRP:HD1	1.95	0.77
1:B:198:THR:HG22	2:E:58:VAL:HG13	1.71	0.73
1:A:210:GLN:HE22	2:C:44:THR:HG21	1.54	0.72
1:A:113:GLU:HG2	6:A:500:HEC:HBC2	1.75	0.68
1:A:202:ARG:HB2	1:A:206:MET:HG3	1.77	0.66
1:B:202[B]:ARG:HG2	1:B:202[B]:ARG:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:HA	1:A:252:ARG:HG3	1.84	0.60
1:A:299:SER:HB2	1:A:333:MET:HG3	1.84	0.60
1:B:198:THR:CG2	2:E:58:VAL:HG13	2.33	0.58
1:B:202[B]:ARG:HB2	1:B:206:MET:HG3	1.88	0.56
2:C:21:GLN:HE22	3:F:14:GLN:HE21	1.52	0.56
1:B:202[A]:ARG:HG2	1:B:202[A]:ARG:HH11	1.71	0.56
3:F:45:ARG:NH2	3:F:343:LYS:O	2.39	0.55
3:D:204:VAL:HG22	3:D:214:ILE:HG12	1.88	0.54
3:D:265:VAL:HG21	3:D:321:GLY:CA	2.36	0.54
3:D:265:VAL:CG2	3:D:321:GLY:HA3	2.37	0.53
2:E:57:0AF:CZ3	2:E:108:TRP:HD1	2.22	0.53
1:A:91:GLN:O	1:A:92:PHE:HB2	2.09	0.52
3:F:179:PRO:HD3	3:F:214:ILE:HD13	1.91	0.52
1:B:210:GLN:HE22	2:E:44:THR:HG21	1.75	0.51
1:A:65:ARG:HH12	1:A:94:ASP:CG	2.19	0.51
3:D:14:GLN:HE21	2:E:21:GLN:HE22	1.59	0.50
1:B:193:TYR:O	1:B:197:ILE:HG12	2.11	0.50
1:B:39:ARG:HD3	1:B:44:PRO:HB3	1.94	0.50
3:F:186:PRO:HB2	3:F:235:GLN:NE2	2.27	0.50
1:A:70:LEU:HD13	1:A:163:GLN:NE2	2.27	0.49
3:D:237:ALA:HB2	3:D:289:ARG:HG3	1.95	0.48
1:B:91:GLN:O	1:B:92:PHE:HB2	2.13	0.48
2:C:91:THR:HB	3:D:306:HIS:CE1	2.48	0.47
1:A:21:PRO:O	1:A:27:ALA:HA	2.14	0.47
1:B:357:LEU:O	1:B:360:GLU:HG2	2.14	0.47
1:A:81:ARG:CZ	1:A:85:GLY:HA2	2.45	0.47
1:B:40:ALA:HA	1:B:354:TYR:CZ	2.50	0.47
1:A:48:LYS:H	1:A:62:HIS:CE1	2.32	0.47
3:D:312:PHE:CE2	3:D:328:GLU:HG2	2.50	0.46
2:E:68:GLN:HB2	2:E:70:TYR:CE1	2.49	0.46
3:D:312:PHE:HE2	3:D:328:GLU:HG2	1.81	0.46
3:F:237:ALA:HB2	3:F:289:ARG:HG3	1.97	0.46
1:A:60:GLN:O	1:A:62:HIS:CD2	2.69	0.46
1:A:98:ASP:OD1	1:A:252:ARG:NH2	2.41	0.46
2:C:130:ALA:O	2:C:131:SER:CB	2.64	0.46
1:B:285:THR:HG22	1:B:286:ASP:OD1	2.16	0.46
2:C:57:0AF:HE3	2:C:108:TRP:CG	2.50	0.46
3:D:20[B]:ARG:NH1	12:D:496:HOH:O	2.49	0.46
3:D:273:ARG:HG2	12:D:1101:HOH:O	2.15	0.45
1:B:212:VAL:HG21	2:E:129:LYS:HG3	1.97	0.45
3:D:92:ILE:HG13	3:D:114:PHE:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:PRO:HB3	1:A:285:THR:HA	1.99	0.44
2:E:88[B]:CYS:SG	2:E:90:ASN:ND2	2.89	0.44
1:A:95:GLY:HA3	1:A:223:TYR:OH	2.18	0.44
3:F:51:ASP:HA	3:F:377:PRO:HA	2.01	0.43
3:F:350:SER:HB3	3:F:353:ASP:HB2	2.00	0.43
1:B:229:PRO:HG3	1:B:314:TRP:O	2.19	0.43
1:A:116:MET:HE1	1:A:125:ARG:HG3	2.01	0.43
2:E:57:0AF:HE3	2:E:108:TRP:CG	2.44	0.43
2:E:57:0AF:HZ3	2:E:108:TRP:HB2	2.01	0.43
3:F:331:HIS:HE1	3:F:366:GLU:OE1	2.02	0.43
1:B:210:GLN:NE2	2:E:44:THR:HG21	2.33	0.43
1:B:226:ILE:O	1:B:297:TYR:OH	2.36	0.43
3:D:82:ASN:HB3	3:D:142:THR:HB	2.00	0.43
1:A:272:VAL:HG21	6:A:600:HEC:HMA2	2.01	0.42
1:A:147:ASP:HB3	1:A:150:ARG:HB2	2.00	0.42
1:B:202[A]:ARG:HG2	1:B:202[A]:ARG:NH1	2.34	0.42
3:F:312:PHE:CE2	3:F:328:GLU:HG2	2.54	0.42
1:A:210:GLN:NE2	2:C:44:THR:HG21	2.26	0.42
1:B:147:ASP:HB3	1:B:150:ARG:HB2	2.01	0.42
3:F:226:PHE:O	3:F:244:THR:HA	2.20	0.42
3:D:347:TYR:HB3	3:D:356:LEU:HD11	2.01	0.42
3:F:153:PHE:CE1	3:F:163:GLY:HA3	2.55	0.42
3:F:227:LEU:HB3	3:F:242:TRP:NE1	2.36	0.41
3:F:153:PHE:CZ	3:F:163:GLY:HA3	2.55	0.41
3:F:181:CYS:C	3:F:182:TYR:CD1	2.98	0.41
1:B:21:PRO:O	1:B:27:ALA:HA	2.20	0.41
3:D:16:GLN:HA	2:E:18:ASN:O	2.20	0.41
3:F:205:ALA:HB3	3:F:213:GLU:HB3	2.02	0.41
3:F:280:GLY:HA3	3:F:301:ARG:CZ	2.51	0.41
2:E:57:0AF:CZ3	2:E:108:TRP:CD1	3.00	0.40
3:D:181:CYS:C	3:D:182:TYR:CD1	3.00	0.40
3:D:284:GLN:O	3:D:296:LEU:HD12	2.21	0.40
3:F:42:PRO:HG3	3:F:116:PRO:HB2	2.03	0.40
1:A:301:ARG:HA	1:A:302:PRO:HD3	1.95	0.40
1:B:68:PRO:HG2	6:B:500:HEC:HBA1	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	353/373 (95%)	344 (98%)	9 (2%)	0	100	100
1	B	354/373 (95%)	345 (98%)	9 (2%)	0	100	100
2	C	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
2	E	123/137 (90%)	120 (98%)	3 (2%)	0	100	100
3	D	375/385 (97%)	364 (97%)	10 (3%)	1 (0%)	36	36
3	F	374/385 (97%)	362 (97%)	11 (3%)	1 (0%)	36	36
All	All	1701/1790 (95%)	1656 (97%)	43 (2%)	2 (0%)	48	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	102	ILE
3	F	102	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	277/292 (95%)	274 (99%)	3 (1%)	65	74
1	B	278/292 (95%)	274 (99%)	4 (1%)	59	67
2	C	104/112 (93%)	103 (99%)	1 (1%)	68	76
2	E	105/112 (94%)	103 (98%)	2 (2%)	50	57
3	D	305/310 (98%)	296 (97%)	9 (3%)	36	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	F	304/310 (98%)	296 (97%)	8 (3%)	40 45
All	All	1373/1428 (96%)	1346 (98%)	27 (2%)	48 55

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	206	MET
1	A	232	GLU
1	A	256	GLU
1	B	167	GLU
1	B	219	THR
1	B	269	LEU
1	B	358	LEU
2	C	71	LEU
3	D	117	VAL
3	D	127	LEU
3	D	174	ARG
3	D	211	THR
3	D	218	GLU
3	D	223	GLU
3	D	260	LYS
3	D	275	ASP
3	D	354	LYS
2	E	56	SER
2	E	71	LEU
3	F	11	GLN
3	F	92	ILE
3	F	117	VAL
3	F	215	THR
3	F	218	GLU
3	F	223	GLU
3	F	262	LEU
3	F	354	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	29	GLN
1	A	62	HIS
1	A	84	ASN

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Mol	Chain	Res	Type
1	A	91	GLN
1	A	163	GLN
1	A	210	GLN
1	B	29	GLN
1	B	91	GLN
1	B	163	GLN
1	B	210	GLN
2	C	21	GLN
2	C	45	ASN
2	E	21	GLN
2	E	68	GLN
2	E	90	ASN
3	F	61	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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
2	0AF	C	57	2	15,16,17	2.49	7 (46%)	14,22,24	1.56	3 (21%)
2	0AF	E	57	2	15,16,17	2.83	5 (33%)	14,22,24	1.52	5 (35%)

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
2	0AF	C	57	2	-	0/5/6/8	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	0AF	E	57	2	-	0/5/6/8	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	57	0AF	CD2-CE2	-6.14	1.33	1.41
2	C	57	0AF	CD2-CE2	-6.03	1.33	1.41
2	E	57	0AF	CD2-CG	-5.75	1.34	1.44
2	E	57	0AF	CE2-NE1	-4.65	1.30	1.37
2	C	57	0AF	CD2-CG	-3.74	1.37	1.44
2	E	57	0AF	CD1-NE1	-3.65	1.31	1.37
2	C	57	0AF	CE2-NE1	-3.45	1.32	1.37
2	C	57	0AF	O1-CZ2	-2.90	1.30	1.36
2	C	57	0AF	CD1-NE1	-2.88	1.32	1.37
2	E	57	0AF	O1-CZ2	-2.15	1.32	1.36
2	C	57	0AF	CE2-CZ2	-2.03	1.35	1.40
2	C	57	0AF	CE3-CD2	-2.01	1.36	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	57	0AF	CZ3-CH2-CZ2	-3.41	115.84	120.05
2	C	57	0AF	CH2-CZ2-CE2	3.28	124.37	118.69
2	E	57	0AF	CE3-CD2-CG	-2.83	129.63	133.85
2	E	57	0AF	CH2-CZ2-CE2	2.41	122.86	118.69
2	E	57	0AF	CG-CD1-NE1	-2.39	107.69	110.31
2	C	57	0AF	CG-CD1-NE1	-2.07	108.04	110.31
2	E	57	0AF	CE3-CD2-CE2	2.03	121.42	119.14
2	E	57	0AF	CE2-NE1-CD1	2.02	110.67	108.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	57	0AF	4	0
2	E	57	0AF	7	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	NO	A	375	6	0,1,1	-	-	-		
6	HEC	A	500	1,5	50,50,50	2.74	27 (54%)	68,82,82	1.85	21 (30%)
5	NO	B	375	6	0,1,1	-	-	-		
10	PGE	F	387	-	9,9,9	0.49	0	8,8,8	0.22	0
8	ACT	C	138	-	3,3,3	0.74	0	3,3,3	1.42	0
6	HEC	B	600	1	50,50,50	2.62	25 (50%)	68,82,82	1.81	19 (27%)
11	PG6	F	388	-	17,17,17	0.51	0	16,16,16	0.16	0
6	HEC	A	600	1	50,50,50	2.69	25 (50%)	68,82,82	1.79	19 (27%)
6	HEC	B	500	1,5	50,50,50	2.69	28 (56%)	68,82,82	1.78	20 (29%)
9	EDO	F	1	-	3,3,3	0.49	0	2,2,2	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEC	A	500	1,5	1/1/3/7	2/14/54/54	-
11	PG6	F	388	-	-	5/15/15/15	-
10	PGE	F	387	-	-	3/7/7/7	-
6	HEC	B	600	1	1/1/3/7	4/14/54/54	-
6	HEC	A	600	1	1/1/3/7	2/14/54/54	-
6	HEC	B	500	1,5	1/1/3/7	2/14/54/54	-
9	EDO	F	1	-	-	1/1/1/1	-

All (105) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	500	HEC	CHA-C1A	5.53	1.49	1.38
6	A	600	HEC	CHA-C1A	5.25	1.48	1.38
6	B	500	HEC	CHA-C1A	5.25	1.48	1.38
6	A	500	HEC	CHB-C4A	5.18	1.48	1.38
6	A	500	HEC	CHD-C1D	5.11	1.48	1.38
6	B	500	HEC	CHD-C1D	5.10	1.48	1.38
6	B	600	HEC	CHA-C1A	5.10	1.48	1.38
6	A	600	HEC	CHB-C4A	5.02	1.48	1.38
6	B	500	HEC	CHB-C4A	5.01	1.48	1.38
6	A	600	HEC	CHD-C1D	4.96	1.48	1.38
6	B	600	HEC	CHB-C4A	4.86	1.47	1.38
6	A	500	HEC	FE-NB	4.82	2.09	1.94
6	A	500	HEC	CHC-C4B	4.73	1.48	1.38
6	B	600	HEC	FE-NB	4.73	2.09	1.94
6	A	500	HEC	FE-ND	4.71	2.09	1.94
6	B	500	HEC	FE-ND	4.71	2.09	1.94
6	A	600	HEC	CHC-C4B	4.70	1.47	1.38
6	B	600	HEC	CHC-C4B	4.69	1.47	1.38
6	B	500	HEC	CHC-C4B	4.67	1.47	1.38
6	B	500	HEC	FE-NB	4.61	2.09	1.94
6	B	500	HEC	FE-NC	4.60	2.10	1.95
6	A	600	HEC	FE-NB	4.55	2.08	1.94
6	A	600	HEC	FE-ND	4.54	2.08	1.94
6	B	600	HEC	FE-ND	4.47	2.08	1.94
6	A	600	HEC	FE-NC	4.45	2.09	1.95
6	B	600	HEC	CHD-C1D	4.42	1.47	1.38
6	A	500	HEC	FE-NC	4.41	2.09	1.95
6	B	600	HEC	FE-NA	4.29	2.09	1.95
6	A	500	HEC	FE-NA	4.29	2.09	1.95
6	B	600	HEC	FE-NC	4.26	2.09	1.95
6	A	500	HEC	CHA-C4D	4.26	1.48	1.39
6	A	600	HEC	FE-NA	4.23	2.09	1.95
6	A	600	HEC	CHA-C4D	4.21	1.48	1.39
6	B	600	HEC	CHA-C4D	4.16	1.48	1.39
6	A	600	HEC	CHC-C1C	4.14	1.48	1.39
6	A	500	HEC	CHC-C1C	4.03	1.48	1.39
6	A	600	HEC	CHD-C4C	4.01	1.48	1.39
6	B	500	HEC	CHA-C4D	4.01	1.48	1.39
6	B	500	HEC	FE-NA	3.99	2.08	1.95
6	A	500	HEC	CHD-C4C	3.94	1.48	1.39
6	B	500	HEC	CHB-C1B	3.94	1.48	1.39
6	B	600	HEC	CHC-C1C	3.92	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	500	HEC	CHC-C1C	3.87	1.48	1.39
6	A	500	HEC	CHB-C1B	3.79	1.47	1.39
6	B	500	HEC	CHD-C4C	3.75	1.47	1.39
6	B	600	HEC	CHD-C4C	3.73	1.47	1.39
6	A	600	HEC	CHB-C1B	3.67	1.47	1.39
6	B	600	HEC	CHB-C1B	3.63	1.47	1.39
6	B	500	HEC	C4B-NB	-3.59	1.34	1.40
6	A	600	HEC	C4B-NB	-3.50	1.34	1.40
6	B	500	HEC	C1D-ND	-3.47	1.34	1.40
6	A	500	HEC	C4B-NB	-3.46	1.34	1.40
6	A	500	HEC	C1D-ND	-3.31	1.34	1.40
6	A	600	HEC	C1D-ND	-3.27	1.34	1.40
6	B	600	HEC	C4B-NB	-3.23	1.34	1.40
6	B	600	HEC	C1D-ND	-3.17	1.34	1.40
6	A	600	HEC	C4A-NA	-3.13	1.33	1.39
6	A	600	HEC	C4C-NC	-3.12	1.33	1.39
6	B	600	HEC	C4A-NA	-3.00	1.34	1.39
6	A	500	HEC	C1C-NC	-2.97	1.34	1.39
6	A	600	HEC	C1C-NC	-2.95	1.34	1.39
6	A	500	HEC	C1A-NA	-2.93	1.34	1.39
6	A	600	HEC	C1A-NA	-2.86	1.34	1.39
6	A	500	HEC	C4A-NA	-2.84	1.34	1.39
6	B	500	HEC	C4A-NA	-2.81	1.34	1.39
6	A	500	HEC	C4C-NC	-2.80	1.34	1.39
6	B	600	HEC	C4C-NC	-2.80	1.34	1.39
6	B	500	HEC	C1C-NC	-2.76	1.34	1.39
6	A	500	HEC	C1C-C2C	2.62	1.49	1.43
6	A	600	HEC	C1B-NB	-2.61	1.33	1.38
6	B	500	HEC	C4C-C3C	2.61	1.49	1.44
6	B	500	HEC	C1A-NA	-2.61	1.34	1.39
6	B	600	HEC	C1C-NC	-2.61	1.34	1.39
6	B	500	HEC	C4C-NC	-2.60	1.34	1.39
6	B	600	HEC	C1C-C2C	2.59	1.49	1.43
6	B	500	HEC	C1C-C2C	2.57	1.49	1.43
6	B	600	HEC	C1A-NA	-2.55	1.34	1.39
6	B	600	HEC	C4B-C3B	2.52	1.49	1.45
6	A	500	HEC	C1A-C2A	2.52	1.49	1.45
6	A	500	HEC	C1B-C2B	2.51	1.49	1.44
6	B	600	HEC	C4D-ND	-2.50	1.33	1.38
6	A	600	HEC	C4B-C3B	2.47	1.49	1.45
6	B	500	HEC	C4D-ND	-2.39	1.34	1.38
6	A	500	HEC	C4B-C3B	2.38	1.49	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	500	HEC	C4D-C3D	2.38	1.49	1.45
6	A	600	HEC	C1C-C2C	2.36	1.48	1.43
6	B	600	HEC	C4D-C3D	2.36	1.49	1.45
6	B	600	HEC	C1A-C2A	2.36	1.49	1.45
6	A	500	HEC	C4C-C3C	2.35	1.49	1.44
6	B	500	HEC	C1A-C2A	2.35	1.49	1.45
6	A	600	HEC	C4D-ND	-2.33	1.34	1.38
6	A	500	HEC	C4D-ND	-2.33	1.34	1.38
6	A	600	HEC	C1A-C2A	2.33	1.49	1.45
6	A	500	HEC	C1B-NB	-2.32	1.34	1.38
6	A	500	HEC	C1D-C2D	2.27	1.49	1.44
6	A	600	HEC	C4C-C3C	2.26	1.49	1.44
6	B	500	HEC	C4D-C3D	2.21	1.48	1.45
6	B	600	HEC	C1B-NB	-2.18	1.34	1.38
6	A	600	HEC	C1D-C2D	2.17	1.48	1.44
6	B	500	HEC	C4B-C3B	2.16	1.48	1.45
6	B	600	HEC	C4C-C3C	2.14	1.48	1.44
6	B	500	HEC	C1B-NB	-2.11	1.34	1.38
6	B	500	HEC	O2A-CGA	-2.05	1.24	1.30
6	B	500	HEC	C1D-C2D	2.03	1.48	1.44
6	B	500	HEC	C4A-C3A	2.02	1.49	1.45

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	600	HEC	C2B-C1B-NB	4.04	114.57	109.90
6	A	600	HEC	C2B-C1B-NB	3.94	114.46	109.90
6	A	500	HEC	C3B-C4B-NB	3.87	114.42	110.17
6	B	600	HEC	C2D-C1D-ND	3.87	114.29	109.84
6	B	500	HEC	C3C-C4C-NC	3.81	114.38	110.15
6	B	500	HEC	C3D-C4D-ND	3.72	113.95	110.35
6	A	500	HEC	C3C-C4C-NC	3.66	114.22	110.15
6	B	500	HEC	C2A-C1A-NA	3.65	113.85	110.32
6	B	600	HEC	C3C-C4C-NC	3.65	114.20	110.15
6	A	500	HEC	C2B-C1B-NB	3.64	114.11	109.90
6	B	500	HEC	C2D-C1D-ND	3.60	113.97	109.84
6	A	500	HEC	C2D-C1D-ND	3.57	113.94	109.84
6	B	600	HEC	C1D-C2D-C3D	-3.53	103.27	106.98
6	A	600	HEC	C3D-C4D-ND	3.53	113.76	110.35
6	A	600	HEC	C2A-C1A-NA	3.47	113.67	110.32
6	B	600	HEC	CBD-CAD-C3D	-3.37	103.21	112.53
6	A	600	HEC	C2D-C1D-ND	3.36	113.70	109.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	600	HEC	C3B-C4B-NB	3.32	113.81	110.17
6	B	500	HEC	C2B-C1B-NB	3.31	113.72	109.90
6	B	500	HEC	C3B-C4B-NB	3.28	113.77	110.17
6	B	600	HEC	C2A-C1A-NA	3.24	113.45	110.32
6	A	500	HEC	C3D-C4D-ND	3.20	113.44	110.35
6	A	600	HEC	C3C-C4C-NC	3.19	113.69	110.15
6	A	600	HEC	C3B-C4B-NB	3.18	113.66	110.17
6	A	600	HEC	CBD-CAD-C3D	-3.17	103.77	112.53
6	A	500	HEC	C2A-C1A-NA	3.15	113.37	110.32
6	A	500	HEC	C1D-C2D-C3D	-3.05	103.77	106.98
6	B	600	HEC	C1B-C2B-C3B	-3.02	103.81	106.98
6	A	500	HEC	CHA-C1A-NA	-3.01	121.17	124.45
6	A	600	HEC	C1B-C2B-C3B	-2.96	103.87	106.98
6	A	600	HEC	C1D-C2D-C3D	-2.95	103.87	106.98
6	A	500	HEC	CHB-C1B-NB	-2.90	121.30	124.42
6	A	500	HEC	C1B-C2B-C3B	-2.86	103.97	106.98
6	B	500	HEC	C1B-C2B-C3B	-2.82	104.01	106.98
6	B	500	HEC	C1D-C2D-C3D	-2.81	104.03	106.98
6	B	500	HEC	C2C-C1C-NC	2.71	114.49	110.14
6	A	500	HEC	C2C-C1C-NC	2.68	114.43	110.14
6	A	500	HEC	C1C-C2C-C3C	-2.66	103.78	106.82
6	A	500	HEC	CBD-CAD-C3D	-2.62	105.30	112.53
6	B	600	HEC	C3D-C4D-ND	2.61	112.87	110.35
6	A	500	HEC	CHD-C1D-ND	-2.58	121.18	124.37
6	A	600	HEC	CHB-C4A-NA	-2.55	121.67	124.45
6	A	600	HEC	CHC-C4B-NB	-2.48	121.29	124.37
6	B	500	HEC	C1A-C2A-C3A	-2.48	103.85	107.11
6	B	500	HEC	CHA-C1A-NA	-2.48	121.76	124.45
6	B	500	HEC	CHA-C4D-ND	-2.45	121.78	124.42
6	A	600	HEC	C3A-C4A-NA	2.45	114.17	109.64
6	A	500	HEC	CHA-C4D-ND	-2.43	121.81	124.42
6	A	600	HEC	CHA-C1A-NA	-2.42	121.82	124.45
6	A	600	HEC	C1C-C2C-C3C	-2.41	104.05	106.82
6	A	600	HEC	CAB-C3B-C4B	2.40	127.92	124.79
6	A	500	HEC	CHC-C4B-NB	-2.40	121.40	124.37
6	B	500	HEC	CHB-C4A-NA	-2.40	121.84	124.45
6	A	600	HEC	C1A-C2A-C3A	-2.36	104.00	107.11
6	A	500	HEC	C1A-C2A-C3A	-2.36	104.00	107.11
6	B	600	HEC	C3A-C4A-NA	2.36	113.99	109.64
6	B	600	HEC	CHA-C1A-NA	-2.33	121.92	124.45
6	B	500	HEC	C1C-C2C-C3C	-2.33	104.15	106.82
6	B	600	HEC	CAD-CBD-CGD	-2.31	107.53	113.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	600	HEC	CHD-C1D-ND	-2.31	121.51	124.37
6	B	500	HEC	CHB-C1B-NB	-2.30	121.95	124.42
6	A	600	HEC	C2C-C1C-NC	2.28	113.80	110.14
6	B	500	HEC	CAC-C3C-C4C	2.26	128.03	124.91
6	A	600	HEC	CHB-C1B-NB	-2.25	122.00	124.42
6	B	500	HEC	CBD-CAD-C3D	-2.24	106.35	112.53
6	B	600	HEC	CBA-CAA-C2A	-2.20	106.45	112.53
6	B	600	HEC	C1A-C2A-C3A	-2.15	104.28	107.11
6	A	500	HEC	C3A-C4A-NA	2.14	113.60	109.64
6	B	600	HEC	C1C-C2C-C3C	-2.10	104.41	106.82
6	B	500	HEC	C3A-C4A-NA	2.09	113.51	109.64
6	B	600	HEC	C2C-C1C-NC	2.08	113.48	110.14
6	B	500	HEC	C4C-C3C-C2C	-2.08	103.64	106.87
6	B	600	HEC	CAB-C3B-C4B	2.08	127.49	124.79
6	B	600	HEC	CHC-C4B-NB	-2.06	121.82	124.37
6	B	500	HEC	CHC-C4B-NB	-2.05	121.83	124.37
6	A	500	HEC	C4B-C3B-C2B	-2.04	103.93	106.89
6	A	500	HEC	O1D-CGD-CBD	-2.03	116.67	123.09
6	B	600	HEC	CHA-C4D-ND	-2.02	122.25	124.42
6	A	500	HEC	CMD-C2D-C1D	2.01	128.18	125.03

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	500	HEC	NA
6	A	600	HEC	NA
6	B	500	HEC	NA
6	B	600	HEC	NA

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	F	388	PG6	O5-C10-C11-O6
9	F	1	EDO	O1-C1-C2-O2
11	F	388	PG6	O1-C2-C3-O2
11	F	388	PG6	C3-C2-O1-C1
11	F	388	PG6	C4-C5-O3-C6
10	F	387	PGE	C4-C3-O2-C2
11	F	388	PG6	C7-C6-O3-C5
6	B	600	HEC	CAD-CBD-CGD-O1D
6	B	600	HEC	C2C-C3C-CAC-CBC
6	B	600	HEC	CAD-CBD-CGD-O2D

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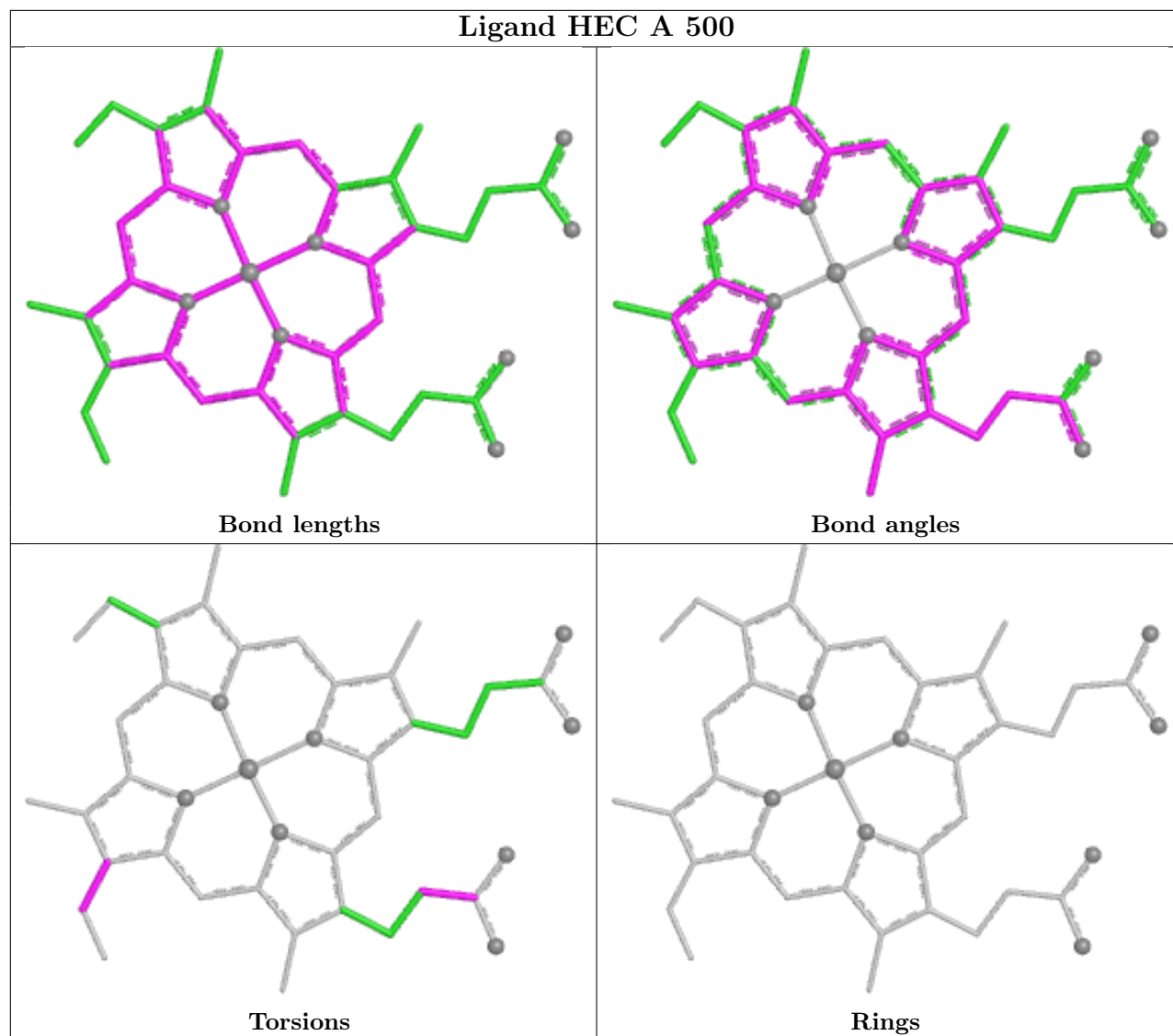
Mol	Chain	Res	Type	Atoms
6	B	600	HEC	C4C-C3C-CAC-CBC
10	F	387	PGE	C1-C2-O2-C3
6	A	600	HEC	CAD-CBD-CGD-O2D
6	B	500	HEC	CAD-CBD-CGD-O2D
6	A	600	HEC	CAD-CBD-CGD-O1D
6	B	500	HEC	CAD-CBD-CGD-O1D
10	F	387	PGE	O1-C1-C2-O2
6	A	500	HEC	C4C-C3C-CAC-CBC
6	A	500	HEC	CAD-CBD-CGD-O2D

There are no ring outliers.

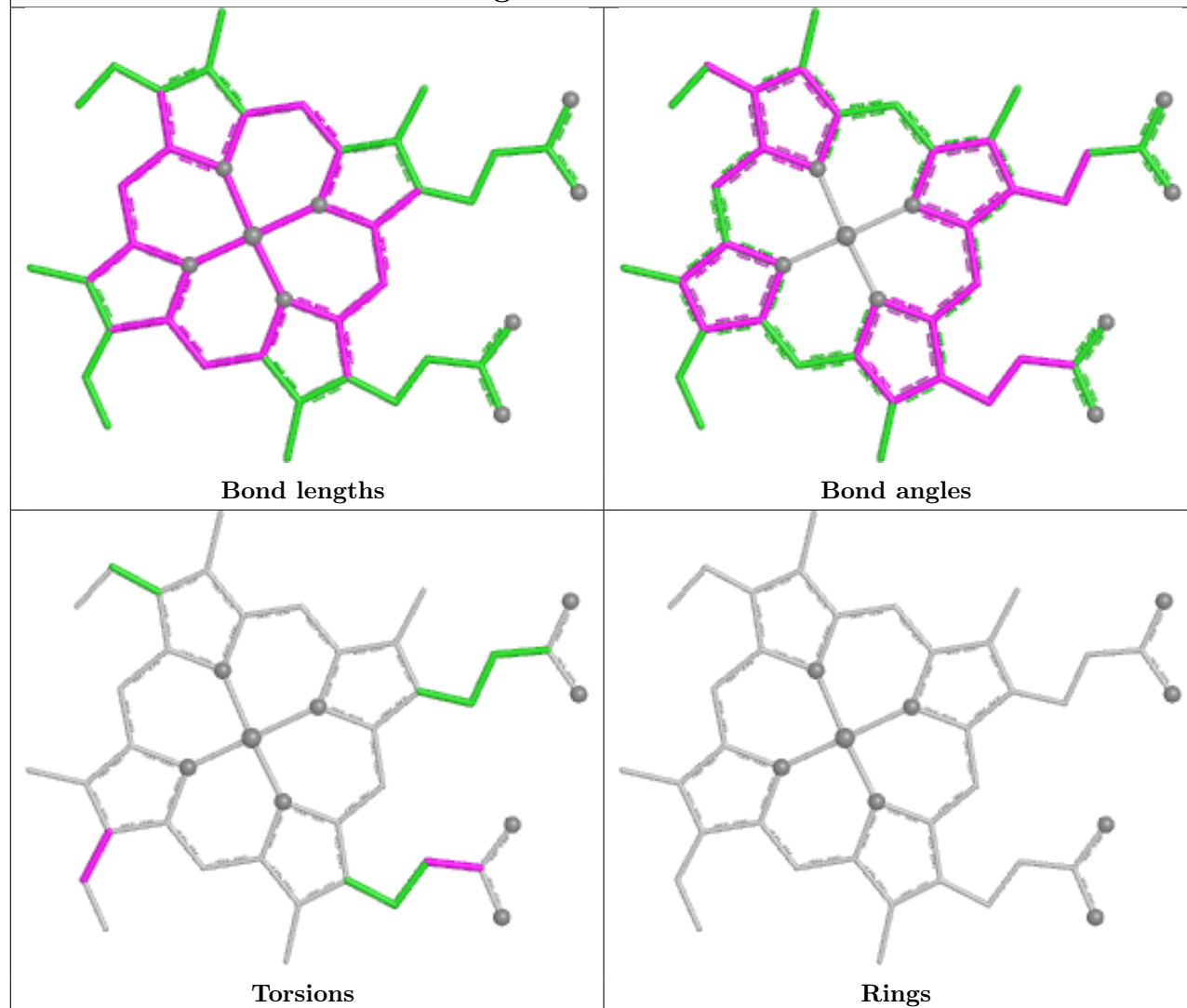
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	500	HEC	1	0
6	A	600	HEC	1	0
6	B	500	HEC	1	0

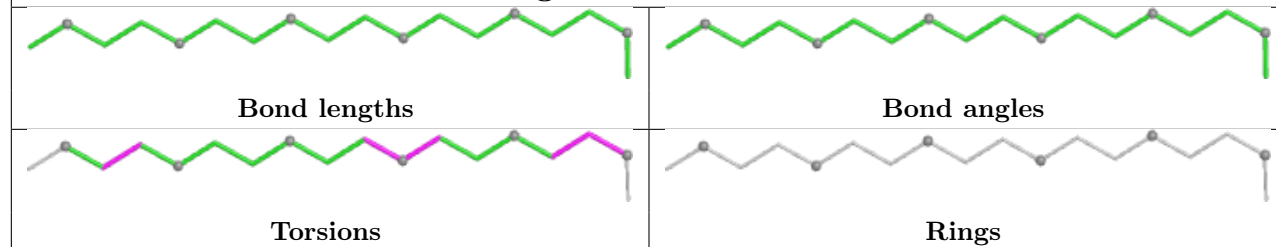
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

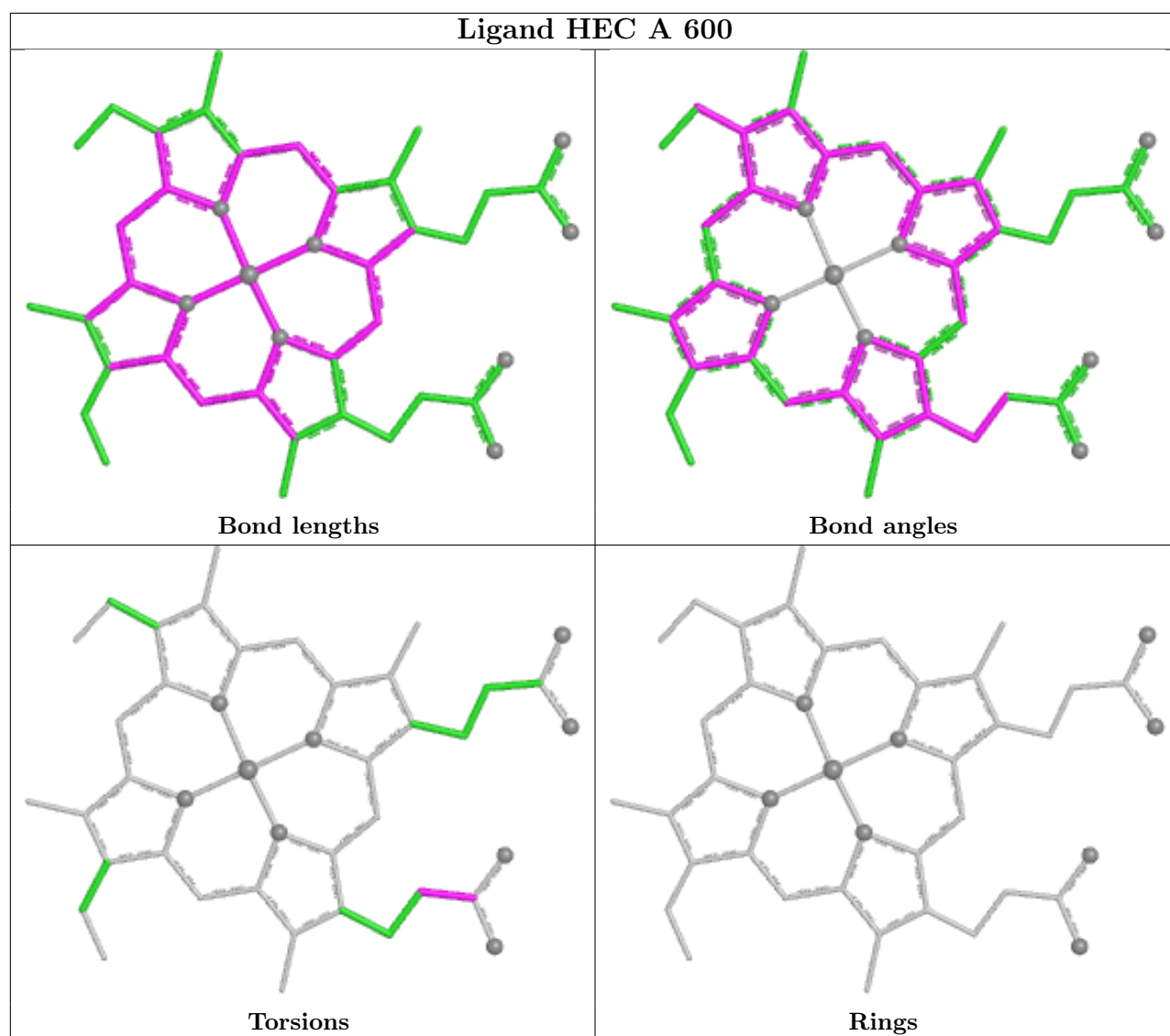


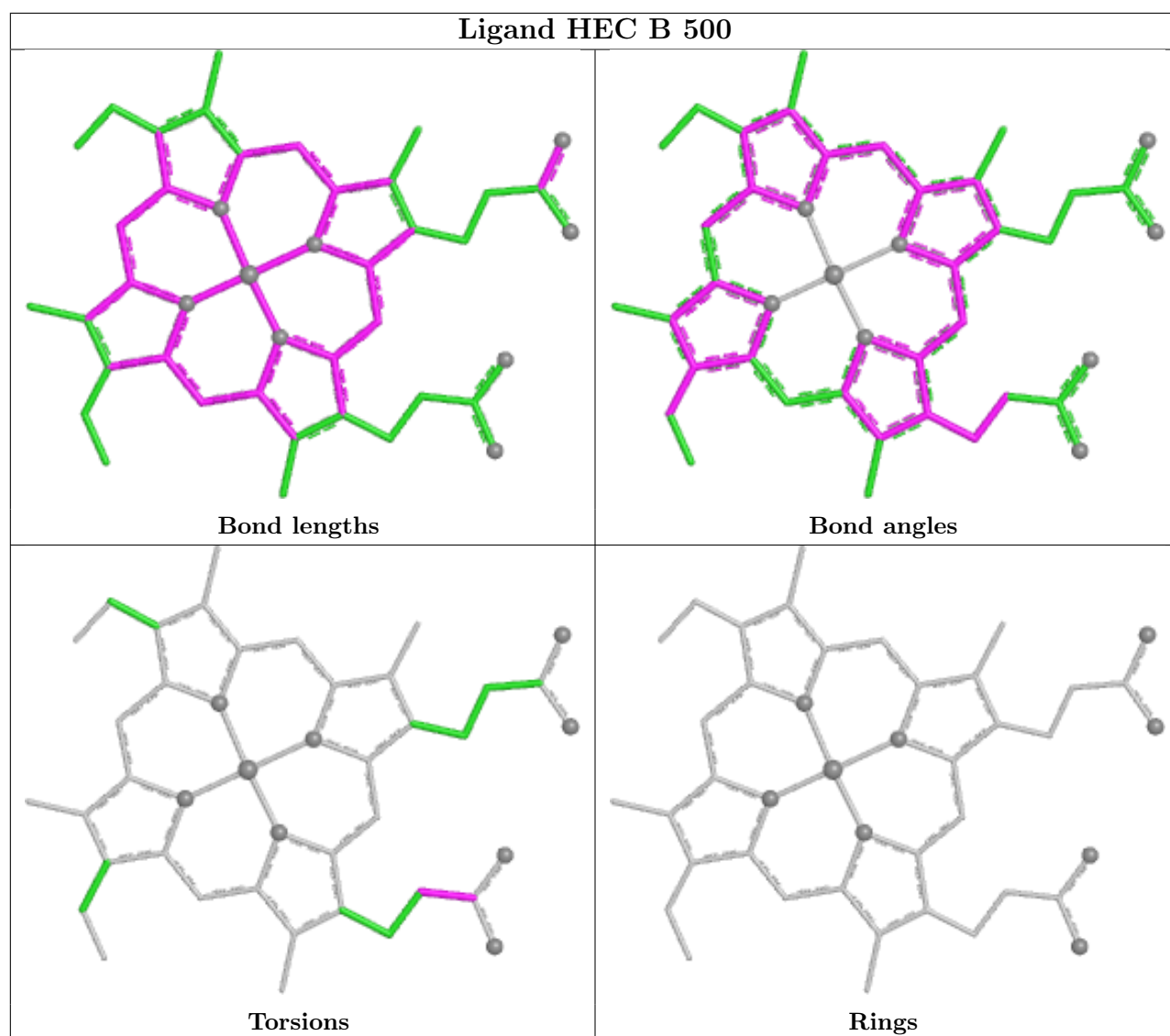
Ligand HEC B 600



Ligand PG6 F 388







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	354/373 (94%)	0.27	2 (0%) 85 87	14, 26, 35, 45	1 (0%)
1	B	355/373 (95%)	0.22	5 (1%) 73 76	12, 26, 38, 49	1 (0%)
2	C	124/137 (90%)	0.09	2 (1%) 70 73	18, 22, 31, 45	0
2	E	124/137 (90%)	0.08	3 (2%) 59 62	13, 21, 30, 44	1 (0%)
3	D	376/385 (97%)	0.19	6 (1%) 70 73	14, 26, 39, 50	1 (0%)
3	F	376/385 (97%)	0.01	2 (0%) 87 89	15, 22, 33, 41	0
All	All	1709/1790 (95%)	0.16	20 (1%) 76 79	12, 25, 36, 50	4 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	131	SER	4.4
1	B	6	ALA	4.3
3	D	209	GLU	4.0
3	D	207	GLY	3.8
3	D	208	THR	3.5
1	B	7	ASP	3.1
3	D	20[A]	ARG	3.1
1	A	84	ASN	2.8
2	E	130	ALA	2.8
2	C	130	ALA	2.6
3	F	208	THR	2.5
2	E	131	SER	2.4
3	D	280	GLY	2.3
2	E	127	VAL	2.2
3	D	386	GLY	2.2
1	B	186	THR	2.1
1	A	178	VAL	2.1
1	B	320	ALA	2.1
3	F	207	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	85	GLY	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(Å ²)	Q<0.9
2	0AF	E	57	15/16	0.81	0.14	28,30,33,33	0
2	0AF	C	57	15/16	0.87	0.11	27,30,32,33	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

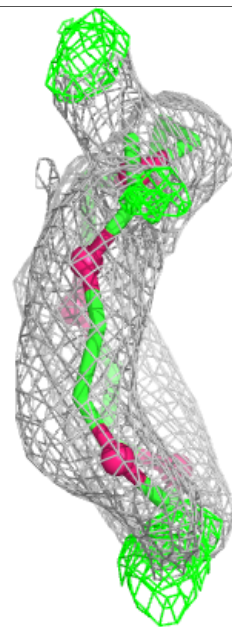
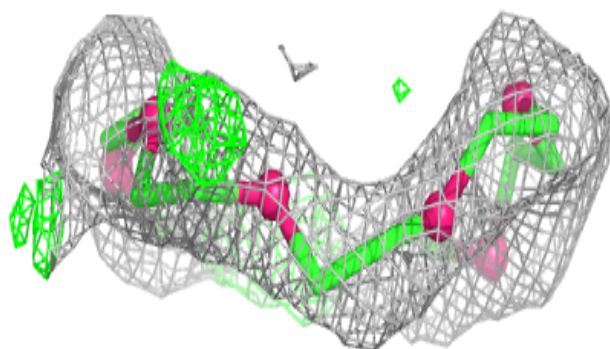
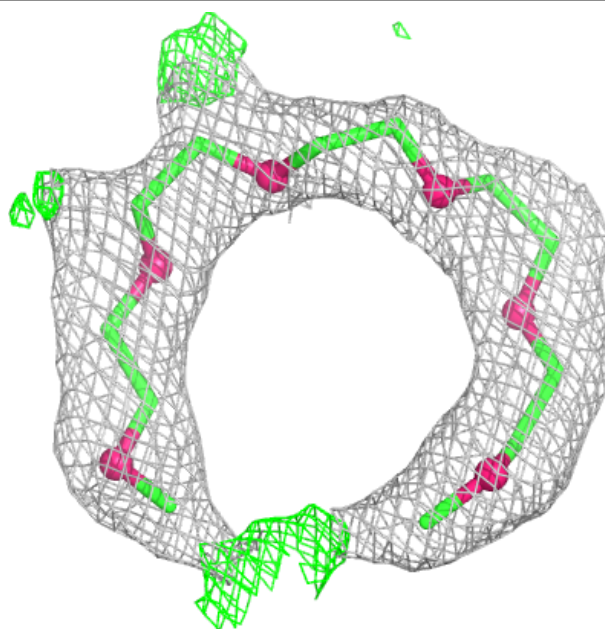
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	PGE	F	387	10/10	0.72	0.21	63,65,65,65	0
9	EDO	F	1	4/4	0.78	0.18	33,37,37,38	0
8	ACT	C	138	4/4	0.79	0.16	32,32,33,33	0
11	PG6	F	388	18/18	0.80	0.16	45,49,53,53	0
4	NA	A	374	1/1	0.94	0.06	35,35,35,35	0
5	NO	B	375	2/2	0.95	0.09	25,25,25,25	0
6	HEC	A	600	43/43	0.96	0.08	18,19,20,21	0
6	HEC	B	600	43/43	0.96	0.08	16,18,21,22	0
5	NO	A	375	2/2	0.96	0.12	21,21,21,22	0
6	HEC	B	500	43/43	0.97	0.07	18,20,22,22	0
6	HEC	A	500	43/43	0.97	0.08	19,21,22,22	0
4	NA	B	374	1/1	0.97	0.04	28,28,28,28	0
7	CA	A	400	1/1	0.99	0.03	20,20,20,20	0
7	CA	B	400	1/1	0.99	0.02	21,21,21,21	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.

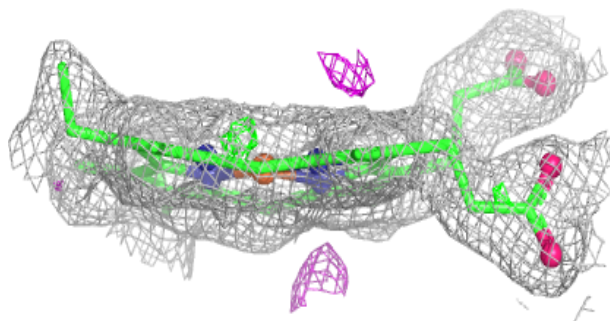
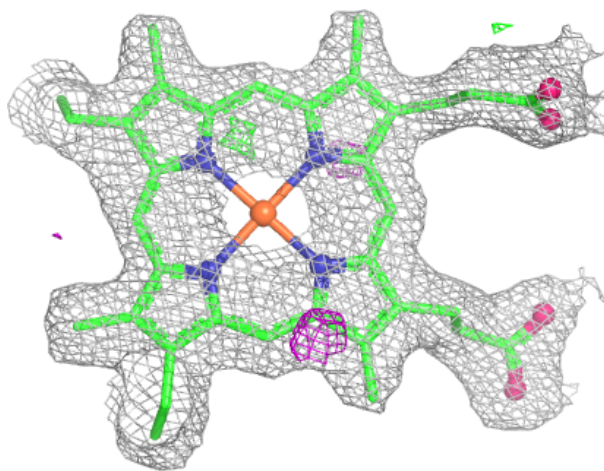
Electron density around PG6 F 388:

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



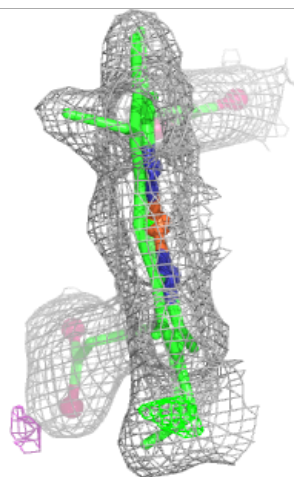
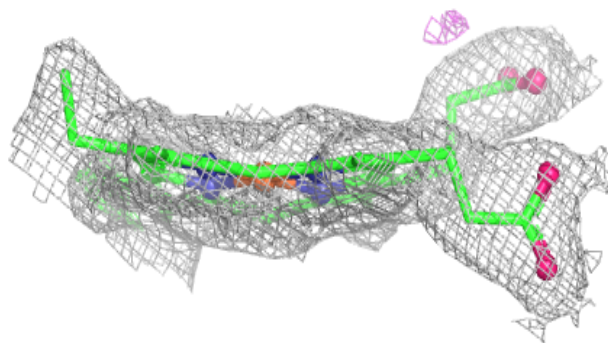
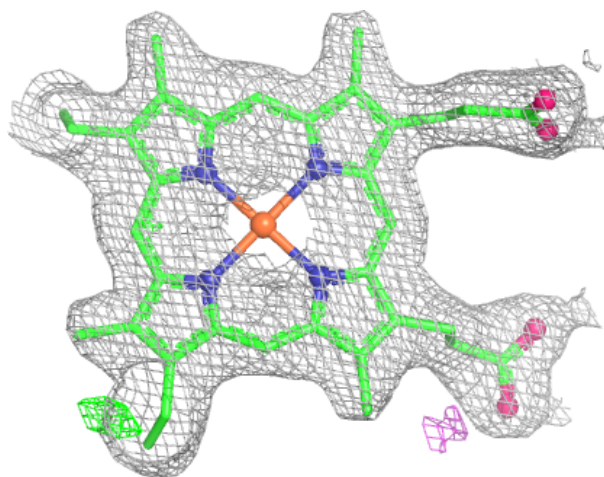
Electron density around HEC A 600:

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



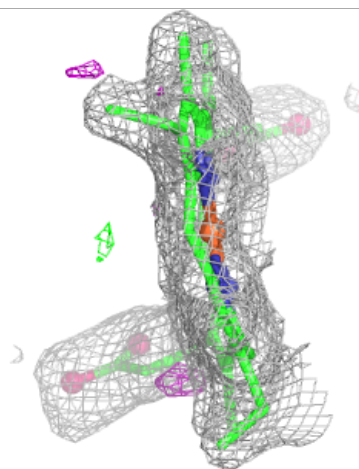
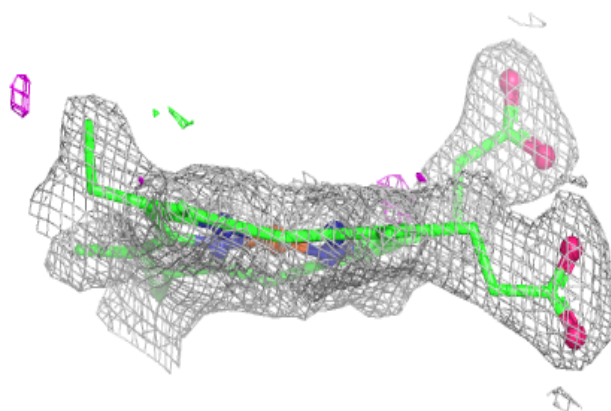
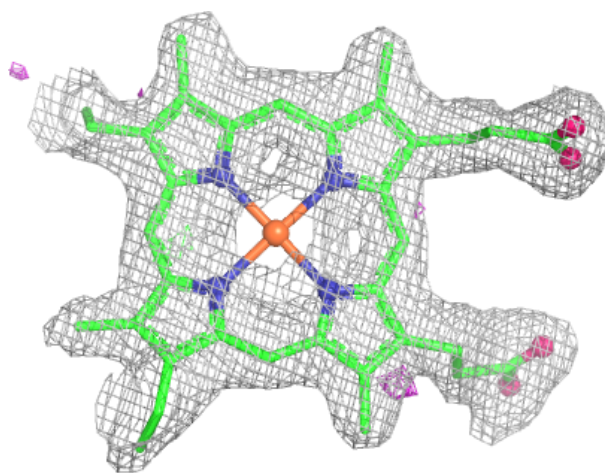
Electron density around HEC B 600:

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



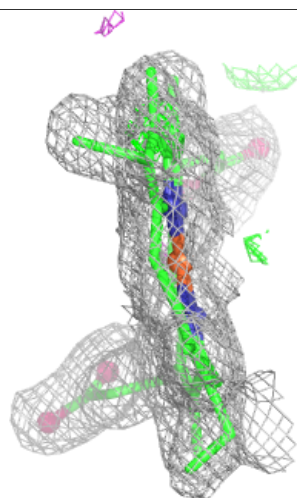
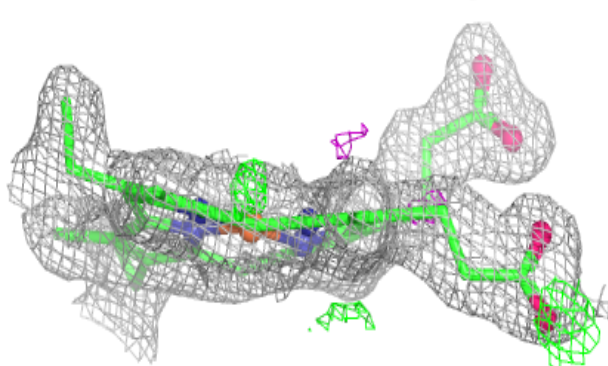
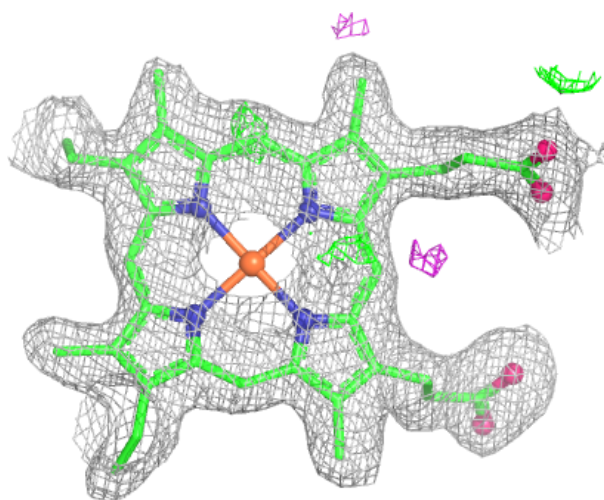
Electron density around HEC B 500:

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



Electron density around HEC A 500:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.