wwPDB X-ray Structure Validation Summary Report (i)

Aug 25, 2026 – 04:33 pm BST

PDB ID	:	4AUM / pdb_00004aum
Title	:	Crystal structure, recombinant expression and mutagenesis studies of the bi-functional catalase-phenol oxidase from Scytalidium thermophilum
Authors	:	Yuzugullu, Y.; Trinh, C.H.; Smith, M.A.; Pearson, A.R.; Phillips, S.E.V.; Sutay Kocabas, D.; Bakir, U.; Ogel, Z.B.; McPherson, M.J.
Deposited on	:	2012-05-18
Resolution	:	1.40 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 (i) 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 (i)) were used in the production of this report:

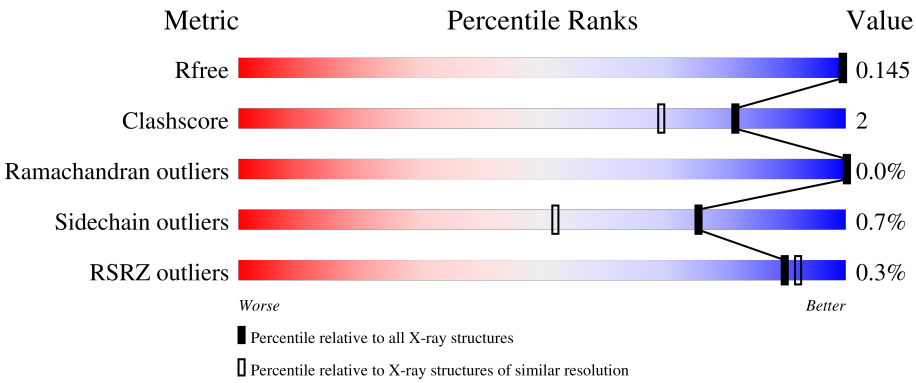
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (1.40-1.40)

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 <=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	89% · 6%
1	B	719	89% 5% 6%
1	C	719	89% 5% 7%
1	D	719	% 89% · 7%

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	HDD	A	900	X	-	-	-
2	HDD	B	900	X	-	-	-
2	HDD	C	900	X	-	-	-
2	HDD	D	900	X	-	-	-

2 Entry composition (i)

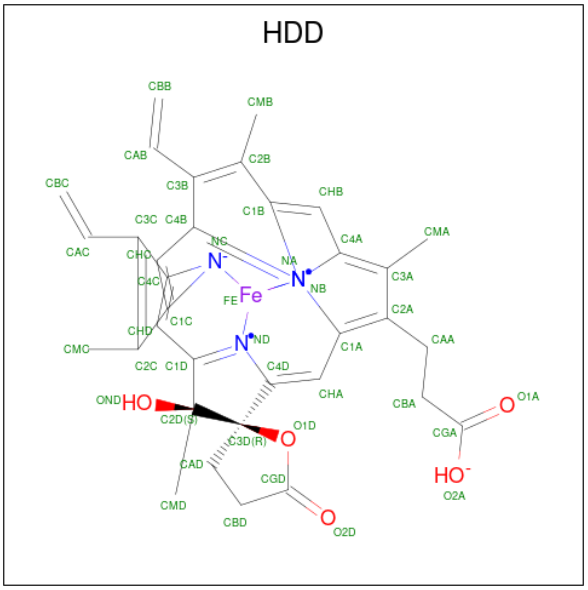
There are 5 unique types of molecules in this entry. The entry contains 24907 atoms, of which 0 are hydrogens and 0 are deuteriums.

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-PHENOL OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	673	5587	3526	976	1072	13	0	48	0
1	B	673	5590	3526	980	1072	12	0	47	0
1	C	671	5545	3502	972	1057	14	0	45	0
1	D	671	5520	3489	966	1051	14	0	41	0

- Molecule 2 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE (CCD ID: HDD) (formula: $C_{34}H_{32}FeN_4O_5$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	44	34	1	4	5	0	0
2	B	1	44	34	1	4	5	0	0

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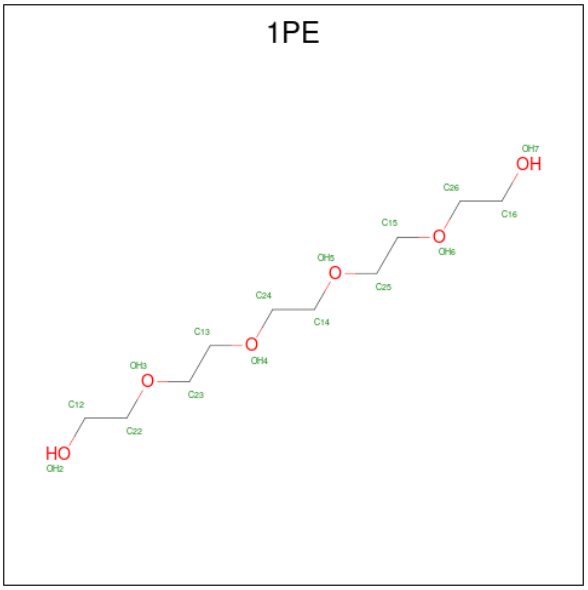
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	C	1	44	34	1	4	5	0	0
			Total	C	Fe	N	O		
2	D	1	44	34	1	4	5	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	3	3	3	0	0
			Total	Ca		
3	B	3	3	3	0	0
			Total	Ca		
3	C	2	2	2	0	0
			Total	Ca		
3	D	2	2	2	0	0

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	16	10	6	0	0

- Molecule 5 is water.

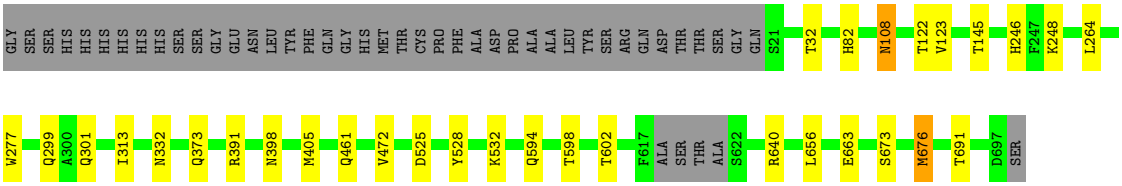
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	772	772	772	0	0
			Total	O		
5	B	694	694	694	0	0
			Total	O		
5	C	524	524	524	0	0
			Total	O		
5	D	473	473	473	0	0

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.

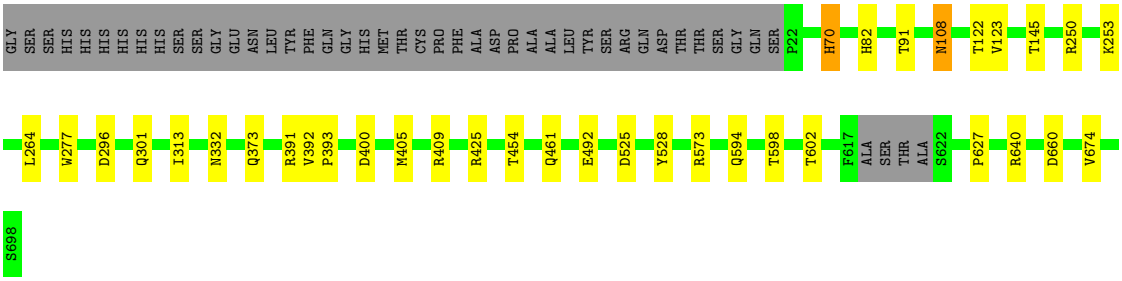
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain A:



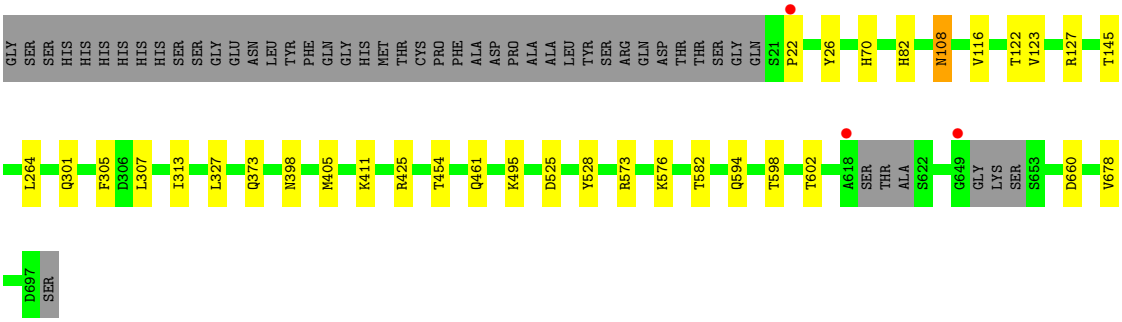
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain B:



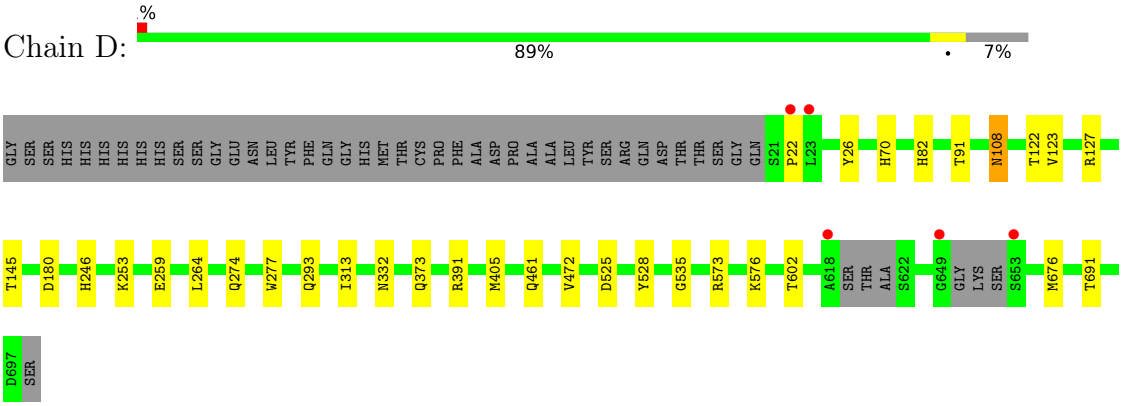
• Molecule 1: CATALASE-PHENOL OXIDASE

Chain C:



• Molecule 1: CATALASE-PHENOL OXIDASE

Chain D:


%
89%
7%
GLY SER SER HIS HIS HIS HIS HIS SER SER GLY GLU ASN LEU TYR PHE GLN GLY HIS MET THR CYS PRO PHE ALA ASP PRO ALA ALA LEU TYR SER ARG GLN ASP THR THR SER GLY GLN S21 P22 L23 Y26 H70 H82 T91 N108 T122 V123 R127
T145 D180 H246 K253 E259 L264 Q274 W277 Q293 I313 N332 Q373 R391 M405 Q461 V472 D525 Y528 G535 R573 K576 T602 A618 SER THR ALA S622 G649 GLY LYS SER S653 M676 T691
D697 SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	201.42Å 121.45Å 125.21Å 90.00° 115.51° 90.00°	Depositor
Resolution (Å)	113.00 – 1.40 113.00 – 1.40	Depositor EDS
% Data completeness (in resolution range)	95.2 (113.00-1.40) 95.2 (113.00-1.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.96 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.118 , 0.145 0.117 , 0.145	Depositor DCC
R_{free} test set	25334 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	10.1	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 41.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	24907	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.82 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0392e-03.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, HDD, 1PE

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	0.72	1/5794 (0.0%)	0.74	0/7862
1	B	0.69	0/5788	0.74	0/7853
1	C	0.72	1/5751 (0.0%)	0.75	0/7803
1	D	0.70	0/5714	0.76	0/7754
All	All	0.71	2/23047 (0.0%)	0.75	0/31272

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	398	ASN	C-N	-6.59	1.25	1.33
1	C	398	ASN	C-N	-5.70	1.26	1.33

There are no bond angle outliers.

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	5587	0	5397	24	0
1	B	5590	0	5399	37	0
1	C	5545	0	5367	27	0
1	D	5520	0	5342	28	0
2	A	44	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	44	0	31	0	0
2	C	44	0	31	0	0
2	D	44	0	31	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	16	0	22	0	0
5	A	772	0	0	6	0
5	B	694	0	0	14	0
5	C	524	0	0	6	0
5	D	473	0	0	5	0
All	All	24907	0	21651	110	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 2.

The worst 5 of 110 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:409[B]:ARG:HH11	1:B:409[B]:ARG:HG2	1.09	1.13
1:B:627:PRO:HB3	1:D:259[B]:GLU:OE2	1.59	1.01
1:D:313:ILE:H	1:D:461:GLN:HE22	1.14	0.95
1:C:313:ILE:H	1:C:461:GLN:HE22	1.16	0.92
1:A:313:ILE:H	1:A:461:GLN:HE22	1.17	0.90

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	717/719 (100%)	701 (98%)	16 (2%)	0	100	100
1	B	716/719 (100%)	700 (98%)	15 (2%)	1 (0%)	48	21
1	C	710/719 (99%)	695 (98%)	15 (2%)	0	100	100
1	D	706/719 (98%)	692 (98%)	14 (2%)	0	100	100
All	All	2849/2876 (99%)	2788 (98%)	60 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	400	ASP

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	606/596 (102%)	602 (99%)	4 (1%)	76	52
1	B	605/596 (102%)	600 (99%)	5 (1%)	73	48
1	C	600/596 (101%)	596 (99%)	4 (1%)	76	52
1	D	596/596 (100%)	592 (99%)	4 (1%)	76	52
All	All	2407/2384 (101%)	2390 (99%)	17 (1%)	76	52

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	108	ASN
1	D	576	LYS
1	B	296	ASP
1	B	660	ASP
1	C	70	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	375	ASN
1	D	373	GLN
1	D	461	GLN
1	D	375	ASN
1	B	108	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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	$\#\|Z\| > 2$
2	HDD	D	900	1,5	50,52,52	2.11	19 (38%)	56,89,89	1.79	12 (21%)
2	HDD	B	900	1,5	50,52,52	1.96	17 (34%)	56,89,89	2.05	14 (25%)
4	1PE	A	1698	-	15,15,15	0.42	0	14,14,14	0.34	0
2	HDD	A	900	1,5	50,52,52	2.11	18 (36%)	56,89,89	2.08	16 (28%)
2	HDD	C	900	1,5	50,52,52	2.02	18 (36%)	56,89,89	1.86	14 (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
2	HDD	D	900	1,5	1/1/8/14	2/9/89/89	0/1/9/9
2	HDD	B	900	1,5	1/1/8/14	2/9/89/89	0/1/9/9
4	1PE	A	1698	-	-	1/13/13/13	-
2	HDD	A	900	1,5	1/1/8/14	2/9/89/89	0/1/9/9
2	HDD	C	900	1,5	1/1/8/14	2/9/89/89	0/1/9/9

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	900	HDD	C1D-ND	4.87	1.38	1.35
2	C	900	HDD	C1D-ND	4.78	1.38	1.35
2	A	900	HDD	CHD-C4C	4.75	1.47	1.38
2	A	900	HDD	C1D-ND	4.34	1.38	1.35
2	D	900	HDD	FE-NB	4.27	2.08	1.94

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	900	HDD	C3B-C2B-C1B	-7.52	100.91	106.49
2	B	900	HDD	C3B-C2B-C1B	-7.29	101.08	106.49
2	C	900	HDD	C3B-C2B-C1B	-6.80	101.44	106.49
2	D	900	HDD	C3B-C2B-C1B	-5.62	102.32	106.49
2	B	900	HDD	C3C-C2C-C1C	-4.89	102.41	107.08

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	900	HDD	NC
2	B	900	HDD	NC
2	C	900	HDD	NC
2	D	900	HDD	NC

5 of 9 torsion outliers are listed below:

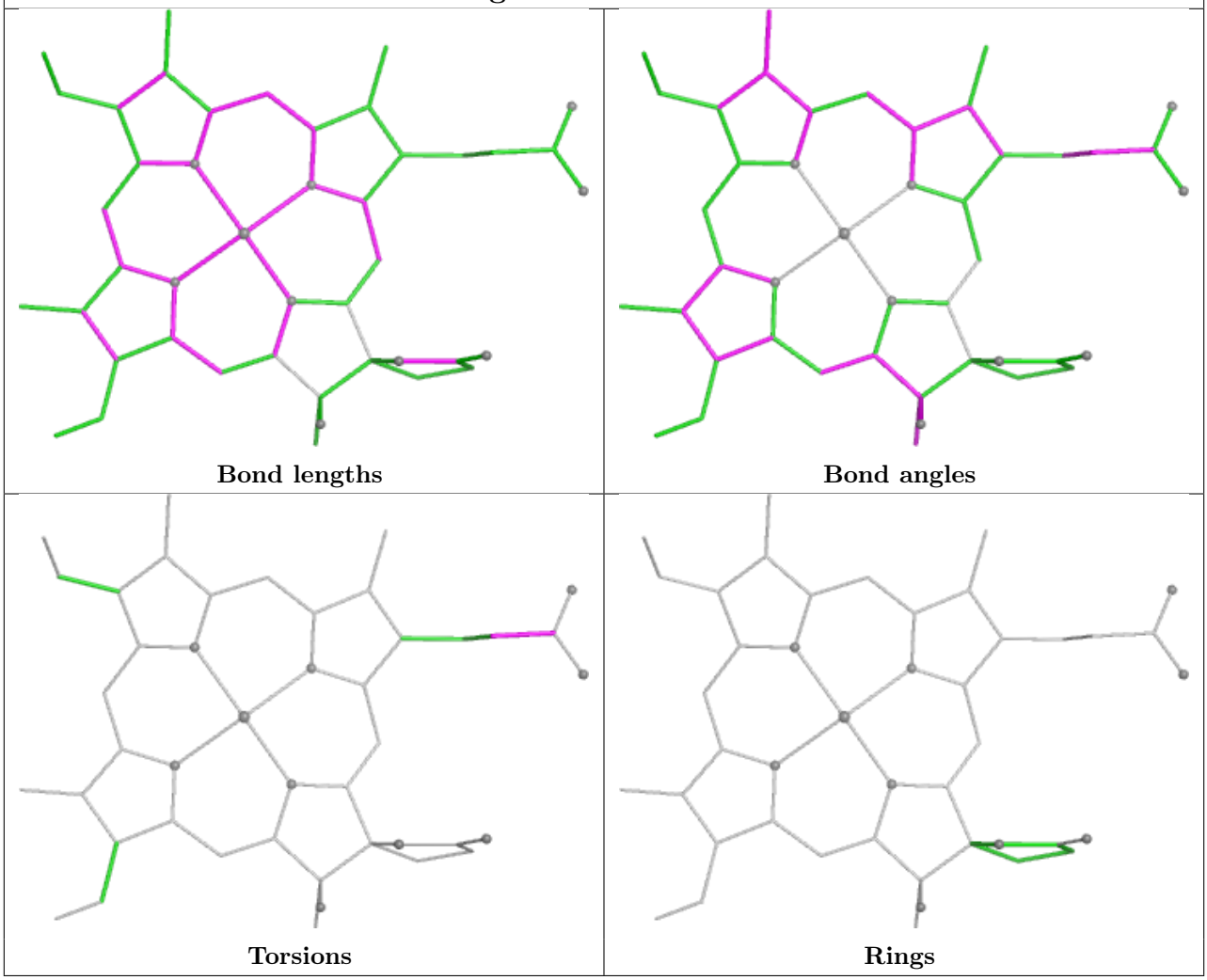
Mol	Chain	Res	Type	Atoms
2	B	900	HDD	CAA-CBA-CGA-O1A
2	D	900	HDD	CAA-CBA-CGA-O2A
2	B	900	HDD	CAA-CBA-CGA-O2A
2	C	900	HDD	CAA-CBA-CGA-O2A
2	A	900	HDD	CAA-CBA-CGA-O1A

There are no ring outliers.

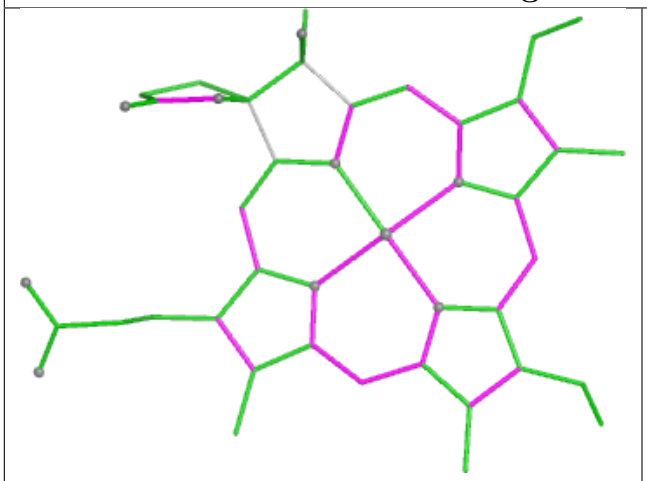
No monomer is involved in short contacts.

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 then 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.

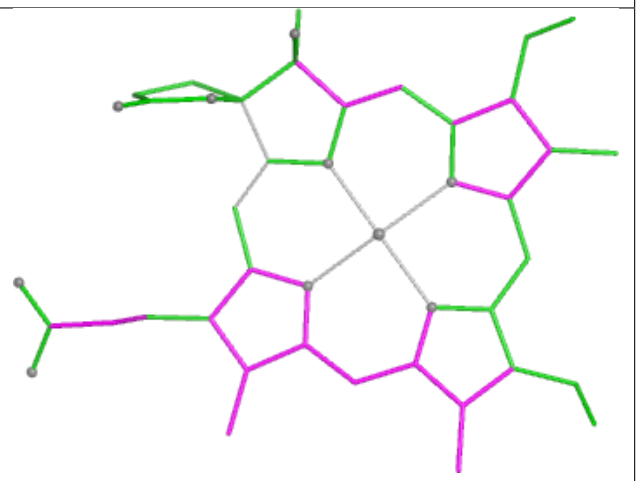
Ligand HDD D 900



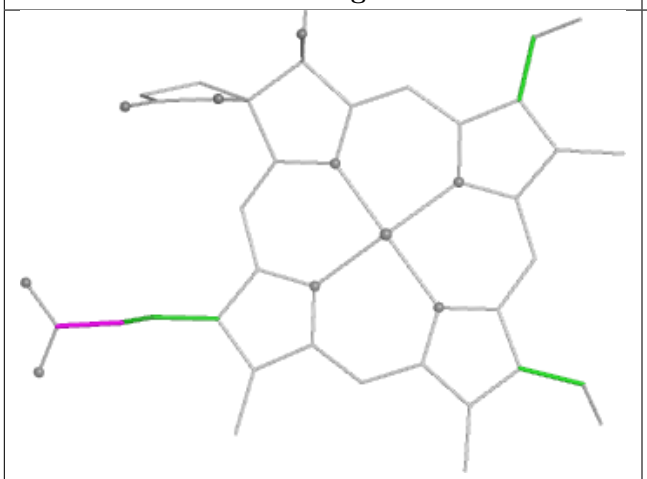
Ligand HDD B 900



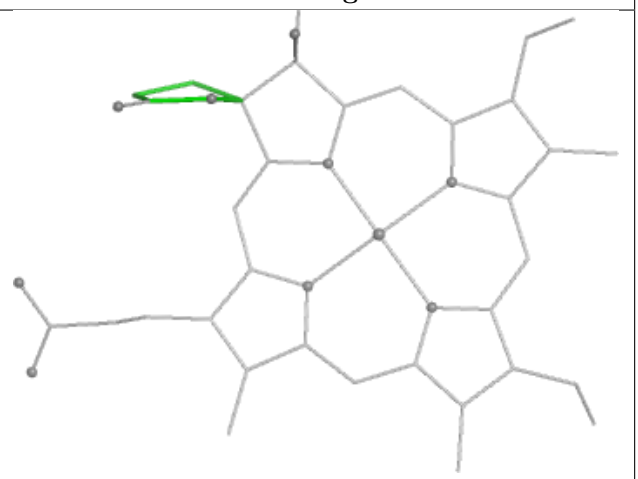
Bond lengths



Bond angles

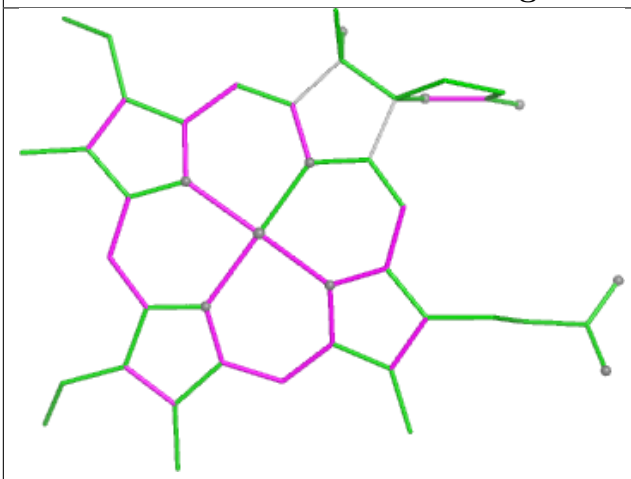


Torsions

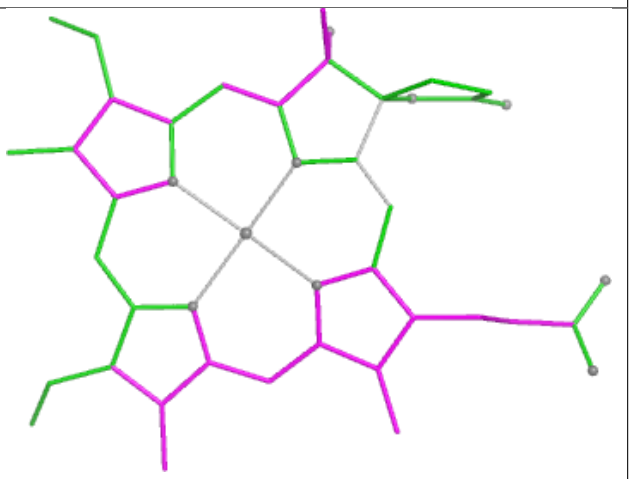


Rings

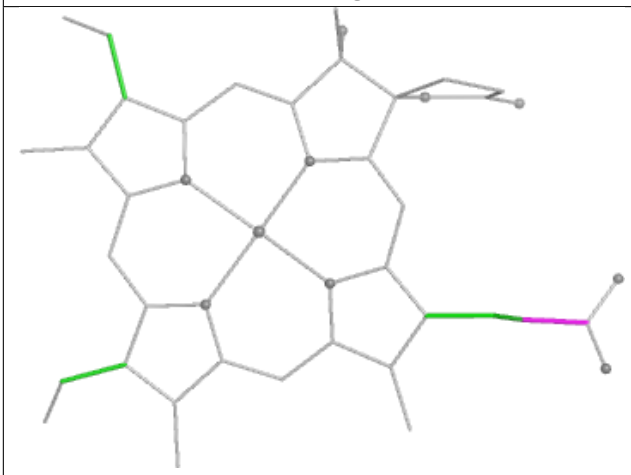
Ligand HDD A 900



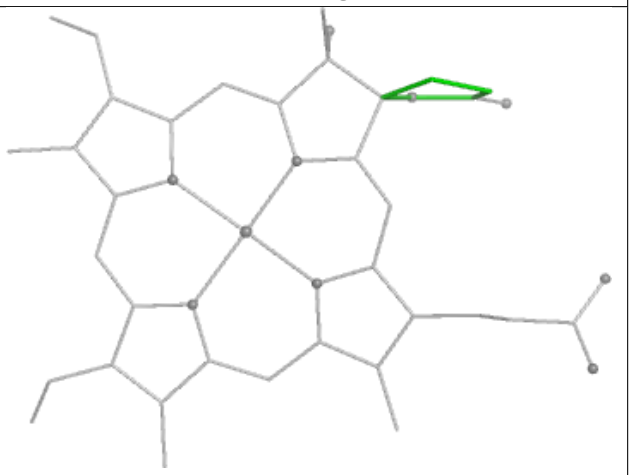
Bond lengths



Bond angles

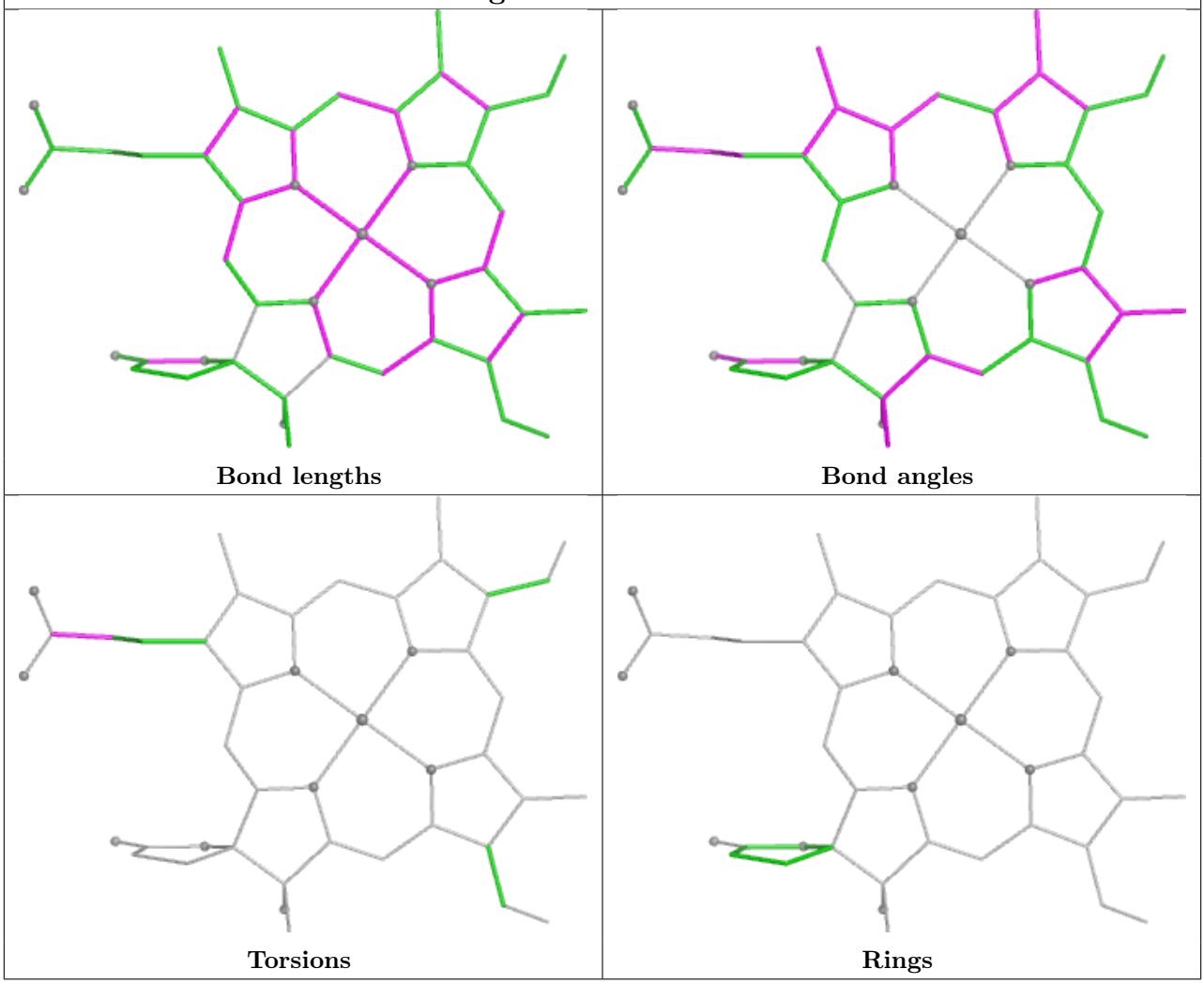


Torsions



Rings

Ligand HDD C 900



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 (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	673/719 (93%)	-0.88	0	100	100	4, 10, 20, 35	48 (7%)
1	B	673/719 (93%)	-0.81	0	100	100	4, 11, 23, 36	47 (6%)
1	C	671/719 (93%)	-0.78	3 (0%)	88	91	3, 10, 26, 66	45 (6%)
1	D	671/719 (93%)	-0.72	5 (0%)	84	87	4, 11, 32, 67	41 (6%)
All	All	2688/2876 (93%)	-0.80	8 (0%)	90	92	3, 11, 25, 67	181 (6%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	649	GLY	3.9
1	D	22	PRO	2.9
1	D	649	GLY	2.6
1	C	22	PRO	2.4
1	D	653	SER	2.3

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 oligosaccharides in this entry.

6.4 Ligands (i)

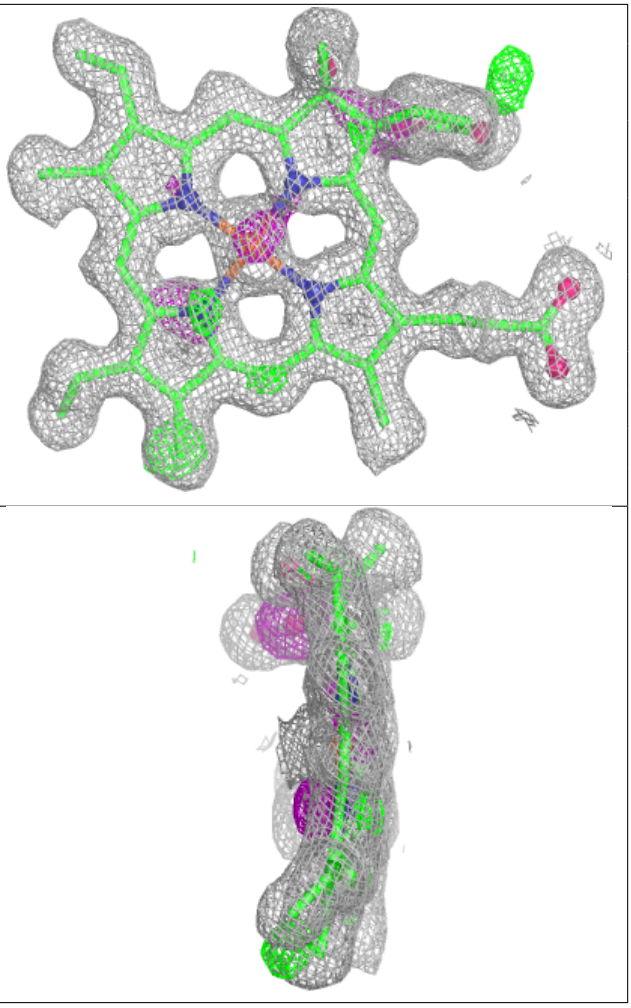
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	1PE	A	1698	16/16	0.84	0.12	9,11,13,15	16
2	HDD	B	900	44/44	0.99	0.04	6,7,10,13	0
2	HDD	C	900	44/44	0.99	0.04	5,6,9,13	0
2	HDD	D	900	44/44	0.99	0.05	5,7,10,14	0
2	HDD	A	900	44/44	0.99	0.04	5,7,9,13	0
3	CA	A	1699	1/1	1.00	0.03	9,9,9,9	1
3	CA	A	1700	1/1	1.00	0.03	12,12,12,12	1
3	CA	B	1699	1/1	1.00	0.01	9,9,9,9	1
3	CA	B	1700	1/1	1.00	0.02	15,15,15,15	1
3	CA	B	1701	1/1	1.00	0.03	13,13,13,13	1
3	CA	C	1698	1/1	1.00	0.01	7,7,7,7	1
3	CA	C	1699	1/1	1.00	0.03	13,13,13,13	1
3	CA	D	1698	1/1	1.00	0.02	11,11,11,11	1
3	CA	D	1699	1/1	1.00	0.01	17,17,17,17	1
3	CA	A	910	1/1	1.00	0.09	11,11,11,11	1

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.

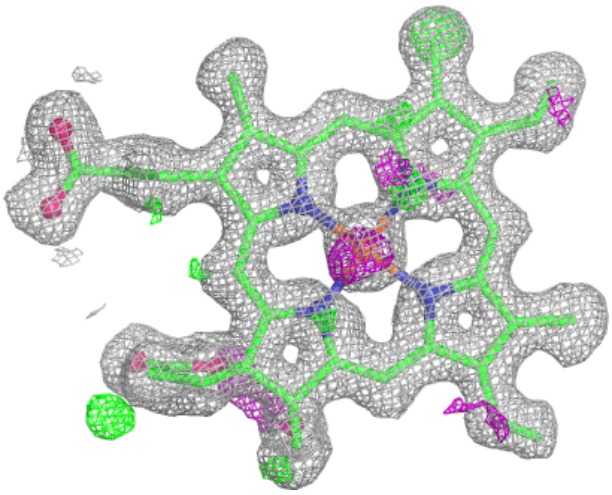
Electron density around HDD B 900:

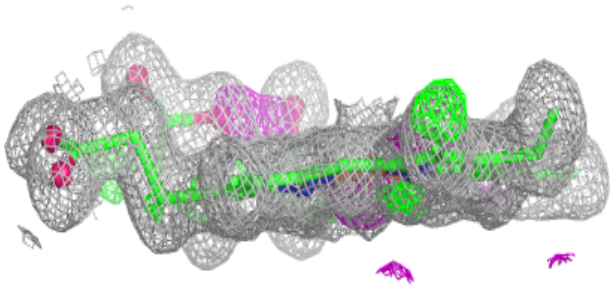
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

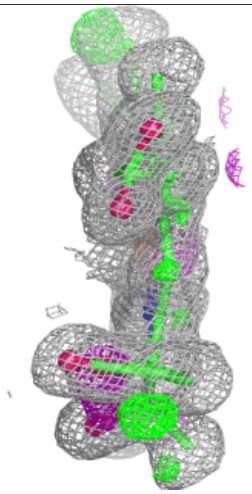


Electron density around HDD C 900:

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

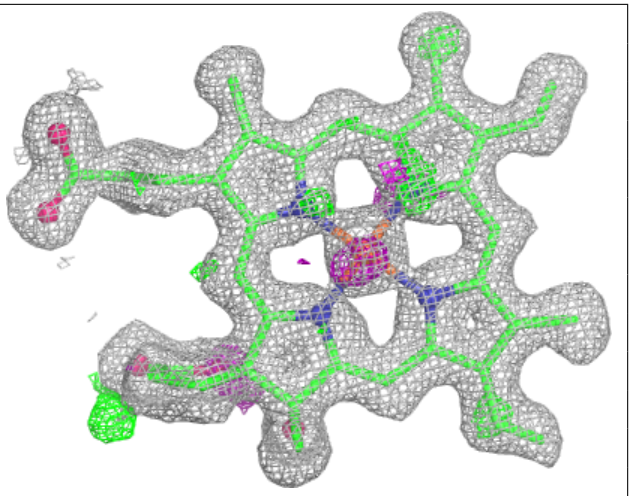


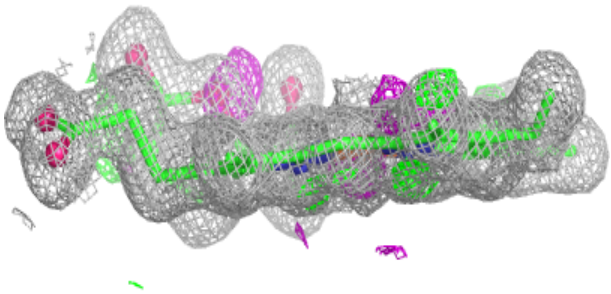


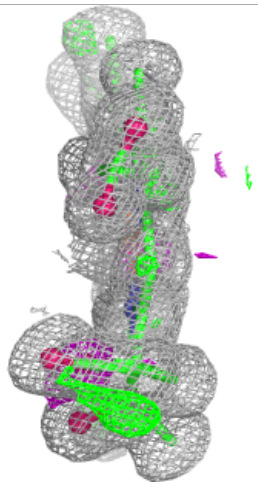


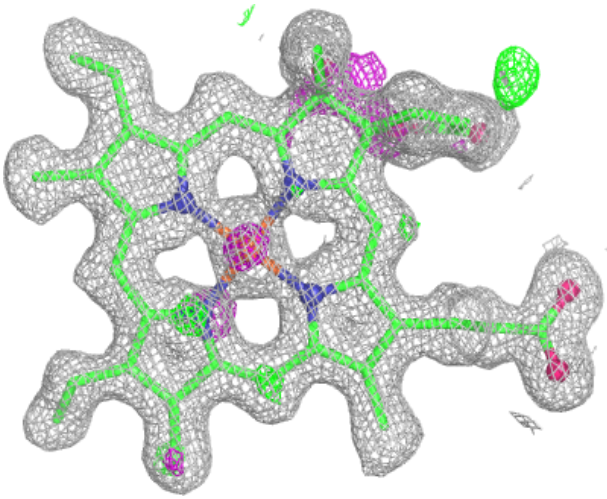
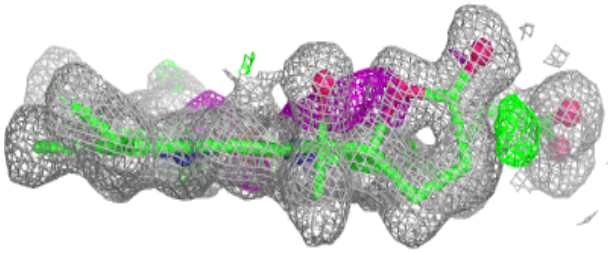
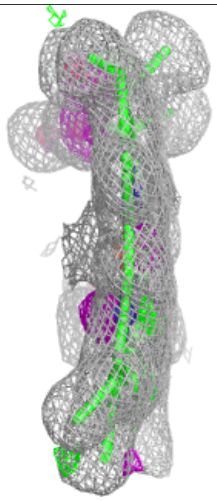
Electron density around HDD D 900:

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







Electron density around HDD A 900: 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.