



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 10:06 pm BST

PDB ID : 6NT1
Title : Catalase 3 from N.Crassa in ferrous state (2.89 MGy)
Authors : Zarate-Romero, A.; Rudino-Pinera, E.; Stojanoff, V.
Deposited on : 2019-01-27
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

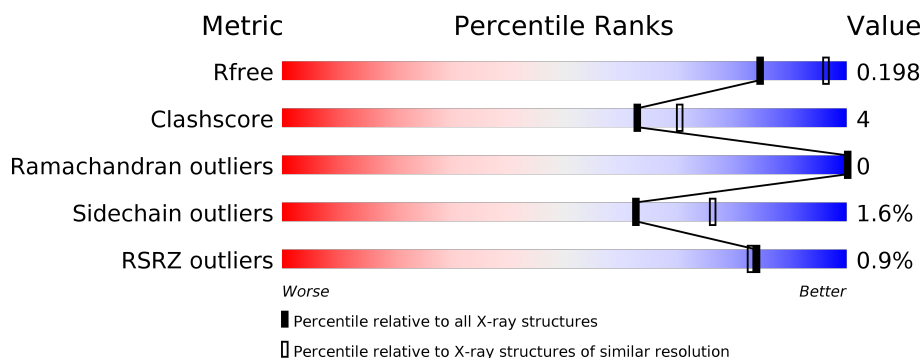
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on 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	719	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> 87% <div style="width: 100%; height: 10px; background-color: yellow;"></div> 8% <div style="width: 100%; height: 10px; background-color: grey;"></div> 5% </div> </div>
1	B	719	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> 84% <div style="width: 100%; height: 10px; background-color: yellow;"></div> 10% <div style="width: 100%; height: 10px; background-color: grey;"></div> 6% </div> </div>
1	C	719	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> 85% <div style="width: 100%; height: 10px; background-color: yellow;"></div> 9% <div style="width: 100%; height: 10px; background-color: grey;"></div> 6% </div> </div>
1	D	719	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> 86% <div style="width: 100%; height: 10px; background-color: yellow;"></div> 8% <div style="width: 100%; height: 10px; background-color: grey;"></div> 6% </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PEG	A	806	-	-	X	-
8	P6G	C	804	-	-	X	-
9	PG4	C	805	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 23938 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 Catalase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	682	Total	C	N	O	S	0	8	0
			5409	3420	956	1027	6			
1	B	677	Total	C	N	O	S	0	6	0
			5359	3392	951	1010	6			
1	C	679	Total	C	N	O	S	0	11	0
			5411	3420	962	1023	6			
1	D	678	Total	C	N	O	S	0	9	0
			5385	3408	956	1015	6			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by author).



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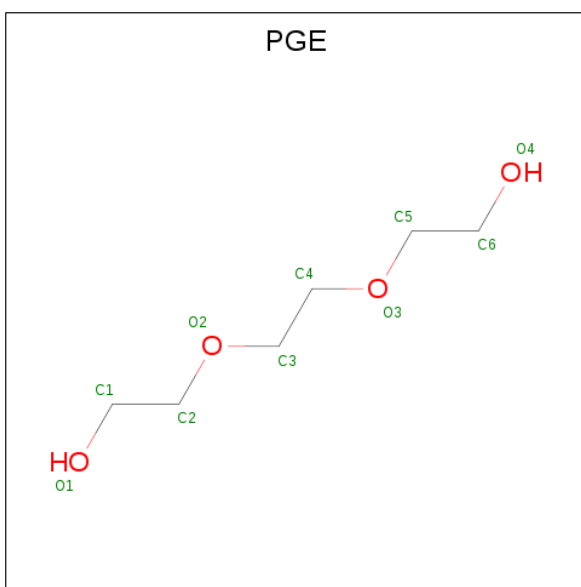
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



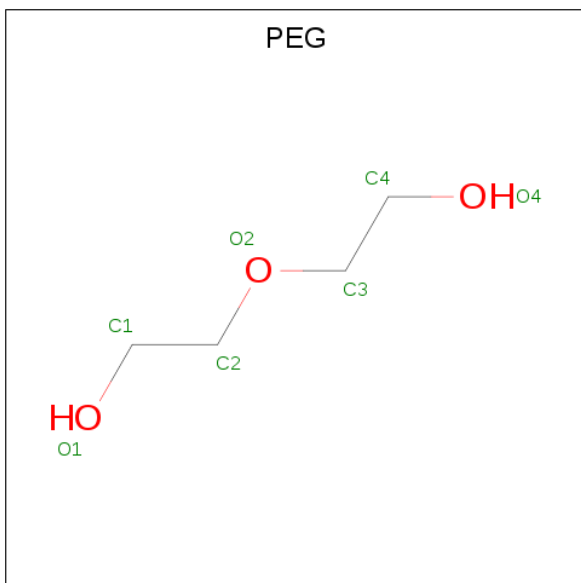
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



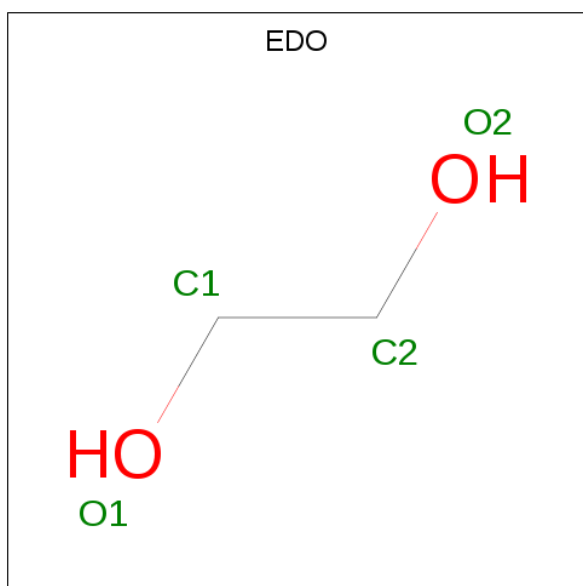
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	C	1	Total	C	O	0	0
			10	6	4		
4	D	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



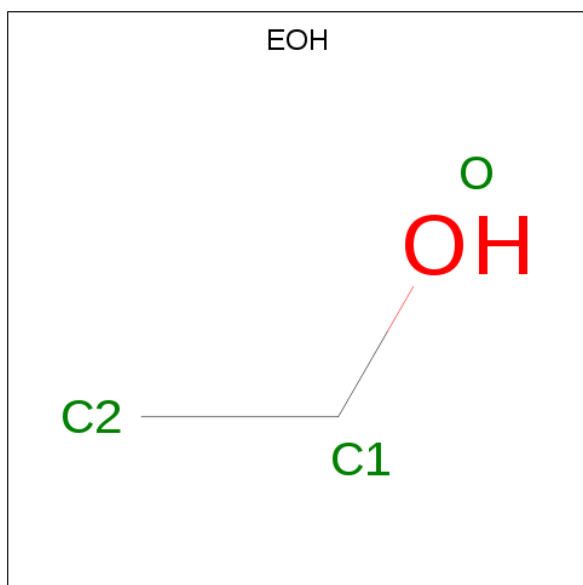
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0

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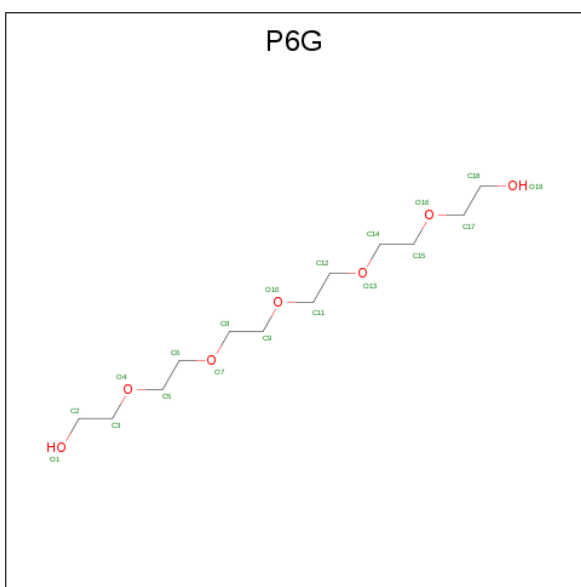
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is ETHANOL (three-letter code: EOH) (formula: C_2H_6O).



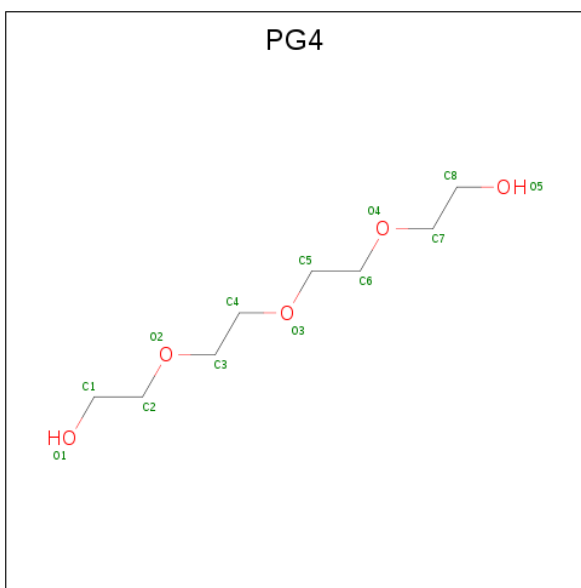
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			3	2	1		
7	B	1	Total	C	O	0	0
			3	2	1		
7	B	1	Total	C	O	0	0
			3	2	1		
7	D	1	Total	C	O	0	0
			3	2	1		
7	D	1	Total	C	O	0	0
			3	2	1		
7	D	1	Total	C	O	0	0
			3	2	1		

- Molecule 8 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			19	12	7		

- Molecule 9 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			13	8	5		

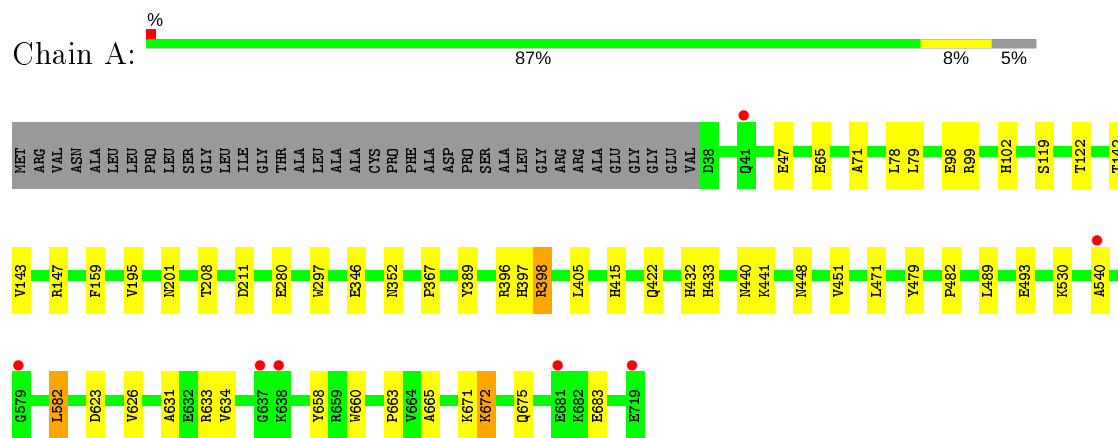
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	492	Total 492	O 492	0	0
10	B	507	Total 507	O 507	0	0
10	C	510	Total 510	O 510	0	0
10	D	500	Total 500	O 500	0	0

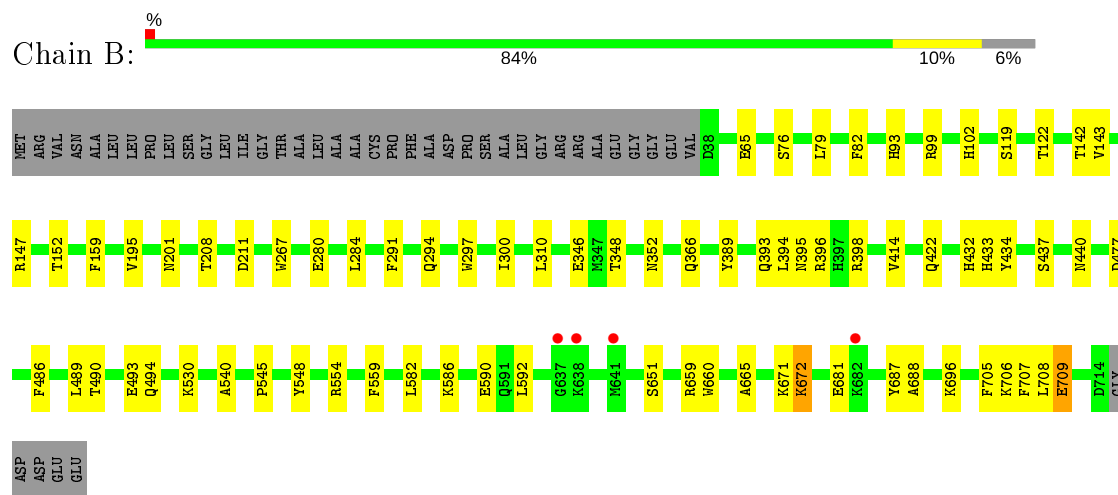
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

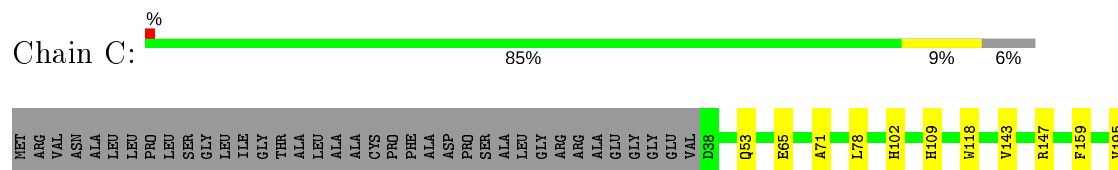
• Molecule 1: Catalase-3

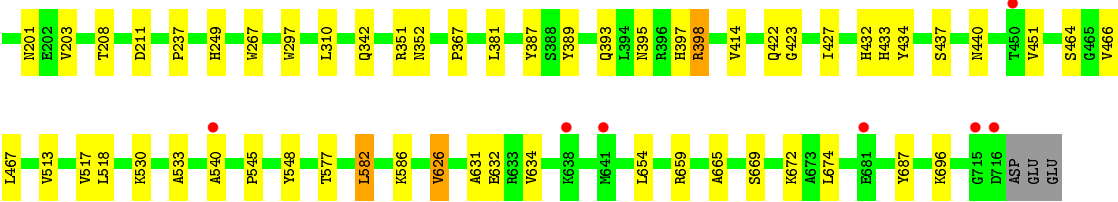


• Molecule 1: Catalase-3

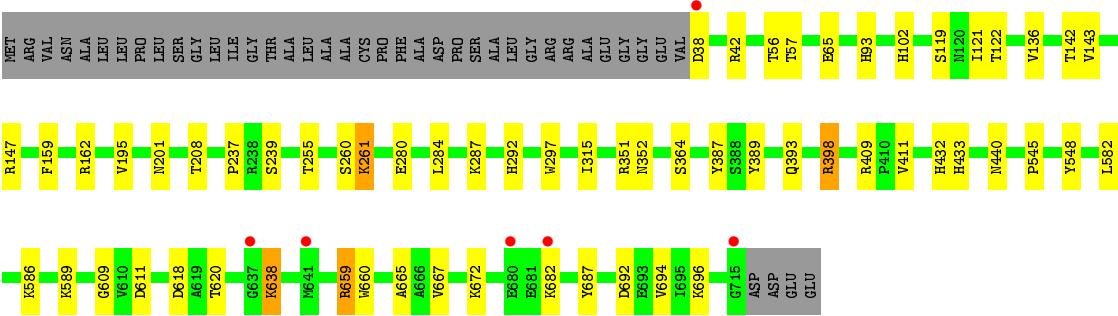
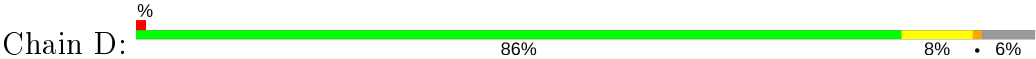


• Molecule 1: Catalase-3





● Molecule 1: Catalase-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	131.10Å 154.50Å 160.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.66 – 2.20 29.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.7 (29.66-2.20) 96.7 (29.65-2.20)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.05 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.12 _2829	Depositor
R, R_{free}	0.150 , 0.198 0.150 , 0.198	Depositor DCC
R_{free} test set	8033 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23938	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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: PGE, EOH, EDO, PG4, P6G, ACT, HEM, PEG

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	0.39	0/5543	0.54	0/7518
1	B	0.40	0/5495	0.55	1/7452 (0.0%)
1	C	0.39	0/5544	0.55	0/7517
1	D	0.39	0/5521	0.54	0/7485
All	All	0.39	0/22103	0.55	1/29972 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	477	ASP	CB-CG-OD1	5.36	123.12	118.30

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	5409	0	5215	47	0
1	B	5359	0	5187	56	0
1	C	5411	0	5227	56	0
1	D	5385	0	5213	45	0
2	A	43	0	30	0	0
2	B	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	43	0	30	0	0
2	D	43	0	30	0	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
3	C	8	0	6	2	0
3	D	8	0	6	2	0
4	A	10	0	14	0	0
4	B	10	0	14	0	0
4	C	10	0	14	0	0
4	D	10	0	14	2	0
5	A	14	0	20	5	0
5	B	7	0	10	0	0
5	C	14	0	20	1	0
6	A	4	0	6	0	0
6	B	8	0	12	1	0
6	C	12	0	18	1	0
6	D	12	0	18	0	0
7	A	3	0	6	0	0
7	B	6	0	12	1	0
7	D	9	0	18	1	0
8	C	19	0	26	9	0
9	C	13	0	18	7	0
10	A	492	0	0	5	0
10	B	507	0	0	6	0
10	C	510	0	0	8	0
10	D	500	0	0	5	0
All	All	23938	0	21226	184	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 4.

All (184) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:398:ARG:HE	1:C:398:ARG:HE	1.15	0.93
1:C:398:ARG:NH1	10:C:901:HOH:O	2.02	0.92
1:B:398:ARG:NH1	10:B:902:HOH:O	2.09	0.86
1:C:632:GLU:HB2	1:C:672:LYS:HD2	1.64	0.78
1:A:398:ARG:NH1	10:A:901:HOH:O	2.12	0.78
1:B:346:GLU:OE1	1:B:348:THR:OG1	2.02	0.77
1:B:147[A]:ARG:O	10:B:901:HOH:O	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:ARG:HG3	1:C:398:ARG:HH21	1.50	0.75
1:B:398:ARG:HE	1:C:398:ARG:NE	1.85	0.74
1:D:56:THR:HG22	1:D:57:THR:O	1.88	0.73
1:A:441:LYS:HE3	5:A:806:PEG:H31	1.69	0.73
1:C:530:LYS:HG2	1:C:540:ALA:HB1	1.71	0.72
1:D:147[B]:ARG:O	10:D:901:HOH:O	2.09	0.70
1:B:681:GLU:HG3	1:B:688:ALA:HB3	1.73	0.70
1:D:121:ILE:O	10:D:902:HOH:O	2.11	0.68
1:A:530:LYS:HG2	1:A:540:ALA:HB1	1.78	0.66
1:B:352:ASN:ND2	10:B:905:HOH:O	2.29	0.65
1:D:38:ASP:HA	1:D:351:ARG:NH1	2.12	0.65
1:C:342:GLN:HG2	9:C:805:PG4:H32	1.78	0.64
1:C:659:ARG:HH22	8:C:804:P6G:H52	1.62	0.63
1:D:586:LYS:HE2	1:D:609:GLY:HA3	1.80	0.63
9:C:805:PG4:H31	10:C:1228:HOH:O	1.98	0.62
1:B:707:PHE:HB3	1:B:709:GLU:OE1	2.00	0.61
1:B:651:SER:HB2	8:C:804:P6G:H51	1.84	0.60
1:C:398:ARG:NH2	1:C:398:ARG:HG3	2.13	0.59
1:A:280:GLU:HB2	1:A:660:TRP:CD2	2.37	0.59
1:C:195[A]:VAL:HG21	3:C:802:ACT:H1	1.84	0.59
1:B:708:LEU:HB2	7:B:809:EOH:H11	1.85	0.58
1:A:346:GLU:HG2	10:A:922:HOH:O	2.05	0.57
1:A:79:LEU:HD11	1:C:387:TYR:HB2	1.87	0.56
1:C:414:VAL:HB	6:C:809:EDO:H22	1.87	0.56
1:B:586:LYS:NZ	1:B:590:GLU:OE1	2.36	0.56
1:D:692:ASP:O	1:D:696:LYS:HD3	2.06	0.56
1:B:659:ARG:HD2	10:B:1039:HOH:O	2.05	0.56
1:A:71:ALA:HB2	1:A:78:LEU:HD21	1.87	0.55
6:B:807:EDO:H11	10:B:1369:HOH:O	2.06	0.55
1:B:280:GLU:HB2	1:B:660:TRP:CD2	2.41	0.55
1:D:195[A]:VAL:HG21	3:D:802:ACT:H1	1.89	0.55
1:A:397:HIS:HA	1:C:422:GLN:OE1	2.09	0.53
1:B:398:ARG:NE	1:C:398:ARG:NE	2.56	0.53
1:B:398:ARG:NH1	1:C:398:ARG:HD3	2.25	0.52
1:B:300:ILE:HG22	10:B:905:HOH:O	2.09	0.52
1:C:102:HIS:CE1	1:C:143:VAL:HG22	2.44	0.52
1:B:559:PHE:HB3	1:B:708:LEU:HD11	1.92	0.52
1:D:239:SER:HA	1:D:292:HIS:CD2	2.45	0.52
1:C:545:PRO:HA	1:C:548:TYR:CD2	2.45	0.52
1:A:422:GLN:NE2	1:C:397:HIS:HA	2.24	0.51
1:D:260:SER:C	1:D:261:LYS:HD3	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147[A]:ARG:HD2	10:C:1072:HOH:O	2.10	0.51
1:B:545:PRO:HA	1:B:548:TYR:CD2	2.46	0.51
1:B:398:ARG:HH11	1:C:398:ARG:HD3	1.76	0.51
1:A:297:TRP:CE3	1:D:201:ASN:HB3	2.46	0.51
1:B:152:THR:HG21	1:B:284:LEU:HD23	1.93	0.51
1:C:434:TYR:CE2	1:C:437:SER:HB2	2.46	0.51
1:A:405:LEU:HD21	1:C:423:GLY:HA2	1.93	0.50
1:A:671:LYS:O	1:A:675:GLN:HG3	2.11	0.50
1:A:147[B]:ARG:HD2	10:A:904:HOH:O	2.12	0.50
1:C:626:VAL:HB	1:C:665:ALA:HB3	1.94	0.50
1:A:432:HIS:HB2	1:A:440:ASN:HB3	1.94	0.49
1:A:102:HIS:CE1	1:A:143:VAL:HG22	2.47	0.49
1:C:432:HIS:HB2	1:C:440:ASN:HB3	1.93	0.49
1:A:658:TYR:OH	1:A:683:GLU:OE2	2.26	0.49
1:D:692:ASP:OD2	10:D:903:HOH:O	2.20	0.49
1:A:415:HIS:CE1	1:C:53:GLN:HG3	2.48	0.48
1:A:441:LYS:HE3	5:A:806:PEG:C3	2.42	0.48
1:D:237:PRO:HB3	3:D:803:ACT:H1	1.96	0.48
1:B:297:TRP:CE3	1:C:201:ASN:HB3	2.49	0.48
1:A:398:ARG:HG3	1:C:422:GLN:NE2	2.28	0.48
1:A:672:LYS:HD2	1:A:672:LYS:O	2.13	0.48
1:D:284:LEU:HD13	1:D:620:THR:HB	1.96	0.48
1:B:147[B]:ARG:O	1:C:147[B]:ARG:O	2.32	0.48
1:B:93:HIS:ND1	1:C:395:ASN:HB2	2.29	0.48
1:D:696:LYS:N	1:D:696:LYS:HD2	2.28	0.48
1:A:98:GLU:HB3	1:A:147[B]:ARG:HG3	1.96	0.48
1:B:414:VAL:HA	1:D:56:THR:HG21	1.96	0.48
1:B:102:HIS:CE1	1:B:143:VAL:HG22	2.50	0.47
1:B:284:LEU:HD21	1:B:291:PHE:CD2	2.49	0.47
1:B:490:THR:HB	1:B:493:GLU:HB2	1.96	0.47
1:C:267:TRP:CZ3	1:C:310:LEU:HB2	2.50	0.47
1:C:249:HIS:HE1	1:C:381:LEU:HB3	1.80	0.47
1:C:659:ARG:HH22	8:C:804:P6G:C5	2.28	0.47
1:B:659:ARG:HH12	8:C:804:P6G:H151	1.80	0.47
1:B:651:SER:CB	8:C:804:P6G:H51	2.45	0.46
1:C:659:ARG:HH12	8:C:804:P6G:H52	1.79	0.46
9:C:805:PG4:H12	10:C:1228:HOH:O	2.15	0.46
1:B:102:HIS:HA	1:B:142:THR:O	2.15	0.46
1:D:659:ARG:HH22	4:D:804:PGE:H3	1.81	0.46
1:B:490:THR:HG22	1:B:493:GLU:H	1.81	0.46
1:C:367:PRO:HD3	1:C:389:TYR:CD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195[B]:VAL:HG13	1:B:208:THR:HG22	1.98	0.46
1:D:545:PRO:HA	1:D:548:TYR:CD2	2.51	0.46
1:B:671:LYS:HE3	1:B:672:LYS:NZ	2.31	0.46
1:C:71:ALA:HB2	1:C:78:LEU:HD21	1.98	0.46
1:D:409:ARG:HH12	7:D:808:EOH:H22	1.81	0.46
9:C:805:PG4:H71	9:C:805:PG4:H52	1.69	0.45
1:D:589:LYS:NZ	1:D:611:ASP:OD2	2.43	0.45
1:D:659:ARG:NH2	4:D:804:PGE:H3	2.32	0.45
1:B:705:PHE:CD2	1:B:706:LYS:HG2	2.52	0.45
1:B:389:TYR:O	1:B:393:GLN:HG2	2.16	0.45
1:D:102:HIS:CE1	1:D:143:VAL:HG22	2.52	0.45
1:B:201:ASN:HB3	1:C:297:TRP:CE3	2.51	0.45
1:D:287:LYS:HE3	1:D:618:ASP:OD1	2.16	0.45
1:A:626:VAL:HG22	1:A:665:ALA:HB3	1.98	0.45
8:C:804:P6G:H152	8:C:804:P6G:H121	1.77	0.44
1:A:201:ASN:HB3	1:D:297:TRP:CE3	2.52	0.44
1:B:99:ARG:HA	1:B:396[A]:ARG:HD3	1.99	0.44
1:A:398:ARG:HG3	1:C:422:GLN:HE21	1.83	0.44
1:D:297:TRP:CZ3	1:D:352:ASN:HB3	2.53	0.44
1:A:99:ARG:HA	1:A:396[A]:ARG:HD3	1.98	0.44
1:D:364:SER:HB3	1:D:393:GLN:CD	2.38	0.44
1:A:147[B]:ARG:O	10:A:902:HOH:O	2.21	0.44
1:A:489:LEU:HB3	1:A:493:GLU:HB3	2.00	0.44
1:A:441:LYS:HE3	5:A:806:PEG:H22	1.99	0.44
1:A:415:HIS:ND1	1:C:53:GLN:HG3	2.33	0.44
1:D:638:LYS:HD2	1:D:638:LYS:HA	1.71	0.44
1:C:195[B]:VAL:HG13	1:C:208:THR:HG22	1.99	0.44
1:A:631:ALA:O	1:A:634:VAL:HG22	2.17	0.44
1:A:441:LYS:NZ	5:A:806:PEG:H22	2.33	0.44
1:C:518[A]:LEU:HD11	1:C:533:ALA:HB2	2.00	0.44
1:C:631:ALA:O	1:C:634:VAL:HG22	2.18	0.44
1:D:667:VAL:HG22	1:D:694:VAL:HG21	2.00	0.43
1:B:294:GLN:OE1	1:C:203:VAL:HG11	2.18	0.43
1:A:147[A]:ARG:O	1:D:147[A]:ARG:O	2.36	0.43
1:B:530:LYS:HA	1:B:540:ALA:HB2	2.01	0.43
1:B:82:PHE:HB2	10:D:1319:HOH:O	2.18	0.43
1:C:632:GLU:OE2	1:C:669[B]:SER:OG	2.24	0.43
1:B:422:GLN:NE2	1:D:398:ARG:HG3	2.33	0.43
1:D:195[B]:VAL:HG13	1:D:208:THR:HG22	2.00	0.43
1:A:471:LEU:HD23	1:A:471:LEU:HA	1.83	0.43
1:D:136:VAL:HA	1:D:162:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195[B]:VAL:HG13	1:A:208:THR:HG22	2.00	0.43
1:A:441:LYS:CE	5:A:806:PEG:H22	2.49	0.43
1:B:395:ASN:O	1:B:398:ARG:HD2	2.18	0.43
1:B:489:LEU:HB3	1:B:493:GLU:HB3	2.01	0.43
1:B:582:LEU:HA	1:B:582:LEU:HD12	1.88	0.43
1:C:297:TRP:CZ3	1:C:352:ASN:HB3	2.54	0.43
1:A:47:GLU:HA	1:C:427:ILE:O	2.19	0.43
1:D:432:HIS:HB2	1:D:440:ASN:HB3	2.00	0.43
1:D:682:LYS:HE2	1:D:682:LYS:HB3	1.83	0.43
1:A:102:HIS:HA	1:A:142:THR:O	2.18	0.43
1:C:342:GLN:HB3	9:C:805:PG4:H51	2.01	0.43
1:D:255:THR:HG23	10:D:902:HOH:O	2.19	0.43
1:B:79:LEU:HD11	1:D:387:TYR:HB2	2.00	0.43
1:C:147[A]:ARG:NH2	10:C:919:HOH:O	2.49	0.42
1:C:577:THR:HA	1:C:582:LEU:HD22	2.01	0.42
1:D:102:HIS:HA	1:D:142:THR:O	2.18	0.42
1:B:432:HIS:HB2	1:B:440:ASN:HB3	2.02	0.42
1:B:297:TRP:CZ3	1:B:352:ASN:HB3	2.55	0.42
1:A:367:PRO:HD2	1:A:389:TYR:CG	2.55	0.42
1:C:665:ALA:HA	1:C:687:TYR:O	2.20	0.42
1:D:665:ALA:HA	1:D:687:TYR:O	2.19	0.42
1:C:237:PRO:HB3	3:C:803:ACT:H1	2.01	0.41
1:C:654:LEU:HD21	1:C:674:LEU:HD23	2.02	0.41
1:D:42:ARG:HD2	1:D:411:VAL:HG12	2.01	0.41
1:B:267:TRP:CZ3	1:B:310:LEU:HB2	2.55	0.41
1:C:389:TYR:O	1:C:393:GLN:HG2	2.20	0.41
1:D:280:GLU:HB2	1:D:660:TRP:CD2	2.54	0.41
1:C:118:TRP:CH2	9:C:805:PG4:H61	2.55	0.41
1:D:119:SER:HA	1:D:122:THR:O	2.20	0.41
1:A:398:ARG:HD2	1:D:398:ARG:CD	2.50	0.41
1:A:297:TRP:CZ3	1:A:352:ASN:HB3	2.55	0.41
1:C:109:HIS:HB2	1:C:351:ARG:HB2	2.02	0.41
1:C:466:VAL:HG22	1:C:467:LEU:O	2.20	0.41
8:C:804:P6G:H21	10:C:1320:HOH:O	2.19	0.41
1:B:394:LEU:HD13	1:D:93:HIS:CE1	2.56	0.41
1:A:448:ASN:OD1	1:A:451[A]:VAL:HG22	2.20	0.41
1:B:486:PHE:CZ	1:B:494:GLN:HB3	2.55	0.41
1:A:479:TYR:C	1:A:482:PRO:HD2	2.42	0.41
1:A:633:ARG:HD2	10:A:1368:HOH:O	2.21	0.41
5:C:808:PEG:H22	10:C:1328:HOH:O	2.21	0.41
1:B:434:TYR:CE2	1:B:437:SER:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:389:TYR:O	1:D:393:GLN:HG2	2.20	0.41
1:A:623:ASP:O	1:A:663:PRO:HD2	2.22	0.40
1:C:659:ARG:NH2	8:C:804:PG6:H52	2.34	0.40
1:D:582:LEU:HA	1:D:582:LEU:HD12	1.91	0.40
1:B:119:SER:HA	1:B:122:THR:O	2.22	0.40
1:B:76:SER:HB3	10:C:911:HOH:O	2.20	0.40
9:C:805:PG4:H31	9:C:805:PG4:H12	1.75	0.40
1:A:582:LEU:HD12	1:A:582:LEU:HA	1.87	0.40
1:C:513:VAL:O	1:C:517:VAL:HG23	2.22	0.40
1:B:366:GLN:HG2	1:B:389:TYR:HB3	2.04	0.40
1:A:119:SER:HA	1:A:122:THR:O	2.21	0.40
1:B:665:ALA:HA	1:B:687:TYR:O	2.22	0.40
1:A:398:ARG:CD	1:D:398:ARG:HD2	2.52	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	688/719 (96%)	666 (97%)	22 (3%)	0	100	100
1	B	681/719 (95%)	661 (97%)	20 (3%)	0	100	100
1	C	688/719 (96%)	669 (97%)	19 (3%)	0	100	100
1	D	685/719 (95%)	665 (97%)	20 (3%)	0	100	100
All	All	2742/2876 (95%)	2661 (97%)	81 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	567/585 (97%)	560 (99%)	7 (1%)	71	83
1	B	561/585 (96%)	551 (98%)	10 (2%)	59	72
1	C	567/585 (97%)	556 (98%)	11 (2%)	57	71
1	D	564/585 (96%)	555 (98%)	9 (2%)	62	76
All	All	2259/2340 (96%)	2222 (98%)	37 (2%)	62	76

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	GLU
1	A	159	PHE
1	A	211	ASP
1	A	398	ARG
1	A	433	HIS
1	A	582	LEU
1	A	672	LYS
1	B	65	GLU
1	B	159	PHE
1	B	211	ASP
1	B	433	HIS
1	B	554[A]	ARG
1	B	554[B]	ARG
1	B	592	LEU
1	B	672	LYS
1	B	696	LYS
1	B	709	GLU
1	C	65	GLU
1	C	159	PHE
1	C	211	ASP
1	C	398	ARG
1	C	433	HIS
1	C	451	VAL
1	C	464	SER

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Mol	Chain	Res	Type
1	C	582	LEU
1	C	586	LYS
1	C	626	VAL
1	C	696	LYS
1	D	65	GLU
1	D	159	PHE
1	D	261	LYS
1	D	315	ILE
1	D	398	ARG
1	D	433	HIS
1	D	638	LYS
1	D	659	ARG
1	D	672	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

38 ligands 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
6	EDO	C	809	-	3,3,3	0.46	0	2,2,2	0.30	0
5	PEG	A	806	-	6,6,6	0.46	0	5,5,5	0.55	0
6	EDO	D	805	-	3,3,3	0.46	0	2,2,2	0.37	0
5	PEG	A	805	-	6,6,6	0.48	0	5,5,5	0.53	0
7	EOH	D	810	-	2,2,2	0.46	0	1,1,1	0.18	0
4	PGE	C	806	-	9,9,9	0.32	0	8,8,8	0.37	0
4	PGE	D	804	-	9,9,9	0.37	0	8,8,8	0.24	0
2	HEM	B	801	1	27,50,50	1.75	4 (14%)	17,82,82	1.83	4 (23%)
6	EDO	C	810	-	3,3,3	0.46	0	2,2,2	0.40	0
6	EDO	D	807	-	3,3,3	0.51	0	2,2,2	0.32	0
3	ACT	D	803	-	1,3,3	7.58	1 (100%)	0,3,3	0.00	-
3	ACT	B	803	-	1,3,3	7.23	1 (100%)	0,3,3	0.00	-
7	EOH	A	808	-	2,2,2	0.46	0	1,1,1	0.17	0
3	ACT	A	803	-	1,3,3	7.68	1 (100%)	0,3,3	0.00	-
2	HEM	C	801	1	27,50,50	1.85	4 (14%)	17,82,82	1.86	4 (23%)
7	EOH	B	808	-	2,2,2	0.44	0	1,1,1	0.19	0
7	EOH	D	809	-	2,2,2	0.43	0	1,1,1	0.31	0
3	ACT	B	802	-	1,3,3	6.65	1 (100%)	0,3,3	0.00	-
3	ACT	A	802	-	1,3,3	6.69	1 (100%)	0,3,3	0.00	-
4	PGE	A	804	-	9,9,9	0.34	0	8,8,8	0.25	0
5	PEG	C	808	-	6,6,6	0.47	0	5,5,5	0.51	0
9	PG4	C	805	-	12,12,12	0.50	0	11,11,11	0.52	0
3	ACT	D	802	-	1,3,3	6.10	1 (100%)	0,3,3	0.00	-
6	EDO	D	806	-	3,3,3	0.50	0	2,2,2	0.32	0
6	EDO	B	807	-	3,3,3	0.47	0	2,2,2	0.24	0
2	HEM	A	801	1	27,50,50	1.80	5 (18%)	17,82,82	1.87	4 (23%)
3	ACT	C	802	-	1,3,3	7.02	1 (100%)	0,3,3	0.00	-
7	EOH	D	808	-	2,2,2	0.45	0	1,1,1	0.17	0
4	PGE	B	804	-	9,9,9	0.30	0	8,8,8	0.40	0
5	PEG	C	807	-	6,6,6	0.48	0	5,5,5	0.49	0
8	P6G	C	804	-	18,18,18	0.50	0	17,17,17	0.48	0
6	EDO	C	811	-	3,3,3	0.44	0	2,2,2	0.36	0
5	PEG	B	805	-	6,6,6	0.49	0	5,5,5	0.57	0
2	HEM	D	801	1	27,50,50	1.75	4 (14%)	17,82,82	2.13	6 (35%)
6	EDO	B	806	-	3,3,3	0.42	0	2,2,2	0.39	0
3	ACT	C	803	-	1,3,3	7.49	1 (100%)	0,3,3	0.00	-
6	EDO	A	807	-	3,3,3	0.44	0	2,2,2	0.37	0
7	EOH	B	809	-	2,2,2	0.47	0	1,1,1	0.16	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	EDO	C	809	-	-	0/1/1/1	-
5	PEG	A	806	-	-	3/4/4/4	-
6	EDO	D	805	-	-	0/1/1/1	-
5	PEG	A	805	-	-	3/4/4/4	-
4	PGE	C	806	-	-	3/7/7/7	-
4	PGE	D	804	-	-	5/7/7/7	-
6	EDO	C	810	-	-	1/1/1/1	-
6	EDO	D	807	-	-	0/1/1/1	-
2	HEM	C	801	1	-	0/6/54/54	-
5	PEG	C	807	-	-	0/4/4/4	-
4	PGE	A	804	-	-	3/7/7/7	-
5	PEG	C	808	-	-	0/4/4/4	-
9	PG4	C	805	-	-	5/10/10/10	-
6	EDO	D	806	-	-	0/1/1/1	-
6	EDO	B	807	-	-	1/1/1/1	-
2	HEM	A	801	1	-	0/6/54/54	-
2	HEM	B	801	1	-	0/6/54/54	-
4	PGE	B	804	-	-	4/7/7/7	-
8	P6G	C	804	-	-	9/16/16/16	-
6	EDO	C	811	-	-	0/1/1/1	-
5	PEG	B	805	-	-	1/4/4/4	-
2	HEM	D	801	1	-	0/6/54/54	-
6	EDO	B	806	-	-	0/1/1/1	-
6	EDO	A	807	-	-	0/1/1/1	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	803	ACT	CH3-C	7.68	1.58	1.48
3	D	803	ACT	CH3-C	7.58	1.58	1.48
3	C	803	ACT	CH3-C	7.49	1.58	1.48
3	B	803	ACT	CH3-C	7.23	1.58	1.48
3	C	802	ACT	CH3-C	7.02	1.57	1.48
3	A	802	ACT	CH3-C	6.69	1.57	1.48
3	B	802	ACT	CH3-C	6.65	1.57	1.48
3	D	802	ACT	CH3-C	6.10	1.56	1.48
2	C	801	HEM	C3C-C2C	-4.09	1.34	1.40
2	A	801	HEM	C3C-C2C	-4.03	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	HEM	C3B-C2B	-3.94	1.34	1.40
2	D	801	HEM	C3C-C2C	-3.85	1.35	1.40
2	D	801	HEM	C3B-CAB	3.85	1.55	1.47
2	A	801	HEM	C3B-CAB	3.67	1.55	1.47
2	B	801	HEM	C3C-C2C	-3.65	1.35	1.40
2	C	801	HEM	C3C-CAC	3.57	1.55	1.47
2	C	801	HEM	C3B-CAB	3.56	1.55	1.47
2	A	801	HEM	C3B-C2B	-3.51	1.35	1.40
2	B	801	HEM	C3B-CAB	3.48	1.55	1.47
2	B	801	HEM	C3C-CAC	3.32	1.54	1.47
2	A	801	HEM	C3C-CAC	3.32	1.54	1.47
2	B	801	HEM	C3B-C2B	-3.27	1.35	1.40
2	D	801	HEM	C3B-C2B	-3.12	1.36	1.40
2	D	801	HEM	C3C-CAC	3.09	1.54	1.47
2	A	801	HEM	CAD-C3D	2.11	1.55	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	HEM	CAA-CBA-CGA	-4.99	104.31	112.67
2	C	801	HEM	CAA-CBA-CGA	-4.52	105.09	112.67
2	A	801	HEM	CAA-CBA-CGA	-4.01	105.94	112.67
2	B	801	HEM	CAA-CBA-CGA	-3.85	106.20	112.67
2	B	801	HEM	CMD-C2D-C1D	-3.61	122.91	128.46
2	D	801	HEM	C4C-C3C-C2C	3.03	109.01	106.90
2	D	801	HEM	CMD-C2D-C1D	-3.01	123.83	128.46
2	C	801	HEM	CBD-CAD-C3D	-2.89	107.15	112.48
2	A	801	HEM	CMD-C2D-C1D	-2.87	124.05	128.46
2	C	801	HEM	CMD-C2D-C1D	-2.86	124.07	128.46
2	D	801	HEM	CMB-C2B-C3B	2.63	129.61	124.68
2	A	801	HEM	CMB-C2B-C3B	2.63	129.59	124.68
2	D	801	HEM	CMC-C2C-C3C	2.50	129.35	124.68
2	A	801	HEM	CMA-C3A-C4A	-2.47	124.67	128.46
2	D	801	HEM	CBD-CAD-C3D	-2.34	108.16	112.48
2	B	801	HEM	CMB-C2B-C3B	2.14	128.68	124.68
2	C	801	HEM	CMC-C2C-C3C	2.10	128.61	124.68
2	B	801	HEM	C1D-C2D-C3D	2.08	108.45	107.00

There are no chirality outliers.

All (38) torsion outliers are listed below:

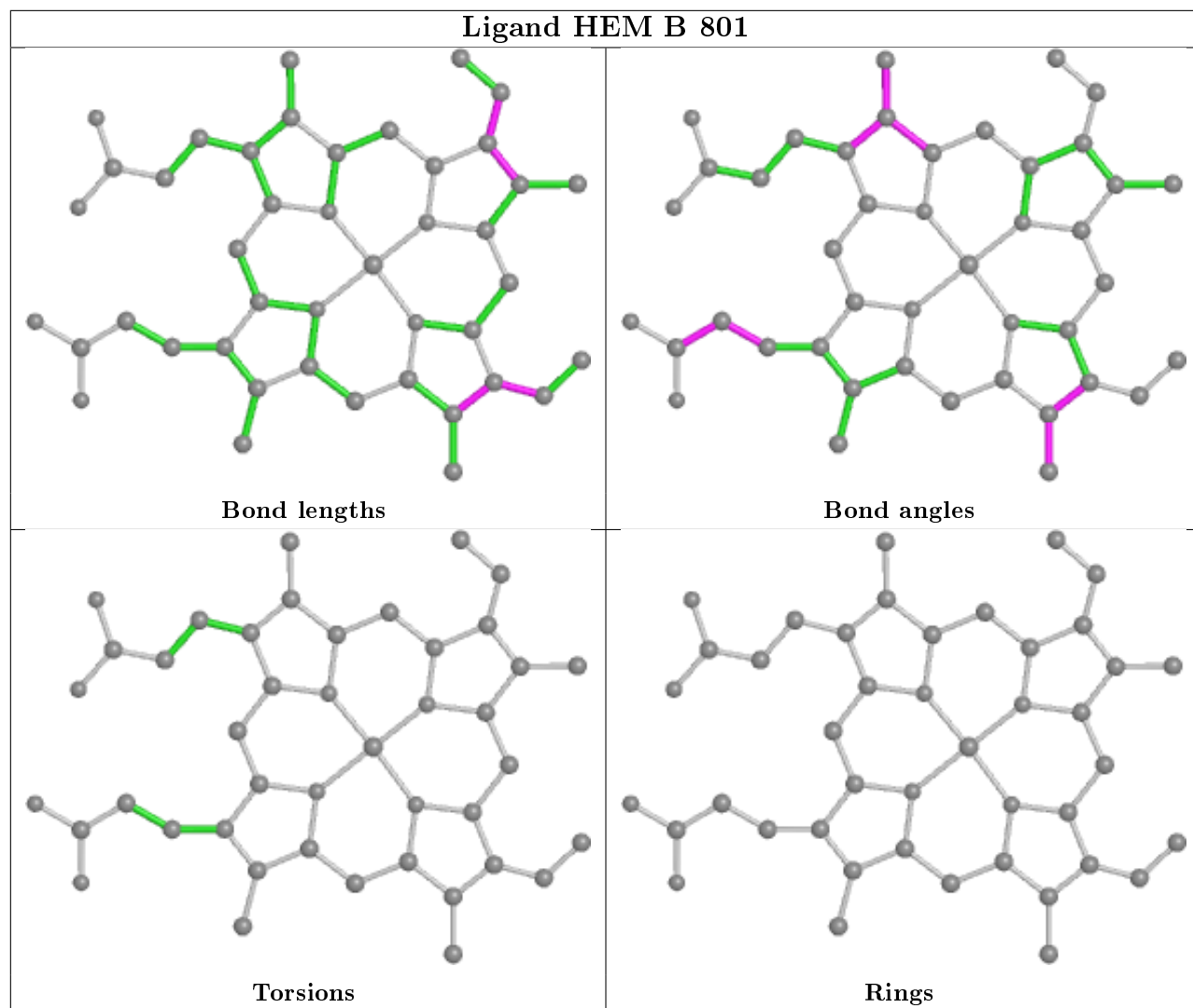
Mol	Chain	Res	Type	Atoms
4	A	804	PGE	O2-C3-C4-O3
4	B	804	PGE	O2-C3-C4-O3
8	C	804	P6G	O7-C8-C9-O10
4	A	804	PGE	C3-C4-O3-C5
9	C	805	PG4	O4-C7-C8-O5
8	C	804	P6G	O1-C2-C3-O4
9	C	805	PG4	C5-C6-O4-C7
4	B	804	PGE	O1-C1-C2-O2
9	C	805	PG4	O2-C3-C4-O3
5	A	805	PEG	O2-C3-C4-O4
8	C	804	P6G	O13-C14-C15-O16
4	D	804	PGE	O2-C3-C4-O3
5	A	806	PEG	O2-C3-C4-O4
4	C	806	PGE	O1-C1-C2-O2
5	B	805	PEG	O1-C1-C2-O2
4	D	804	PGE	O3-C5-C6-O4
4	B	804	PGE	O3-C5-C6-O4
5	A	805	PEG	O1-C1-C2-O2
6	C	810	EDO	O1-C1-C2-O2
4	C	806	PGE	C3-C4-O3-C5
4	A	804	PGE	C4-C3-O2-C2
4	C	806	PGE	O3-C5-C6-O4
4	D	804	PGE	C3-C4-O3-C5
8	C	804	P6G	O16-C17-C18-O19
4	D	804	PGE	C4-C3-O2-C2
8	C	804	P6G	C2-C3-O4-C5
8	C	804	P6G	C9-C8-O7-C6
8	C	804	P6G	C14-C15-O16-C17
9	C	805	PG4	C1-C2-O2-C3
8	C	804	P6G	C15-C14-O13-C12
6	B	807	EDO	O1-C1-C2-O2
5	A	805	PEG	C1-C2-O2-C3
5	A	806	PEG	C1-C2-O2-C3
4	B	804	PGE	C1-C2-O2-C3
8	C	804	P6G	O4-C5-C6-O7
5	A	806	PEG	O1-C1-C2-O2
4	D	804	PGE	O1-C1-C2-O2
9	C	805	PG4	O3-C5-C6-O4

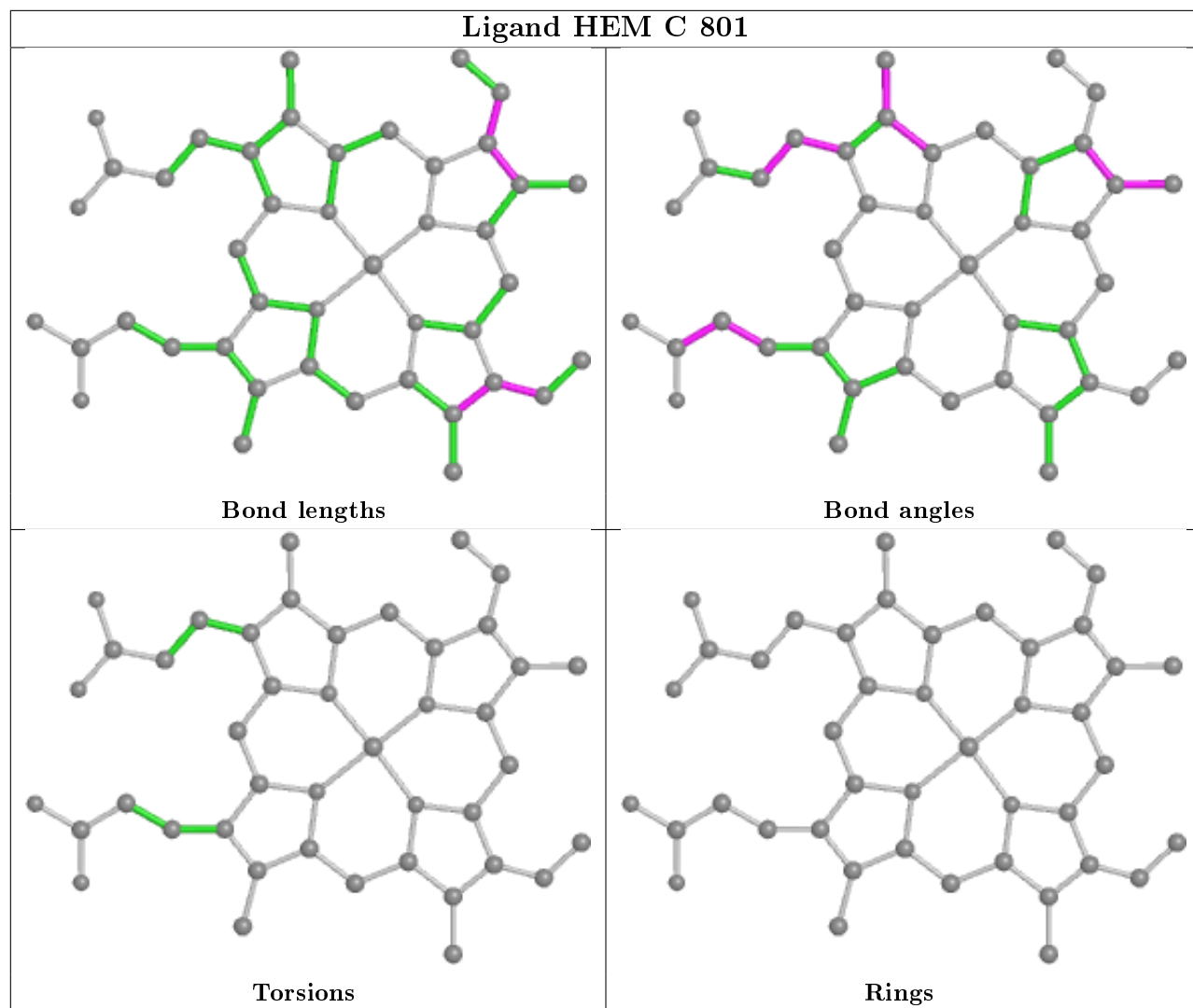
There are no ring outliers.

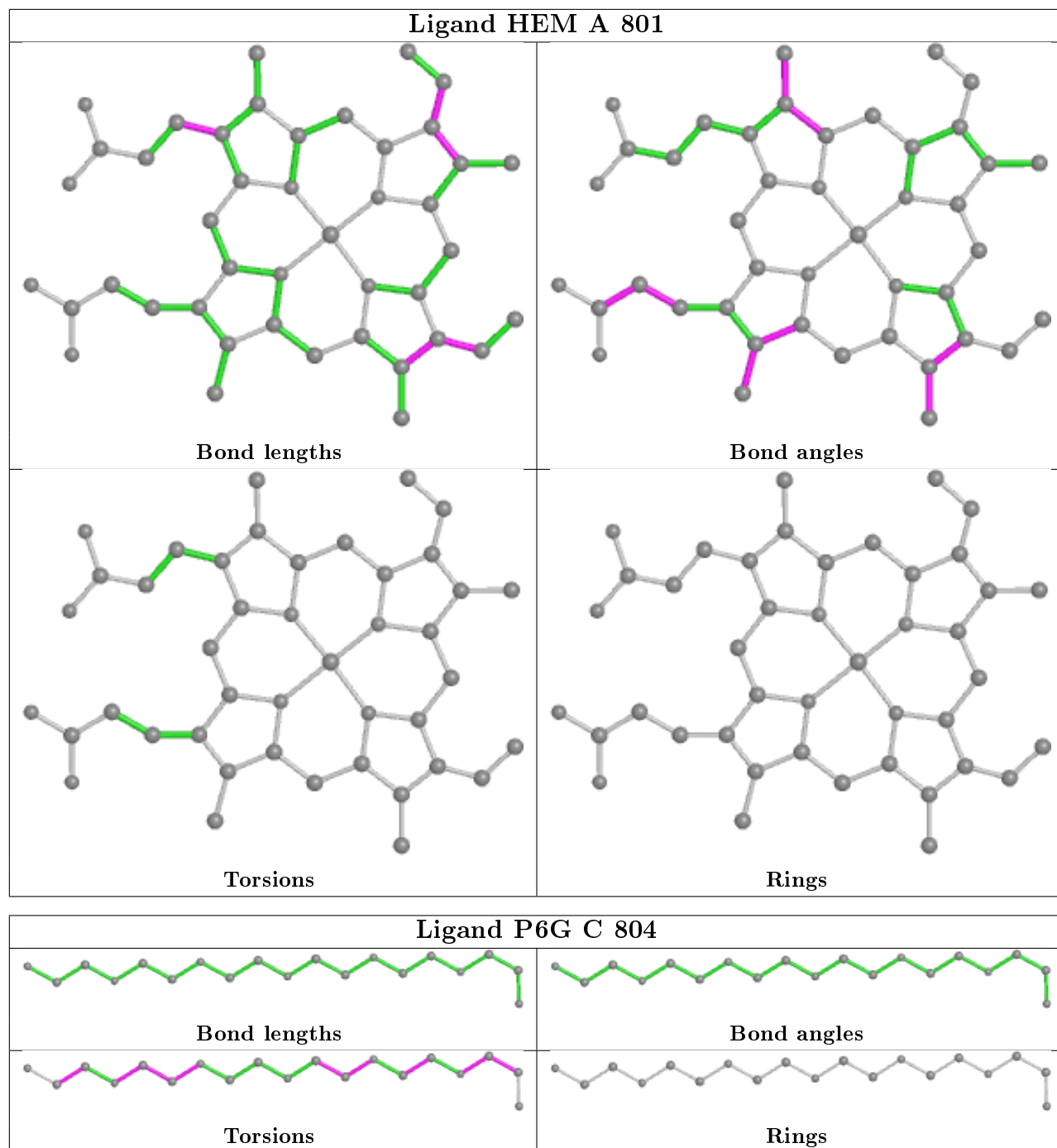
13 monomers are involved in 32 short contacts:

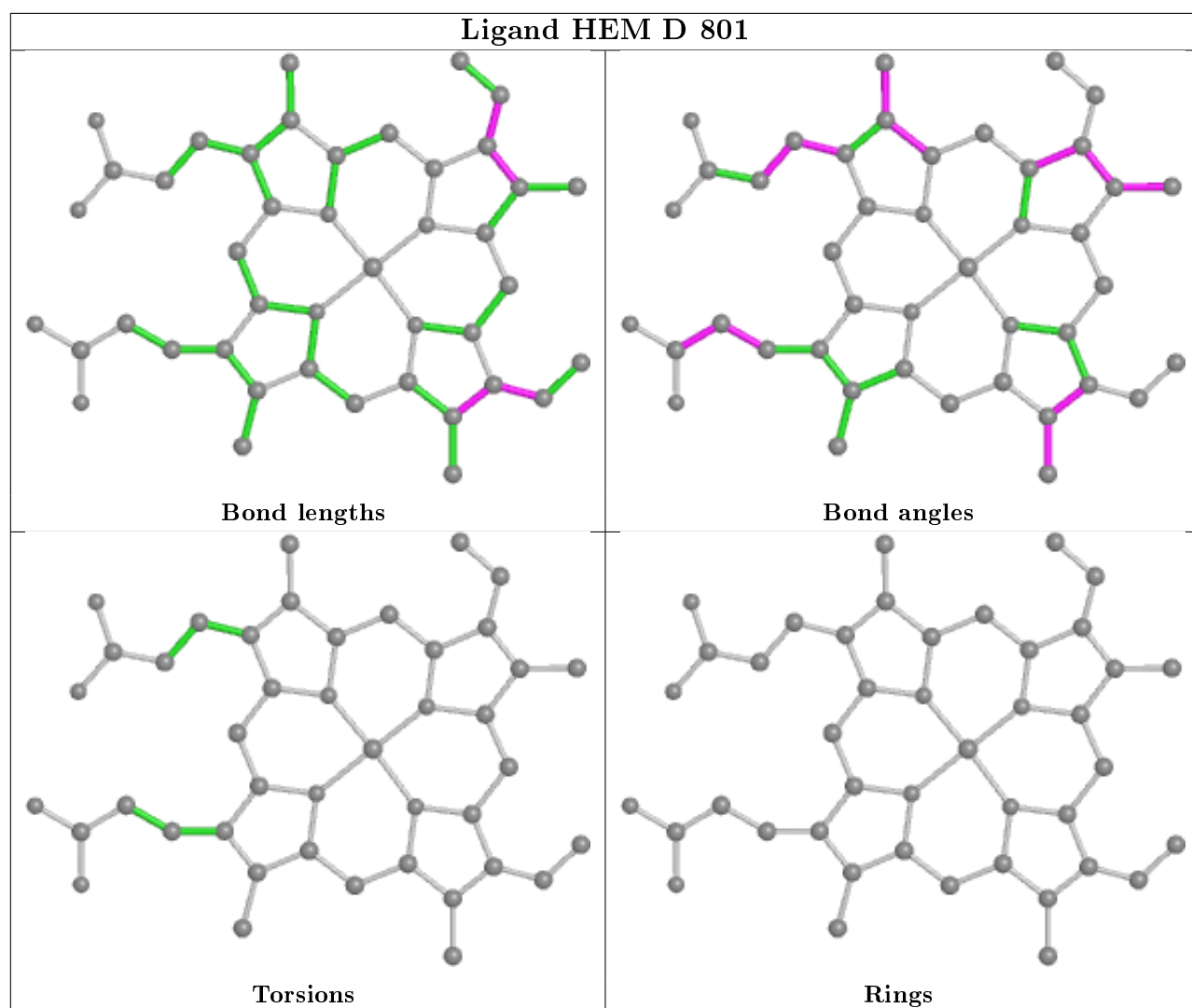
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	809	EDO	1	0
5	A	806	PEG	5	0
4	D	804	PGE	2	0
3	D	803	ACT	1	0
5	C	808	PEG	1	0
9	C	805	PG4	7	0
3	D	802	ACT	1	0
6	B	807	EDO	1	0
3	C	802	ACT	1	0
7	D	808	EOH	1	0
8	C	804	P6G	9	0
3	C	803	ACT	1	0
7	B	809	EOH	1	0

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.









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	682/719 (94%)	-0.56	7 (1%) 82 81	6, 16, 34, 70	0
1	B	677/719 (94%)	-0.67	4 (0%) 89 88	7, 13, 30, 56	0
1	C	679/719 (94%)	-0.65	7 (1%) 82 81	6, 14, 31, 64	0
1	D	678/719 (94%)	-0.63	6 (0%) 84 83	6, 15, 33, 76	0
All	All	2716/2876 (94%)	-0.63	24 (0%) 84 83	6, 15, 32, 76	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	637	GLY	3.7
1	A	719	GLU	3.7
1	D	680	GLU	3.5
1	A	638	LYS	3.5
1	C	715	GLY	3.3
1	C	716	ASP	3.1
1	C	641	MET	3.0
1	B	682	LYS	3.0
1	B	637	GLY	2.9
1	A	637	GLY	2.6
1	D	715	GLY	2.6
1	A	540	ALA	2.5
1	D	641	MET	2.5
1	B	638	LYS	2.4
1	C	540	ALA	2.4
1	B	641	MET	2.4
1	D	682	LYS	2.4
1	C	681	GLU	2.3
1	C	638	LYS	2.3
1	C	450	THR	2.3
1	A	41	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	579	GLY	2.1
1	A	681	GLU	2.1
1	D	38	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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
6	EDO	C	810	4/4	0.72	0.19	27,29,30,32	0
6	EDO	D	806	4/4	0.74	0.23	28,28,29,30	0
4	PGE	D	804	10/10	0.76	0.21	27,29,31,32	0
3	ACT	A	803	4/4	0.79	0.20	17,18,19,24	0
4	PGE	A	804	10/10	0.80	0.28	26,28,29,30	0
7	EOH	D	810	3/3	0.80	0.22	20,20,21,24	0
3	ACT	D	803	4/4	0.81	0.18	18,19,19,22	0
7	EOH	B	808	3/3	0.84	0.13	23,23,25,29	0
4	PGE	C	806	10/10	0.85	0.24	18,21,24,24	0
7	EOH	D	808	3/3	0.86	0.12	27,27,30,34	0
7	EOH	B	809	3/3	0.87	0.31	20,20,21,24	0
5	PEG	B	805	7/7	0.88	0.30	19,20,22,23	0
9	PG4	C	805	13/13	0.88	0.18	25,26,27,28	0
5	PEG	A	806	7/7	0.89	0.28	18,19,24,24	0
5	PEG	A	805	7/7	0.89	0.24	24,26,27,28	0
3	ACT	C	803	4/4	0.89	0.16	15,16,17,17	0
8	P6G	C	804	19/19	0.89	0.29	19,21,24,26	0
6	EDO	C	809	4/4	0.90	0.21	29,29,30,32	0
7	EOH	D	809	3/3	0.91	0.15	19,19,20,23	0
3	ACT	B	803	4/4	0.91	0.13	16,17,17,19	0

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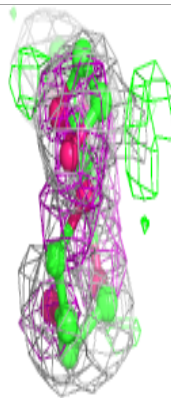
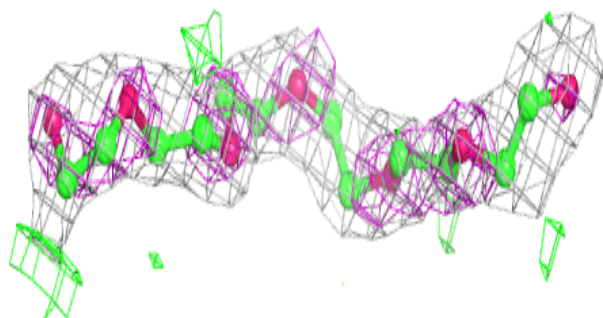
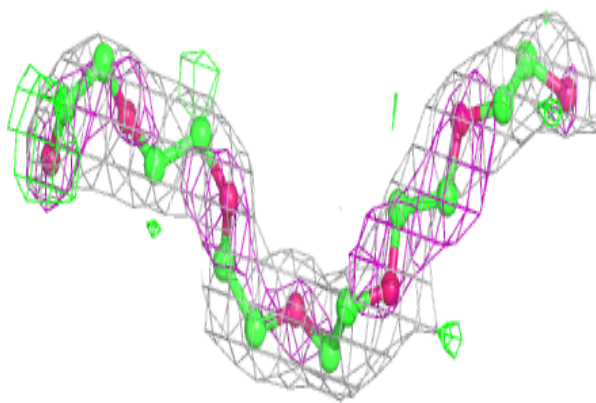
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	EDO	B	807	4/4	0.91	0.18	30,30,31,33	0
6	EDO	D	807	4/4	0.91	0.25	20,21,22,23	0
5	PEG	C	807	7/7	0.91	0.18	28,29,31,34	0
5	PEG	C	808	7/7	0.92	0.17	25,26,28,30	0
6	EDO	B	806	4/4	0.92	0.21	25,25,27,28	0
7	EOH	A	808	3/3	0.92	0.11	22,22,22,25	0
6	EDO	D	805	4/4	0.92	0.29	29,29,31,33	0
6	EDO	C	811	4/4	0.93	0.24	25,26,27,29	0
6	EDO	A	807	4/4	0.94	0.13	26,27,27,30	0
4	PGE	B	804	10/10	0.95	0.15	23,26,29,31	0
3	ACT	C	802	4/4	0.95	0.10	17,19,20,20	0
3	ACT	A	802	4/4	0.95	0.12	15,15,16,16	0
3	ACT	D	802	4/4	0.97	0.09	17,17,19,19	0
2	HEM	C	801	43/43	0.98	0.09	4,7,10,11	0
2	HEM	A	801	43/43	0.98	0.08	4,8,11,11	0
2	HEM	B	801	43/43	0.98	0.08	4,8,11,11	0
2	HEM	D	801	43/43	0.98	0.08	4,7,10,11	0
3	ACT	B	802	4/4	0.99	0.06	13,14,14,16	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.

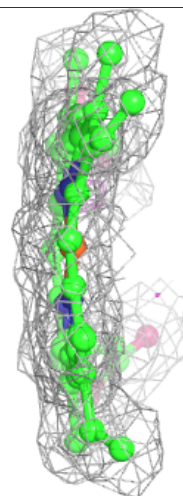
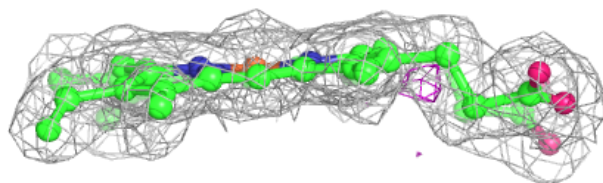
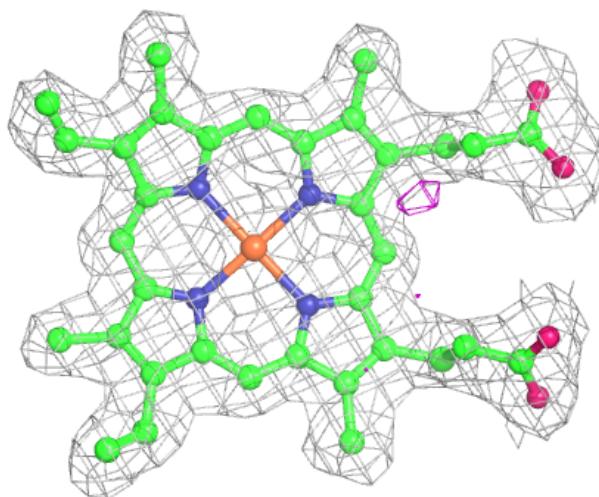
Electron density around P6G C 804:

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



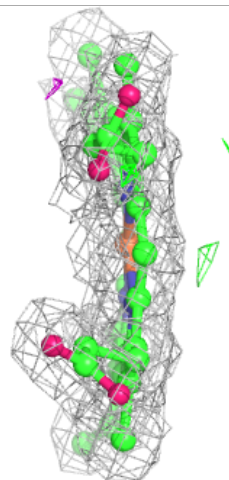
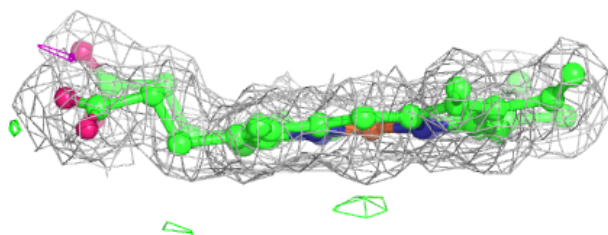
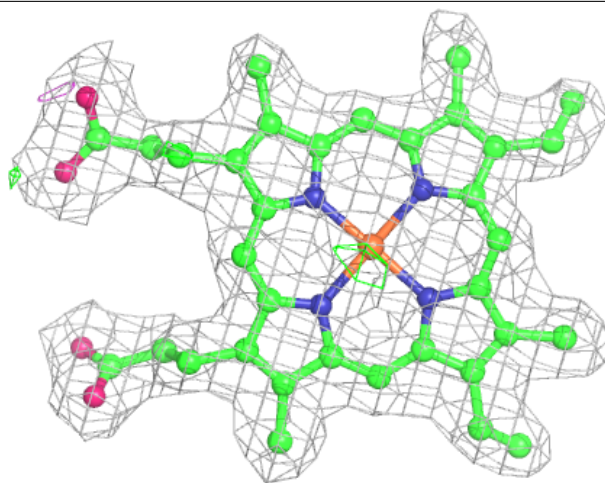
Electron density around HEM C 801:

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



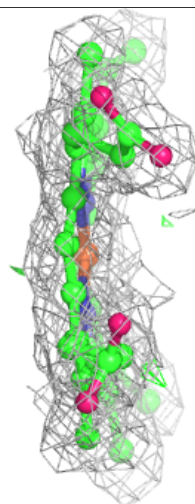
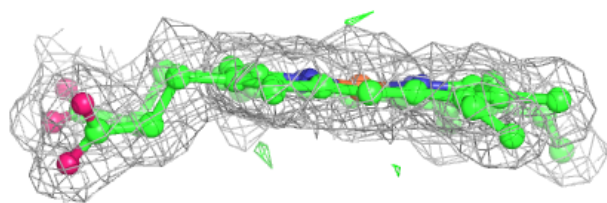
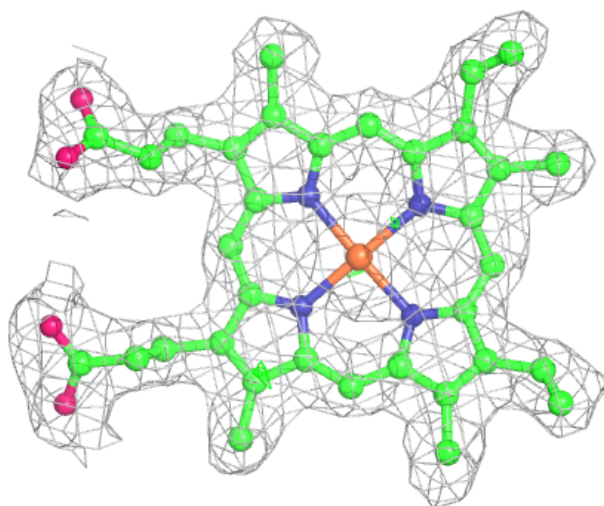
Electron density around HEM A 801:

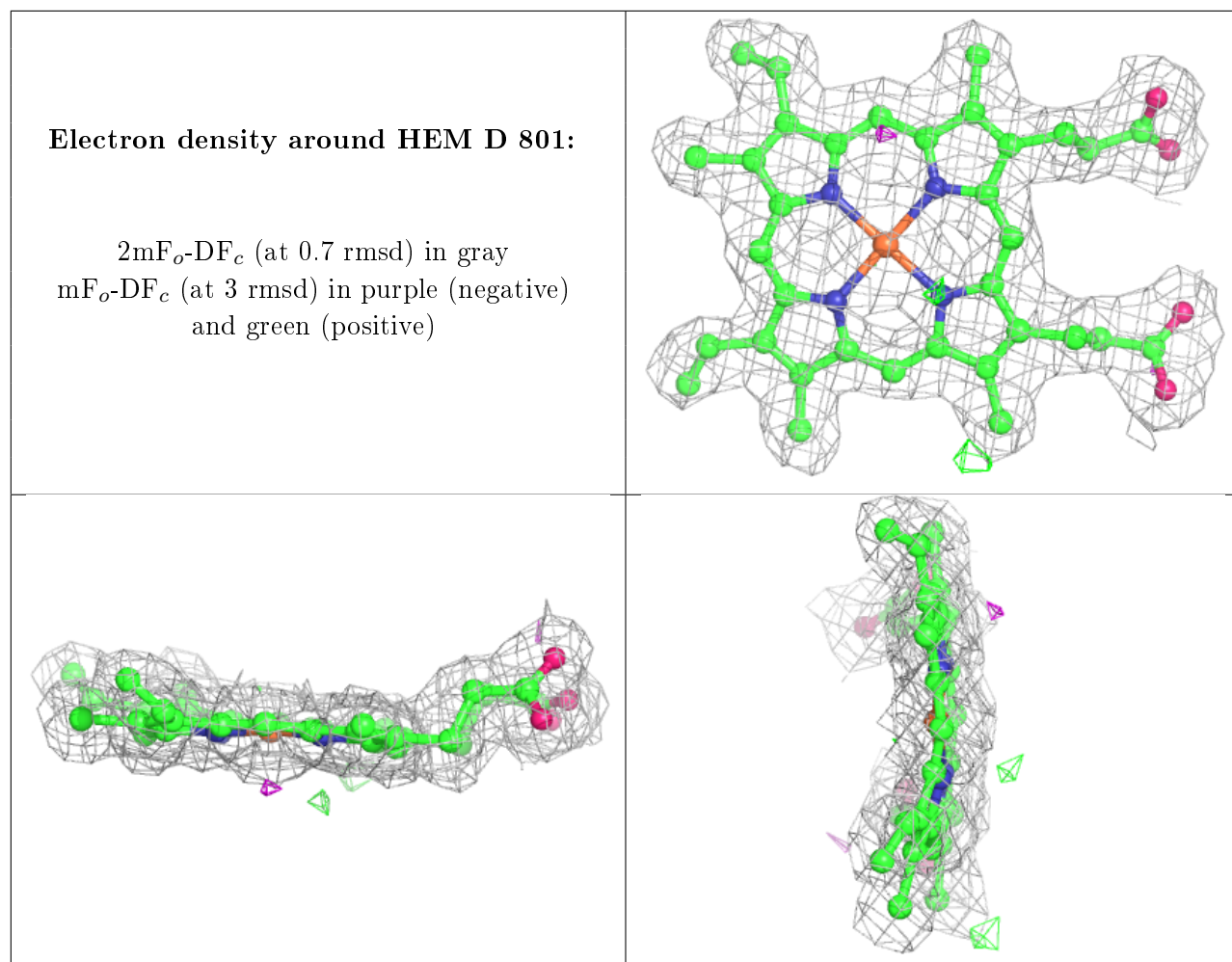
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 801:

$2mF_o-DF_c$ (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.