



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 07:33 PM EDT

PDB ID : 1Y4Z / pdb_00001y4z
Title : The crystal structure of Nitrate Reductase A, NarGHI, in complex with the Q-site inhibitor pentachlorophenol
Authors : Bertero, M.G.; Rothery, R.A.; Boroumand, N.; Palak, M.; Blasco, F.; Ginet, N.; Weiner, J.H.; Strynadka, N.C.J.
Deposited on : 2004-12-01
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

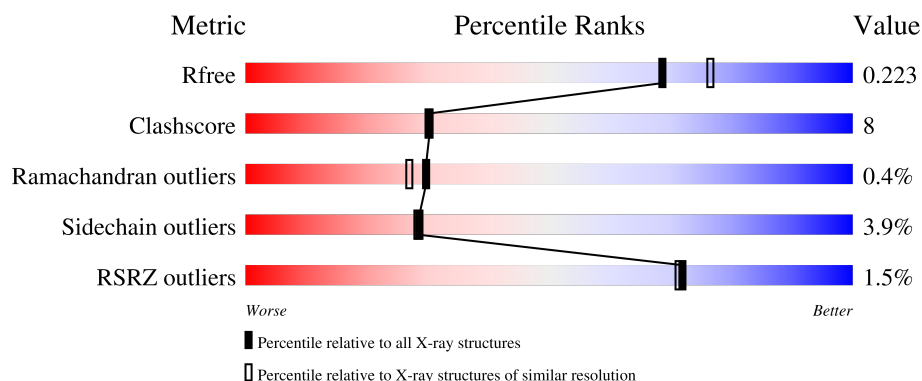
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

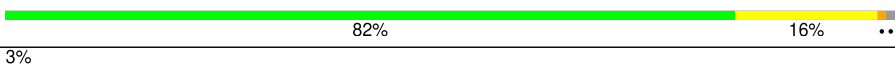
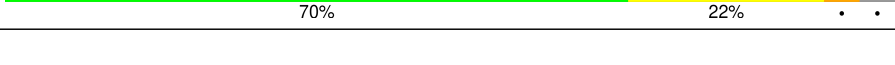
The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1246	
2	B	512	
3	C	225	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	PCI	C	1808	-	X	-	-
8	F3S	B	1803	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 16919 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 Respiratory nitrate reductase 1 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1244	Total	C	N	O	S	0	0	0
			9871	6236	1731	1856	48			

- Molecule 2 is a protein called Respiratory nitrate reductase 1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	509	Total	C	N	O	S	0	0	0
			4049	2562	701	755	31			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	26	ALA	CYS	engineered mutation	UNP P11349

- Molecule 3 is a protein called Respiratory nitrate reductase 1 gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	217	Total	C	N	O	S	0	0	0
			1723	1141	291	278	13			

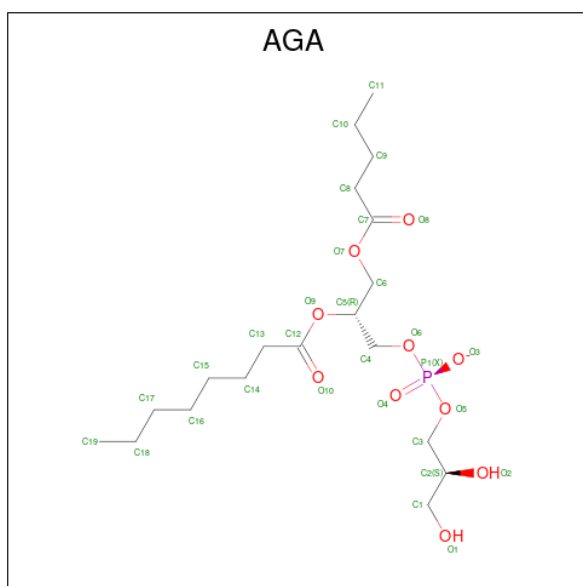
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	FME	MET	modified residue	UNP P11350

- Molecule 4 is PHOSPHORIC ACID 4-(2-AMINO-4-OXO-3,4,5,6,-TETRAHYDRO-PTE RIDIN-6-YL)-2-HYDROXY-3,4-DIMERCAPTO-BUT-3-EN-YL ESTER GUANYLATE ESTER (CCD ID: MD1) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).

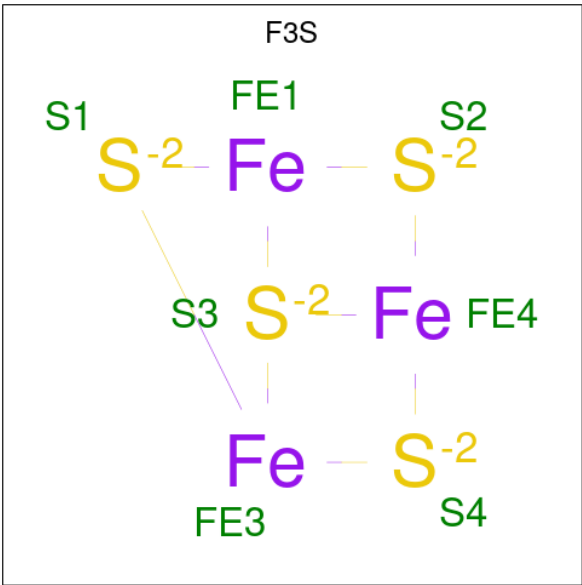
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Fe	S	0	0
			8	4	4		
6	B	1	Total	Fe	S	0	0
			8	4	4		
6	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 7 is (1S)-2-{{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PENTANOYLOXY)METHYL]ETHYL OCTANOATE (CCD ID: AGA) (formula: C₁₉H₃₆O₁₀P).



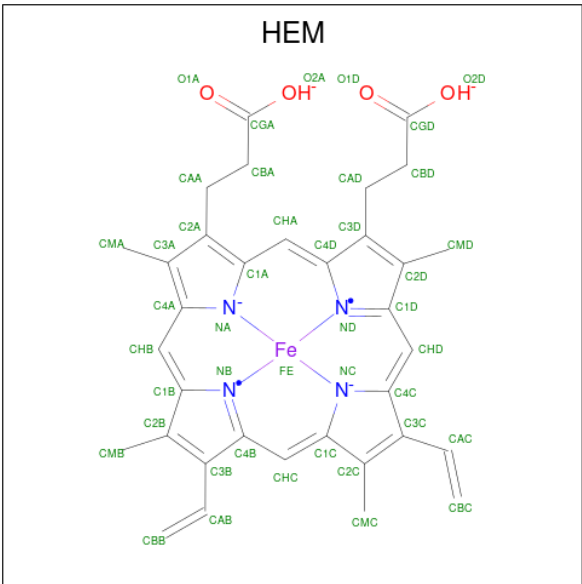
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			25	16	8	1		

- Molecule 8 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe₃S₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	Fe	S		0	0
			7	3	4			
8	B	1	Total	Fe	S		0	0
			7	3	4			

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



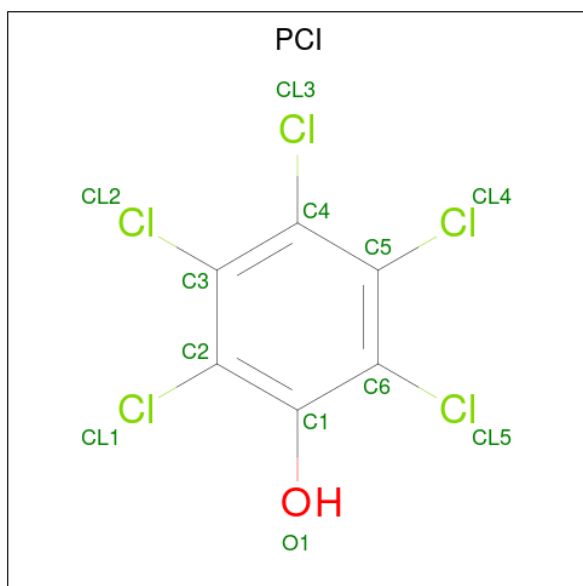
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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

- Molecule 10 is PENTACHLOROPHENOL (CCD ID: PCI) (formula: C_6HCl_5O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	C	1	Total	C	Cl	O		
			12	6	5	1		
							0	0

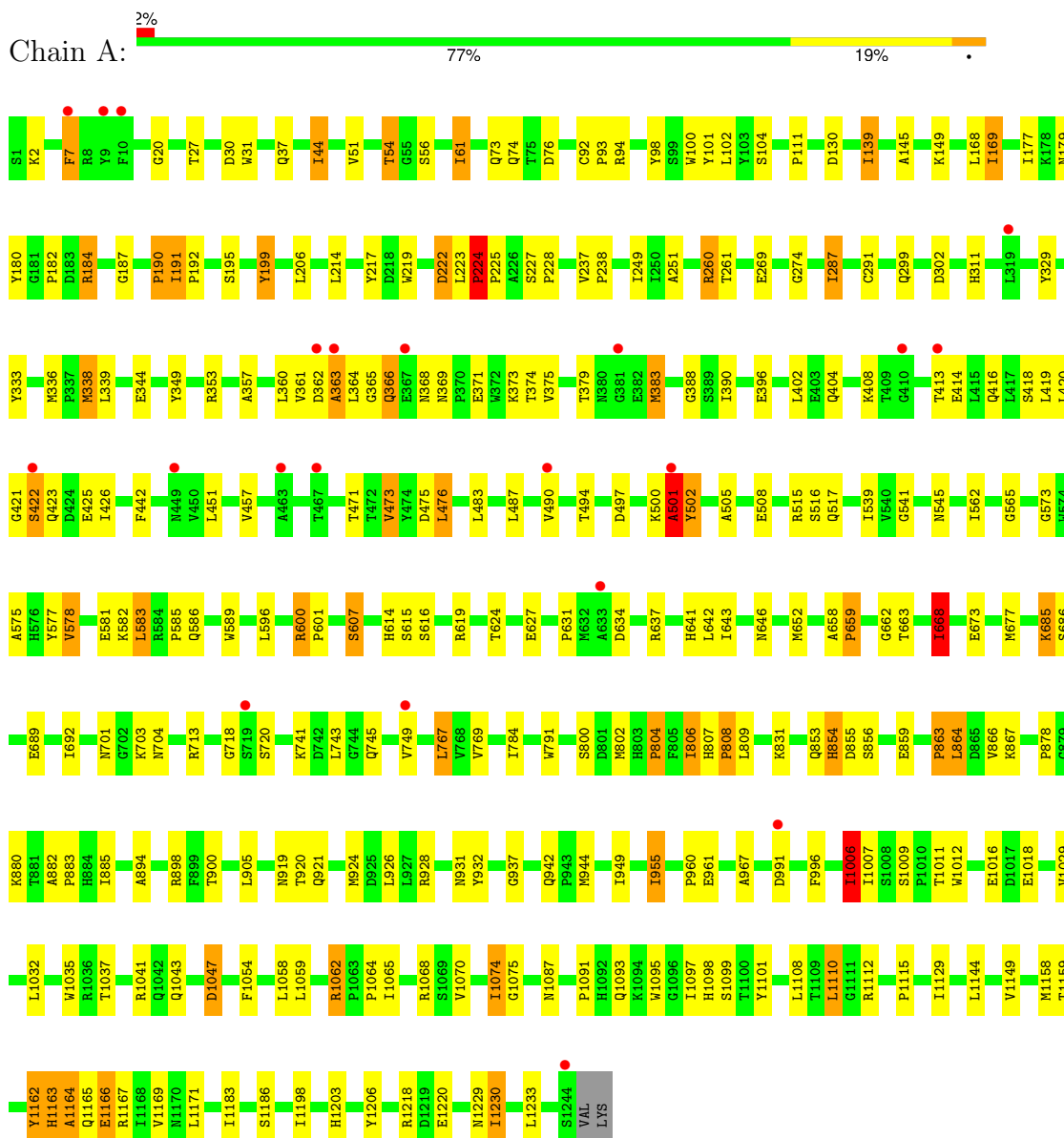
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	595	Total	O		
			595	595	0	0
11	B	368	Total	O		
			368	368	0	0
11	C	57	Total	O		
			57	57	0	0

3 Residue-property plots

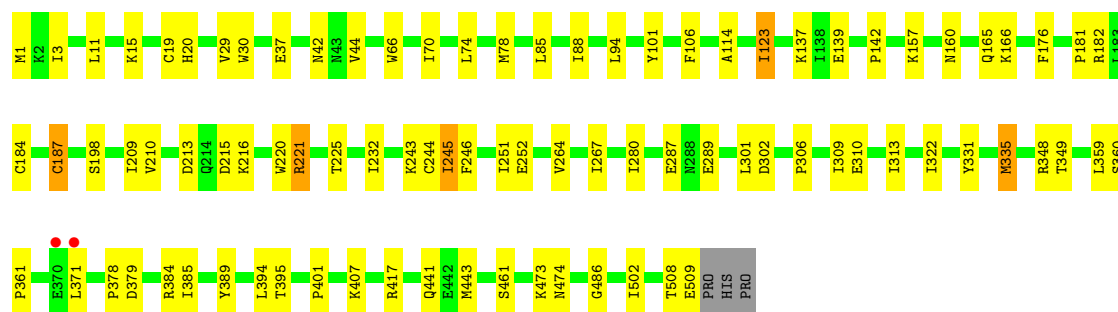
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Respiratory nitrate reductase 1 alpha chain



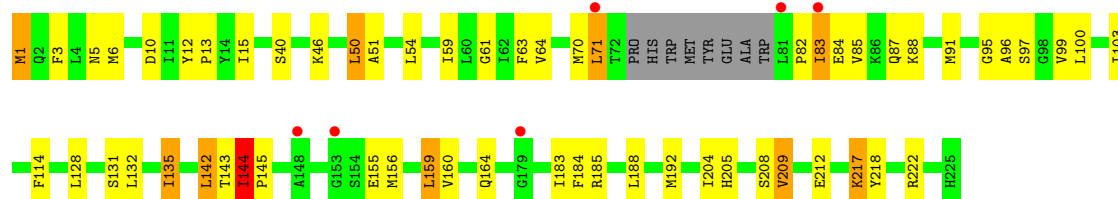
- Molecule 2: Respiratory nitrate reductase 1 beta chain

Chain B:  82% 16% ..



• Molecule 3: Respiratory nitrate reductase 1 gamma chain

Chain C:  3% 70% 22% . .



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	154.46Å 241.34Å 140.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.75 – 2.00 29.75 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.9 (29.75-2.00) 92.0 (29.75-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.188 , 0.233 0.181 , 0.223	Depositor DCC
R_{free} test set	9703 reflections (6.01%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.842	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16919	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PCI, FME, HEM, AGA, 6MO, F3S, MD1, SF4

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	0.88	6/10131 (0.1%)	1.20	78/13753 (0.6%)
2	B	0.91	0/4145	1.14	23/5608 (0.4%)
3	C	0.83	0/1758	1.10	13/2374 (0.5%)
All	All	0.88	6/16034 (0.0%)	1.17	114/21735 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1006	ILE	CA-CB	6.62	1.63	1.54
1	A	338	MET	SD-CE	-6.11	1.64	1.79
1	A	1163	HIS	C-N	-5.89	1.25	1.33
1	A	191	ILE	CA-CB	5.23	1.60	1.54
1	A	501	ALA	C-N	-5.20	1.26	1.33

The worst 5 of 114 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1163	HIS	CA-C-N	21.13	151.66	121.24
1	A	1163	HIS	C-N-CA	21.13	151.66	121.24
1	A	501	ALA	CA-C-N	13.91	148.10	121.54
1	A	501	ALA	C-N-CA	13.91	148.10	121.54
1	A	1163	HIS	CA-C-O	-9.61	110.48	120.96

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	501	ALA	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1163	HIS	Peptide,Mainchain
1	A	501	ALA	Peptide,Mainchain
1	A	502	TYR	Mainchain

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	9871	0	9528	178	0
2	B	4049	0	3974	61	0
3	C	1723	0	1772	33	0
4	A	94	0	42	7	0
5	A	1	0	0	0	0
6	A	8	0	0	0	0
6	B	16	0	0	0	0
7	A	25	0	29	0	0
8	B	14	0	0	3	0
9	C	86	0	60	1	0
10	C	12	0	1	1	0
11	A	595	0	0	7	1
11	B	368	0	0	8	0
11	C	57	0	0	1	0
All	All	16919	0	15406	263	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 263 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:A:641:HIS:HD2	1:A:643:ILE:H	1.14	0.93
1:A:652:MET:HE1	1:A:866:VAL:HG13	1.55	0.87
2:B:3:ILE:HD12	2:B:301:LEU:CD1	2.06	0.86
1:A:338:MET:HE2	1:A:374:THR:OG1	1.77	0.84
2:B:361:PRO:HG2	2:B:384:ARG:HD3	1.59	0.84

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:4064:HOH:O	11:A:4064:HOH:O[3_354]	1.00	1.20

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	1242/1246 (100%)	1174 (94%)	61 (5%)	7 (1%)	21	17
2	B	507/512 (99%)	495 (98%)	12 (2%)	0	100	100
3	C	213/225 (95%)	207 (97%)	6 (3%)	0	100	100
All	All	1962/1983 (99%)	1876 (96%)	79 (4%)	7 (0%)	30	27

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	422	SER
1	A	501	ALA
1	A	578	VAL
1	A	1166	GLU
1	A	195	SER

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	1039/1043 (100%)	995 (96%)	44 (4%)	26	25
2	B	435/438 (99%)	424 (98%)	11 (2%)	42	45
3	C	179/186 (96%)	170 (95%)	9 (5%)	22	20
All	All	1653/1667 (99%)	1589 (96%)	64 (4%)	28	28

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	59	ILE
3	C	97	SER
1	A	743	LEU
1	A	685	LYS
3	C	142	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	160	ASN
2	B	165	GLN
2	B	451	ASN
1	A	559	ASN
1	A	517	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$
3	FME	C	1	3	8,9,10	1.16	1 (12%)	8,9,11	1.71	2 (25%)

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
3	FME	C	1	3	-	5/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	FME	CB-CG	2.17	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	FME	CA-N-CN	3.59	128.34	122.82
3	C	1	FME	CB-CA-N	2.18	114.49	110.52

There are no chirality outliers.

All (5) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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
6	SF4	B	1802	2	0,12,12	-	-	-		
10	PCI	C	1808	-	12,12,12	9.44	11 (91%)	18,18,18	1.47	2 (11%)
8	F3S	B	1805	2	0,9,9	-	-	-		
6	SF4	A	1801	1	0,12,12	-	-	-		
4	MD1	A	1800	5	47,51,51	2.74	9 (19%)	56,78,78	1.45	8 (14%)
9	HEM	C	806	3	50,50,50	1.71	10 (20%)	67,82,82	0.92	2 (2%)
7	AGA	A	1309	-	24,24,29	0.95	1 (4%)	27,29,35	1.66	2 (7%)
9	HEM	C	807	3	50,50,50	1.92	16 (32%)	67,82,82	0.97	5 (7%)
8	F3S	B	1803	2	0,9,9	-	-	-		
4	MD1	A	2800	5	47,51,51	2.79	6 (12%)	56,78,78	1.42	7 (12%)
6	SF4	B	1804	2	0,12,12	-	-	-		

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
6	SF4	B	1802	2	-	-	0/6/5/5
10	PCI	C	1808	-	-	-	0/1/1/1
8	F3S	B	1805	2	-	-	1/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MD1	A	1800	5	-	7/22/59/59	0/5/5/5
9	HEM	C	806	3	-	4/14/54/54	-
6	SF4	A	1801	1	-	-	0/6/5/5
7	AGA	A	1309	-	-	3/26/26/34	-
9	HEM	C	807	3	-	6/14/54/54	-
8	F3S	B	1803	2	-	-	1/3/3/3
4	MD1	A	2800	5	-	1/22/59/59	0/5/5/5
6	SF4	B	1804	2	-	-	0/6/5/5

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1800	MD1	C7-N8	16.01	1.48	1.28
4	A	2800	MD1	C7-N8	15.76	1.48	1.28
10	C	1808	PCI	C6-CL5	-14.30	1.42	1.72
10	C	1808	PCI	C4-CL3	-13.78	1.43	1.72
10	C	1808	PCI	C2-CL1	-13.58	1.44	1.72

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1800	MD1	C17-N18-C20	5.96	122.45	114.20
4	A	2800	MD1	C17-N18-C20	5.85	122.30	114.20
7	A	1309	AGA	C9-C8-C7	5.50	133.86	113.69
7	A	1309	AGA	C14-C13-C12	4.75	131.09	113.69
10	C	1808	PCI	C6-C1-C2	4.74	122.86	117.78

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1800	MD1	C5'-O5'-PA-O3B
4	A	1800	MD1	C5'-O5'-PA-O2A
4	A	1800	MD1	O4'-C4'-C5'-O5'
4	A	1800	MD1	C3'-C4'-C5'-O5'
7	A	1309	AGA	C8-C7-O7-C6

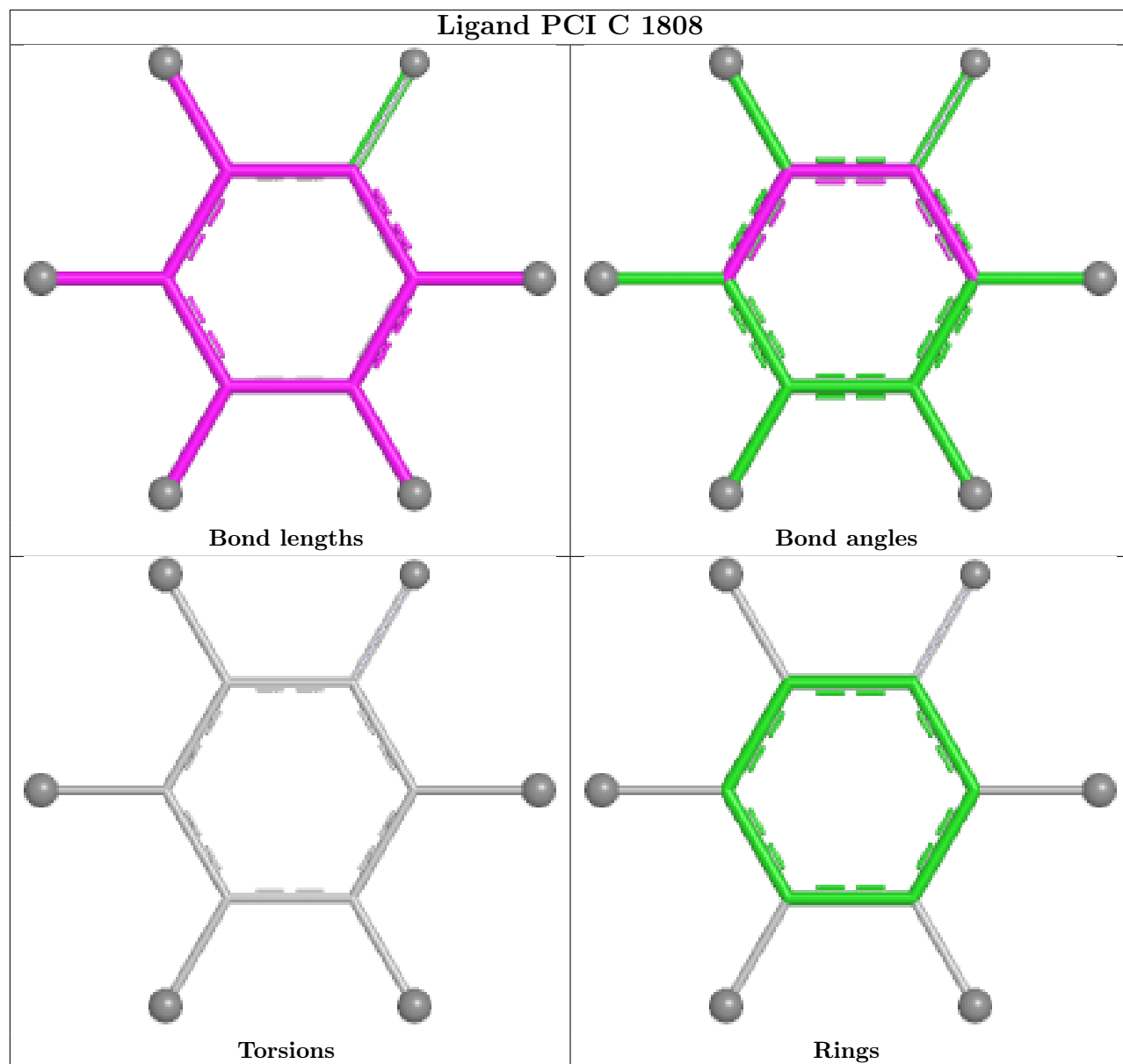
All (2) ring outliers are listed below:

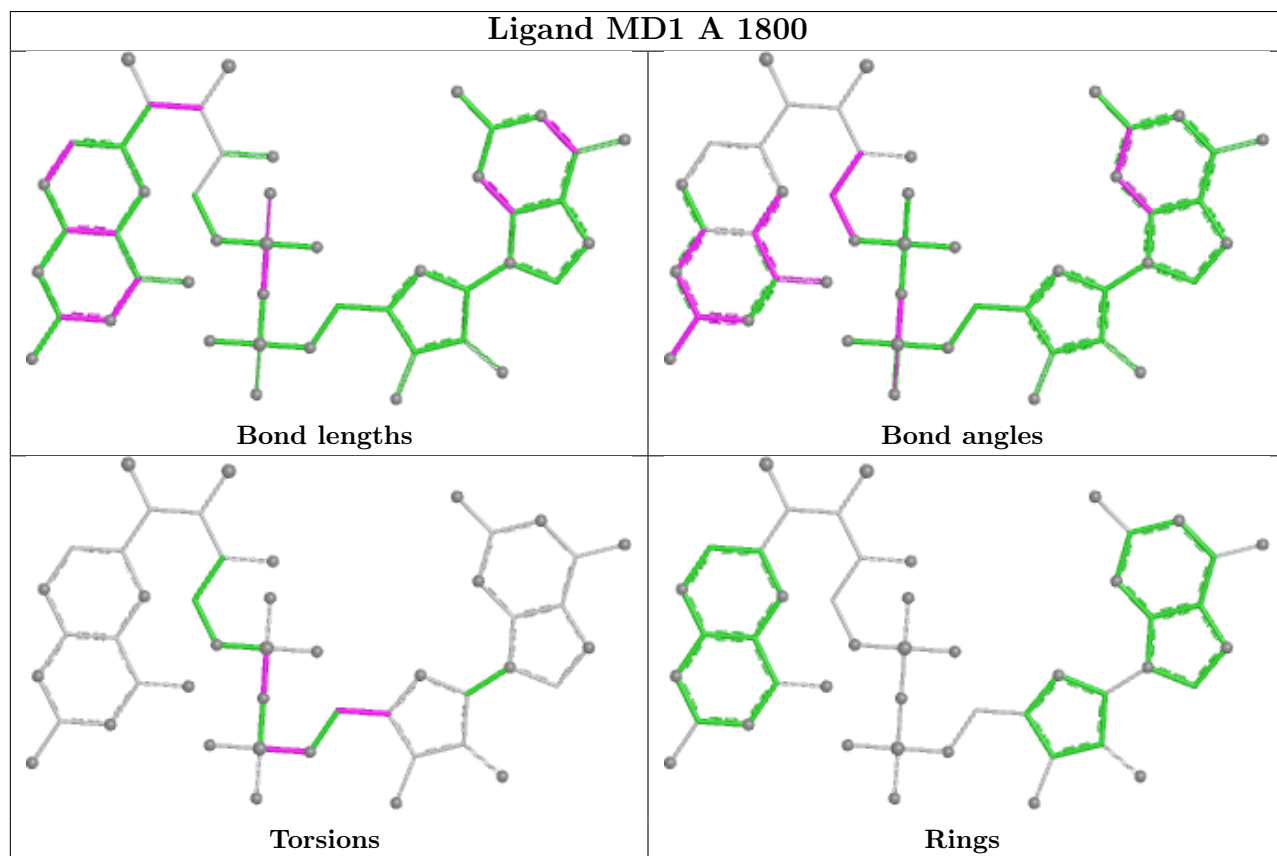
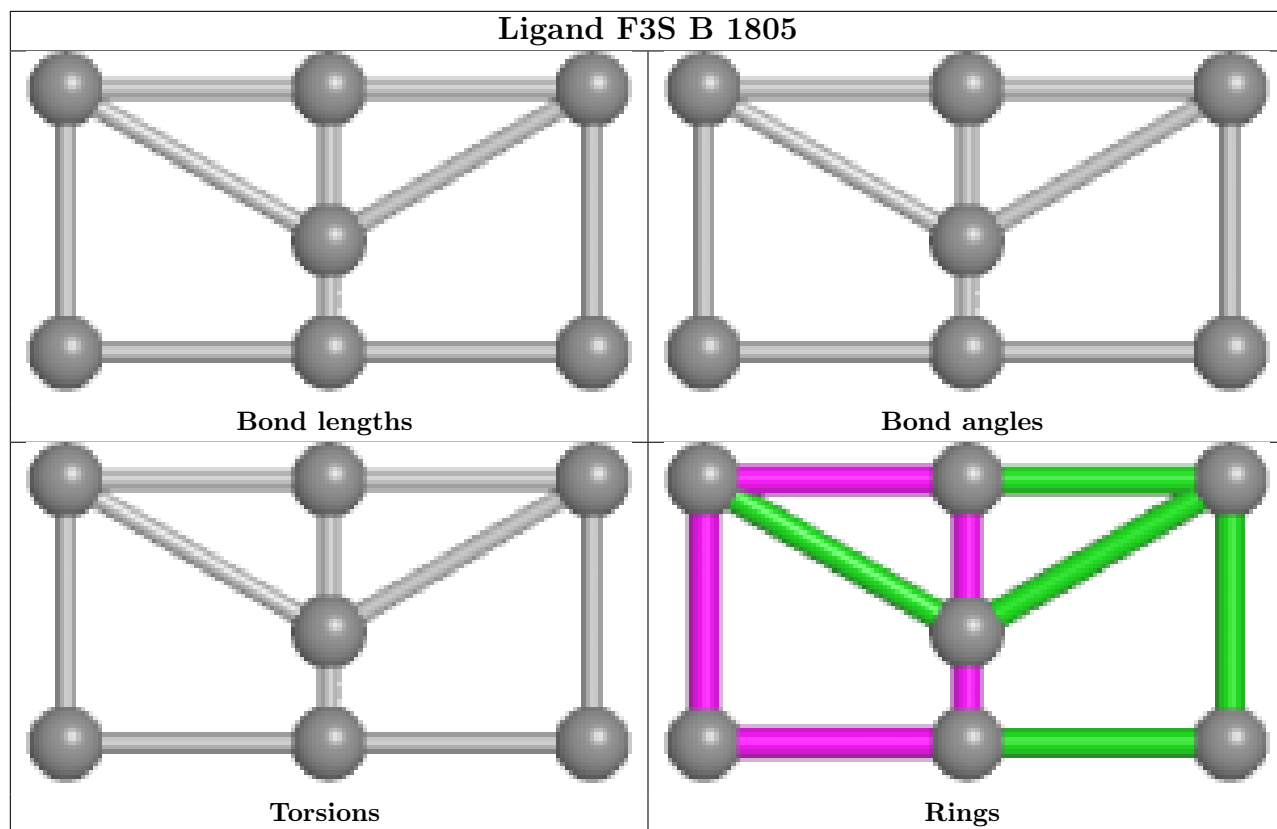
Mol	Chain	Res	Type	Atoms
8	B	1805	F3S	FE1-FE3-S1-S3
8	B	1803	F3S	FE1-FE3-S1-S3

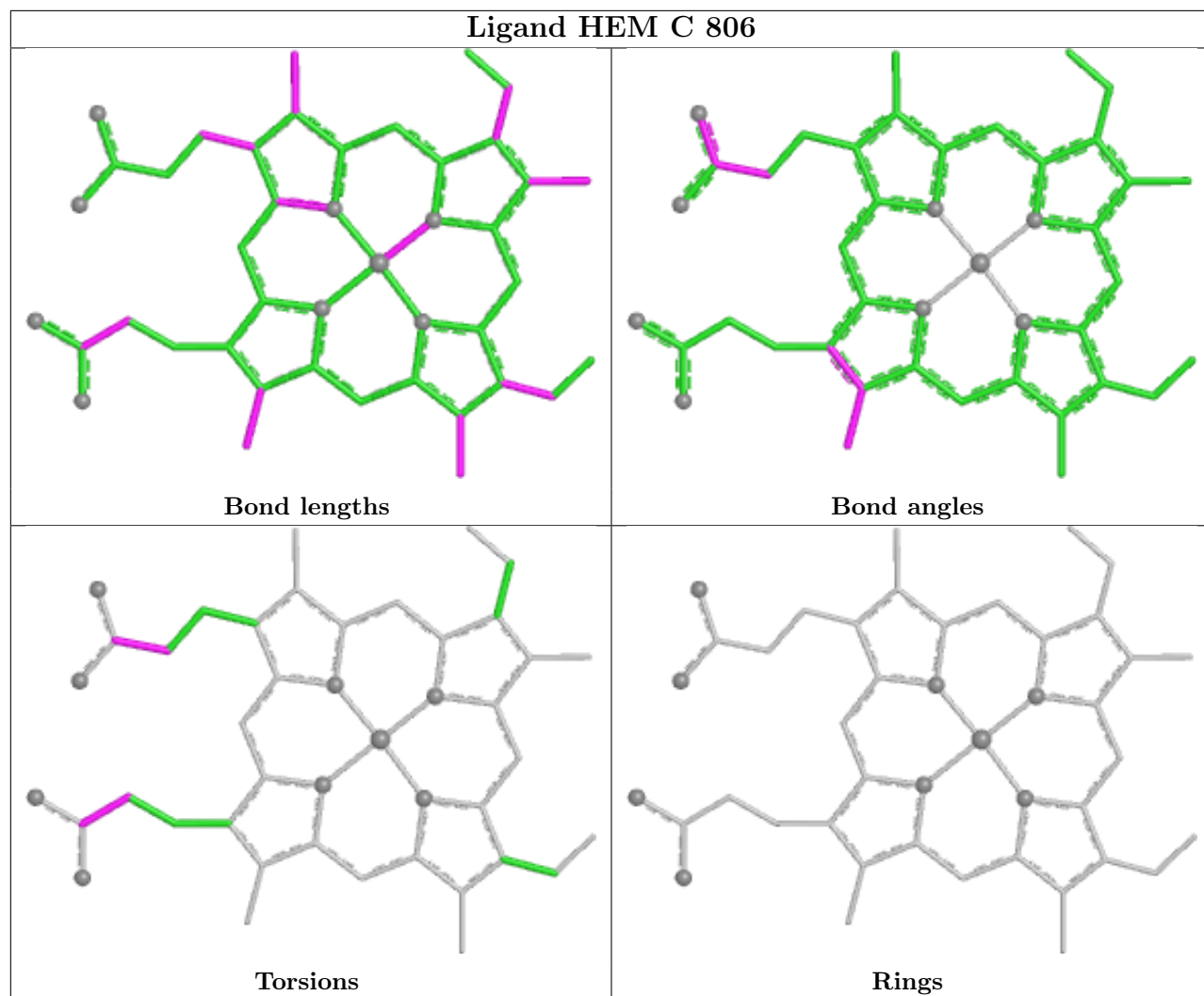
5 monomers are involved in 12 short contacts:

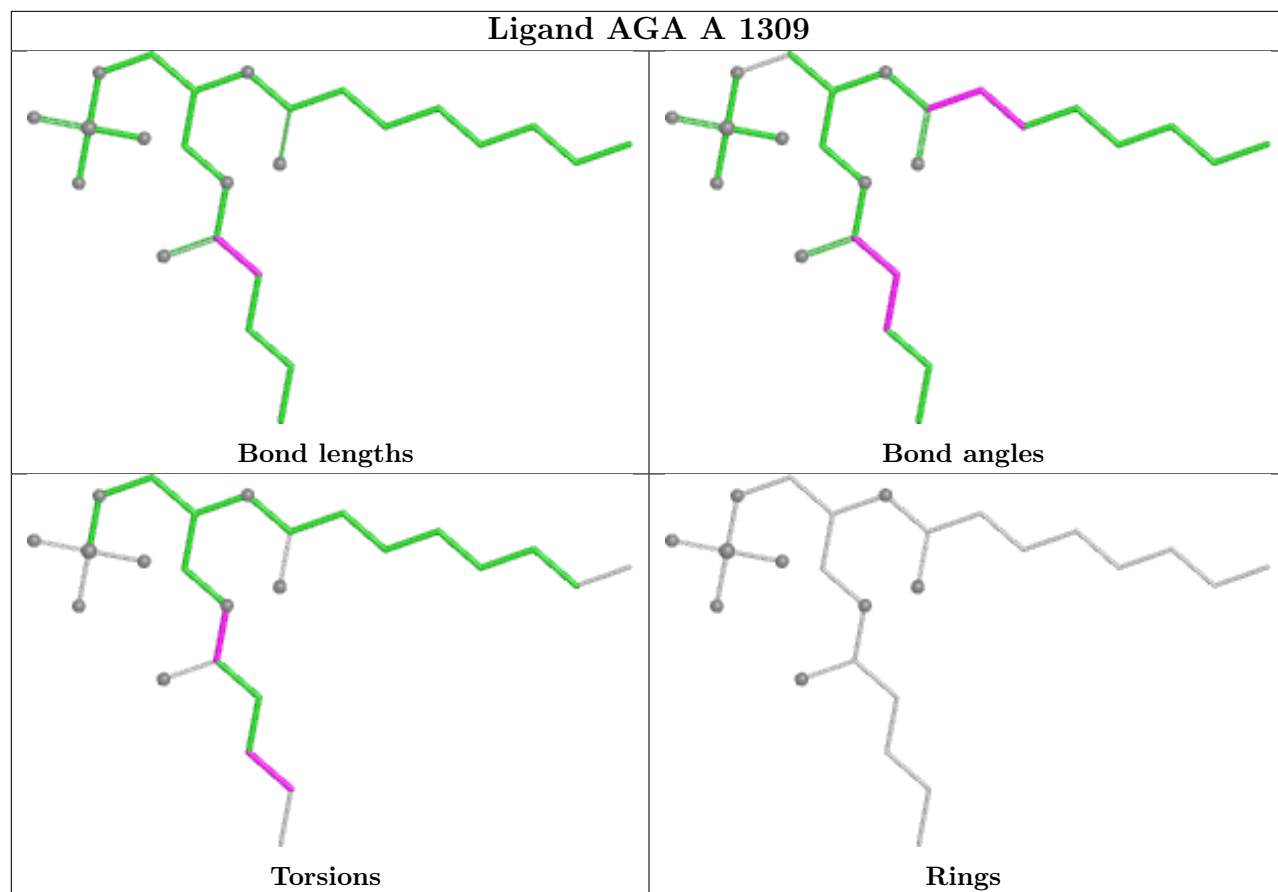
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	C	1808	PCI	1	0
4	A	1800	MD1	4	0
9	C	807	HEM	1	0
8	B	1803	F3S	3	0
4	A	2800	MD1	3	0

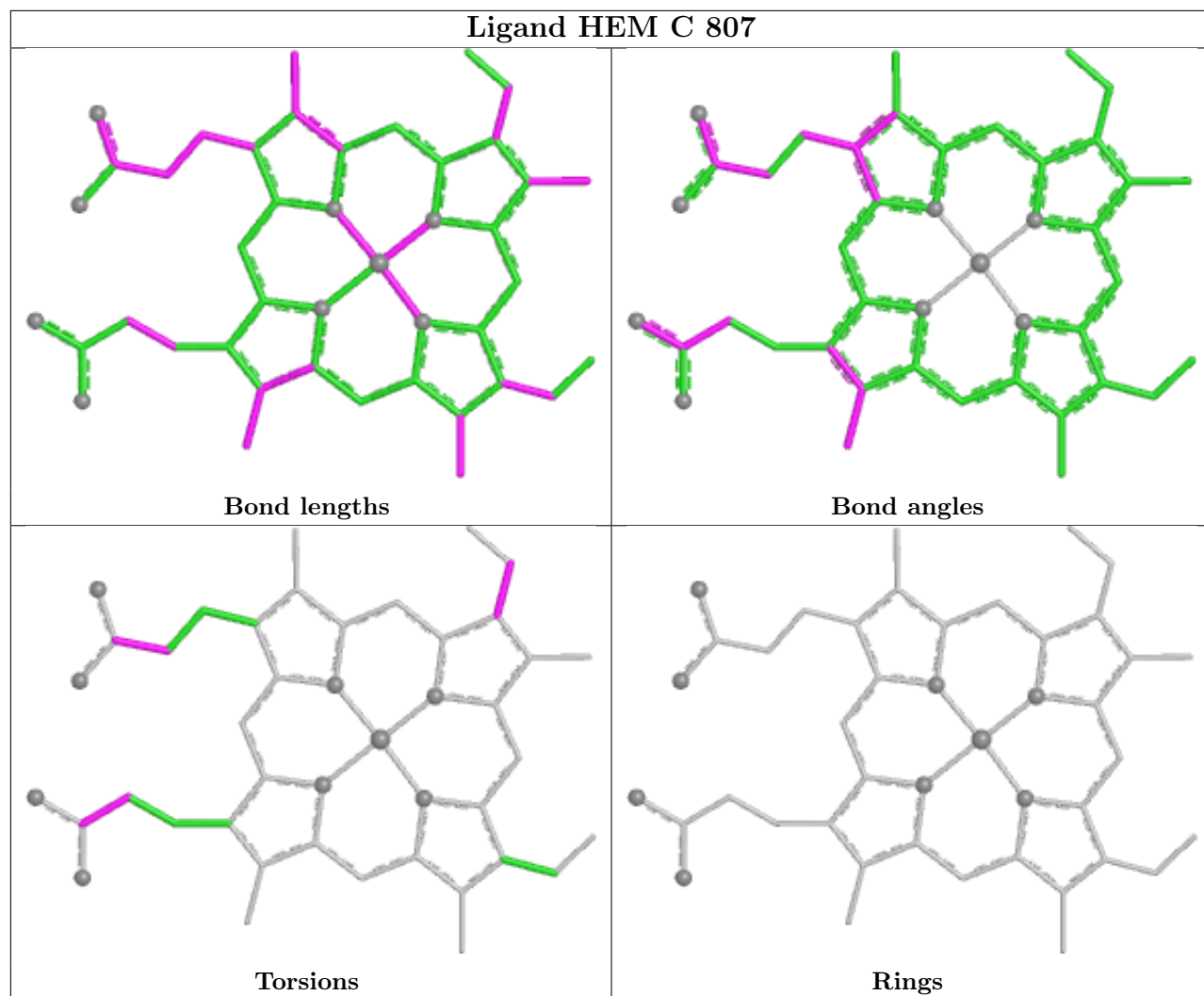
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

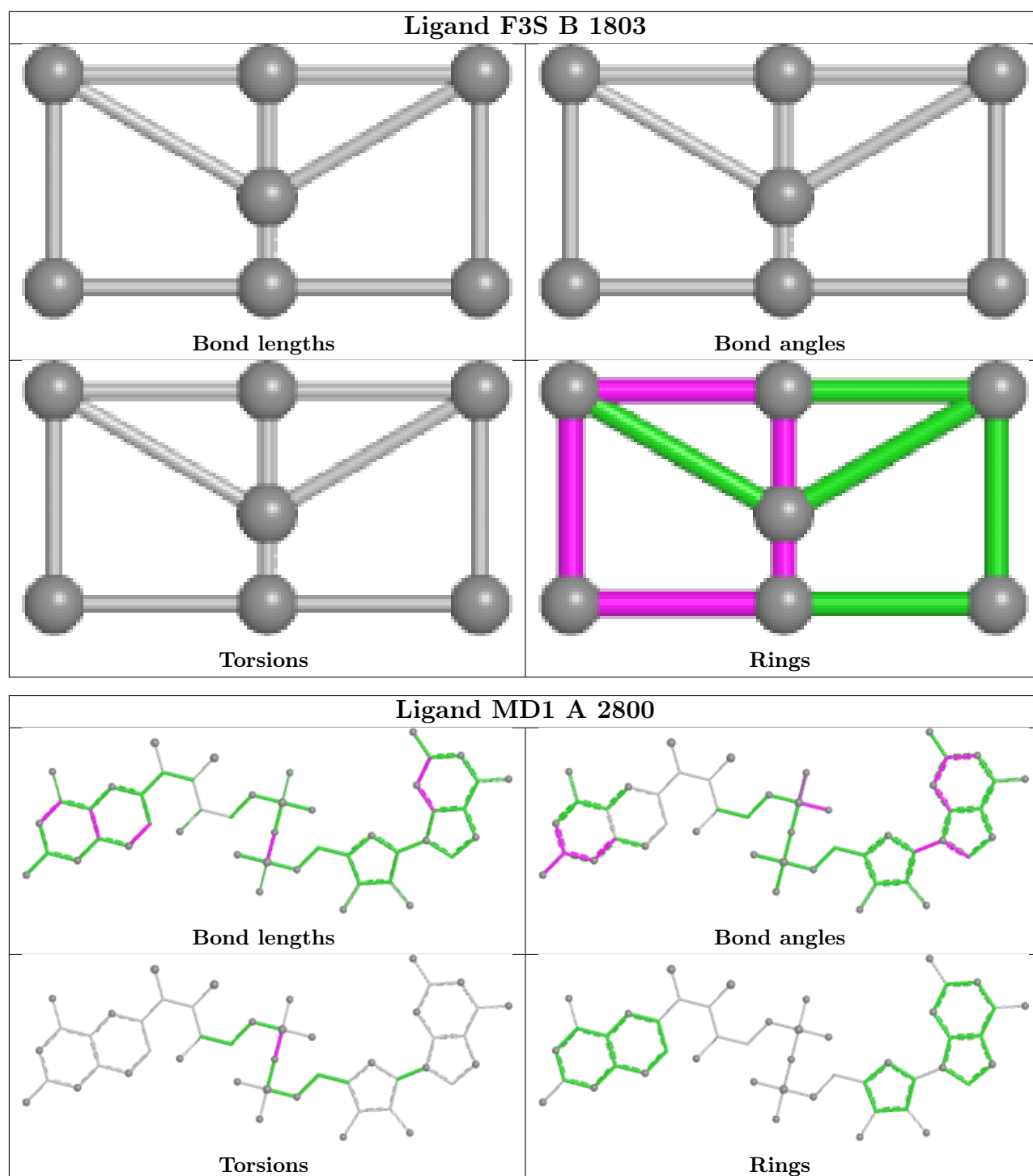












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	1244/1246 (99%)	-0.11	21 (1%) 69 68	14, 26, 47, 69	0
2	B	509/512 (99%)	-0.54	2 (0%) 88 88	14, 21, 33, 61	0
3	C	216/225 (96%)	0.32	6 (2%) 55 54	15, 31, 51, 57	0
All	All	1969/1983 (99%)	-0.17	29 (1%) 72 71	14, 25, 46, 69	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	9	TYR	4.8
1	A	10	PHE	4.2
1	A	501	ALA	3.4
1	A	7	PHE	3.0
1	A	362	ASP	2.8

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
3	FME	C	1	10/11	0.85	0.13	49,56,65,65	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

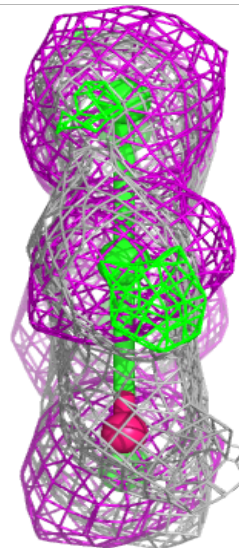
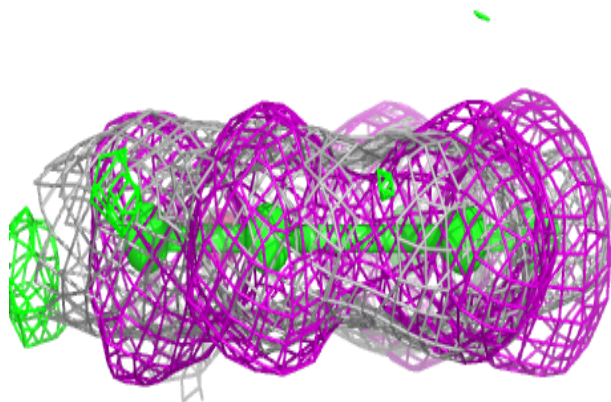
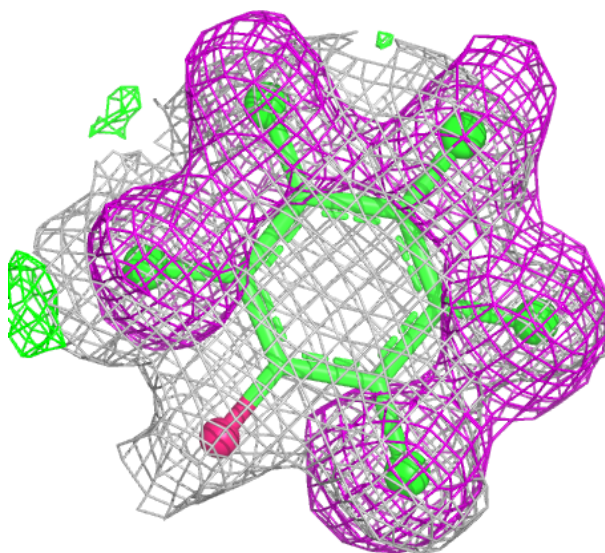
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	PCI	C	1808	12/12	0.84	0.16	33,38,40,40	0
9	HEM	C	807	43/43	0.94	0.12	35,39,45,50	0
7	AGA	A	1309	25/30	0.94	0.10	22,27,42,44	0
5	6MO	A	3800	1/1	0.95	0.19	52,52,52,52	0
4	MD1	A	2800	47/47	0.95	0.07	19,24,33,39	0
4	MD1	A	1800	47/47	0.96	0.07	14,23,36,40	0
6	SF4	B	1804	8/8	0.97	0.05	25,29,31,33	0
6	SF4	A	1801	8/8	0.98	0.05	21,22,28,29	0
9	HEM	C	806	43/43	0.98	0.06	16,22,25,32	0
6	SF4	B	1802	8/8	0.99	0.03	21,23,24,25	0
8	F3S	B	1803	7/7	0.99	0.03	19,21,22,23	0
8	F3S	B	1805	7/7	0.99	0.02	18,19,20,21	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.

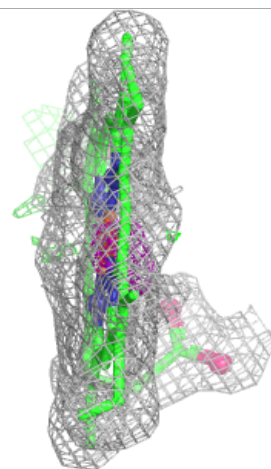
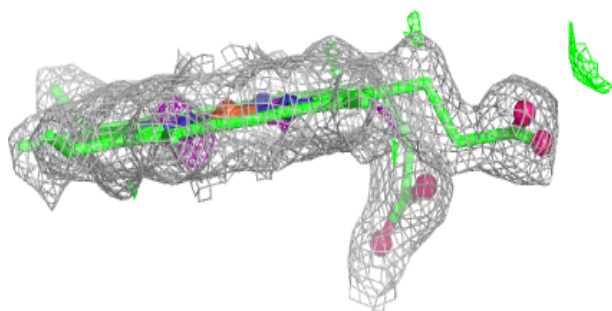
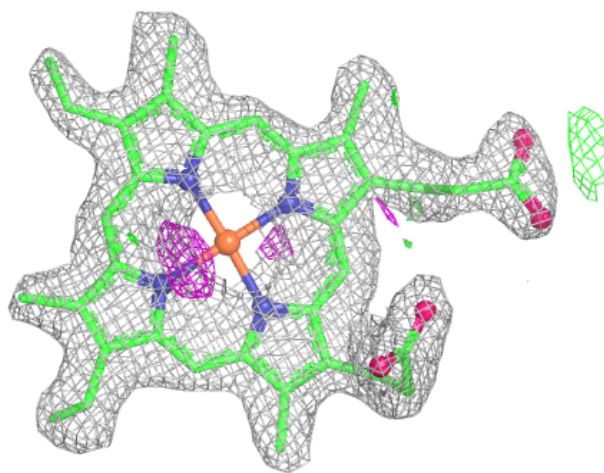
Electron density around PCI C 1808:

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



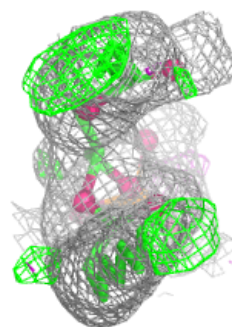
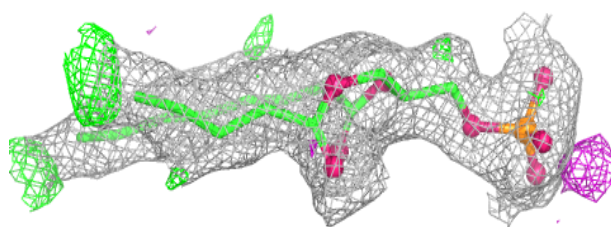
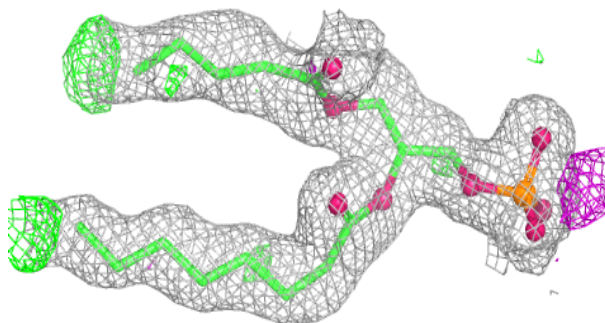
Electron density around HEM C 807:

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

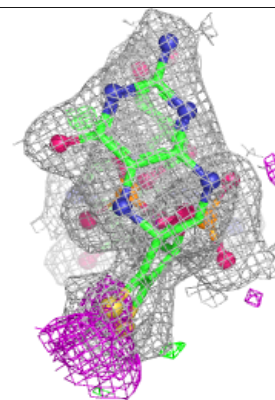
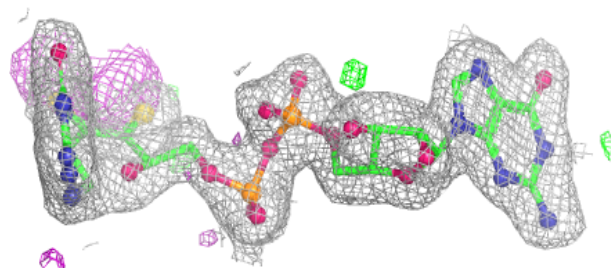
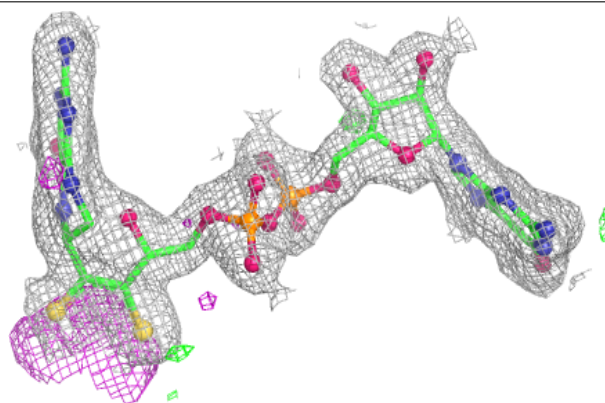


Electron density around AGA A 1309:

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

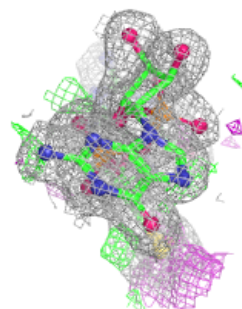
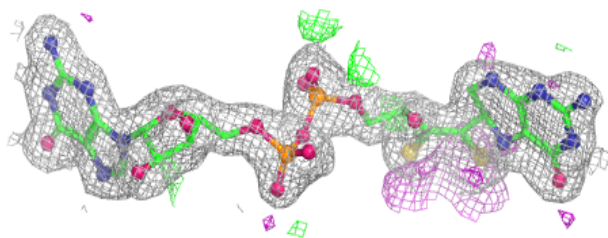
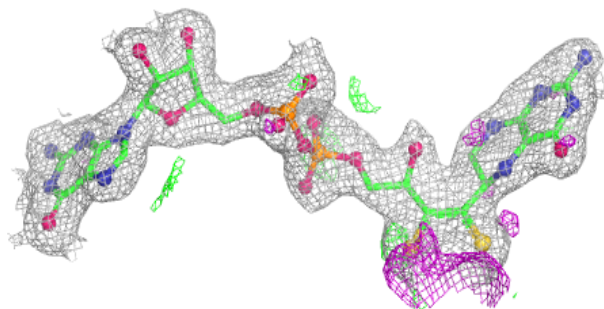
**Electron density around MD1 A 2800:**

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



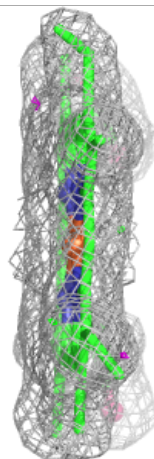
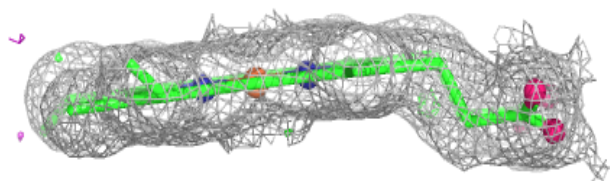
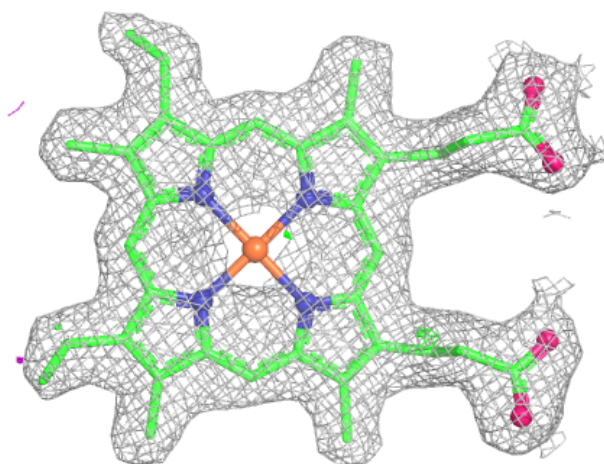
Electron density around MD1 A 1800:

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



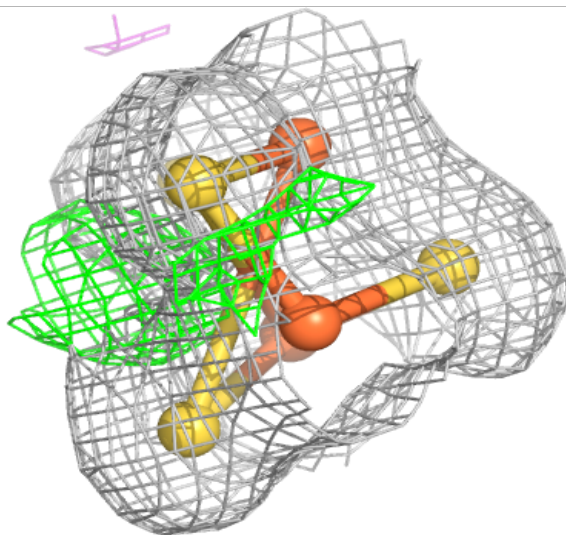
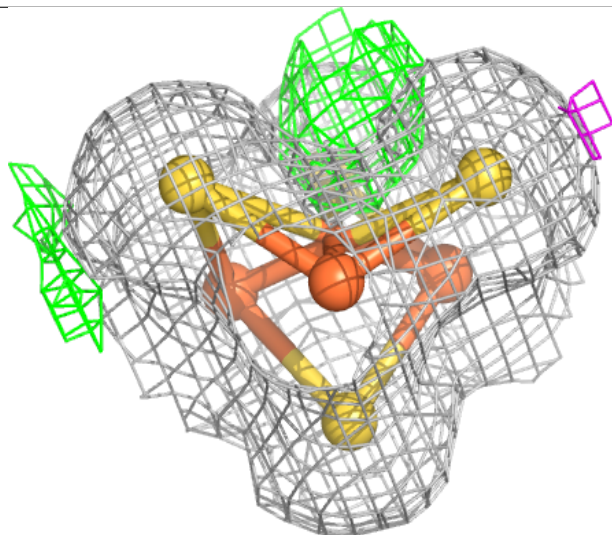
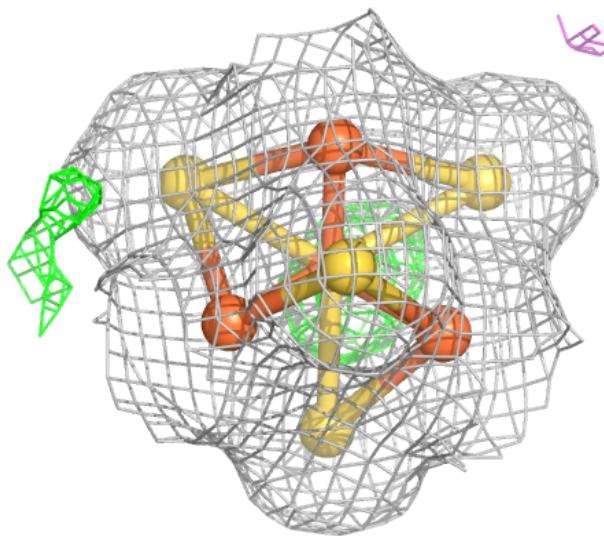
Electron density around HEM C 806:

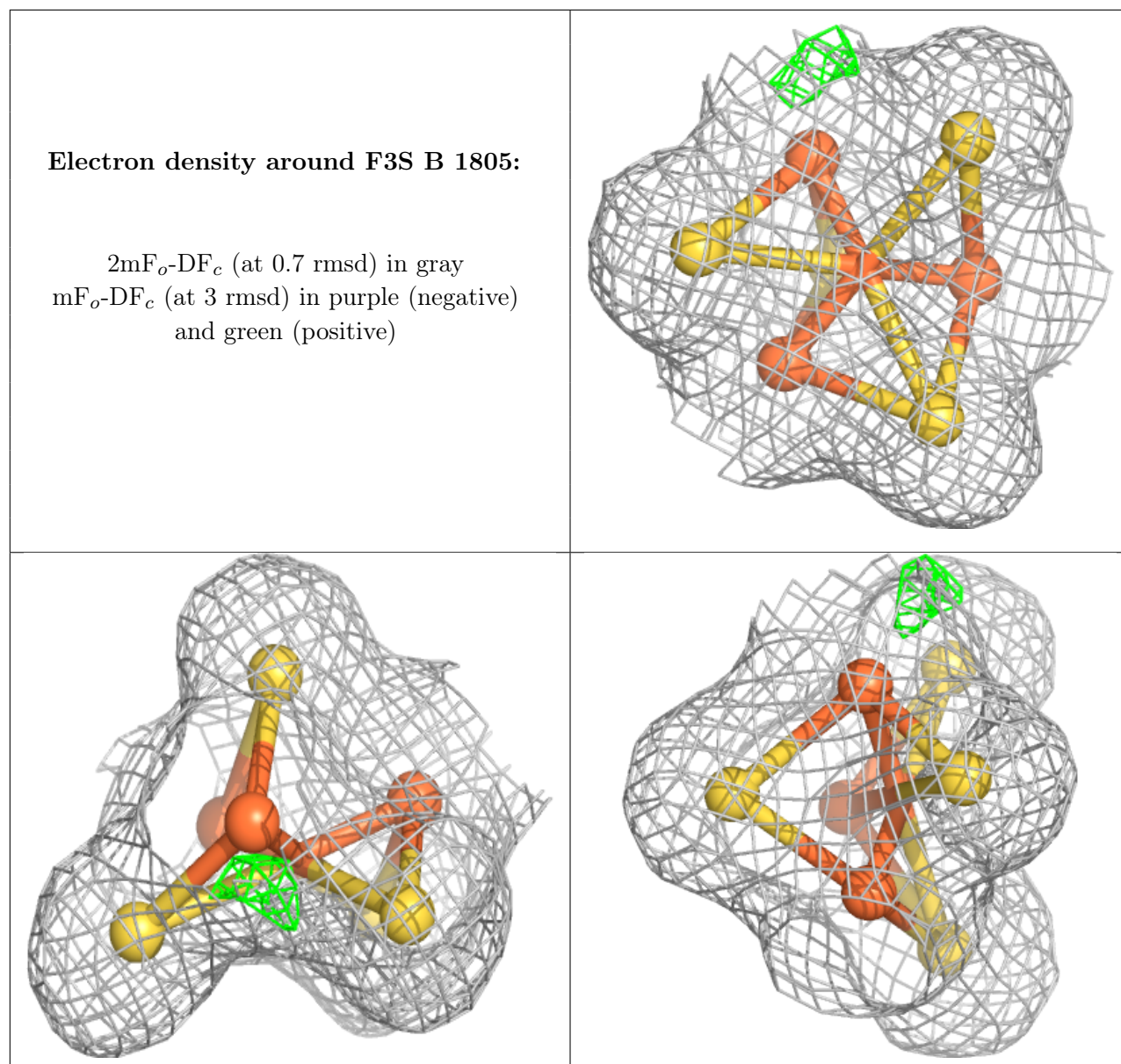
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around F3S B 1803:

$2mF_o-DF_c$ (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.