wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 11:14 AM EDT

PDB ID	:	3PQ8 / pdb_00003pq8
Title	:	Structure of I274C variant of E. coli KatE[] - Images 37-42
Authors	:	Loewen, P.C.; Jha, V.; Louis, S.; Chelikani, P.; Carpena, X.; Fita, I.
Deposited on	:	2010-11-25
Resolution	:	1.80 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:

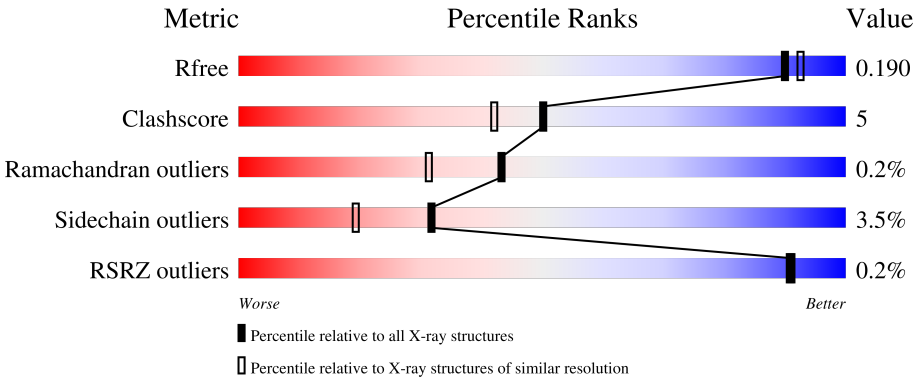
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

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

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	753	86% 9%
1	B	753	85% 10%
1	C	753	85% 10%
1	D	753	84% 11%

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	760[A]	X	-	-	-
2	HDD	B	760[A]	X	-	-	-
2	HDD	C	760[A]	X	-	-	-
2	HDD	D	760[A]	X	-	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 26810 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.

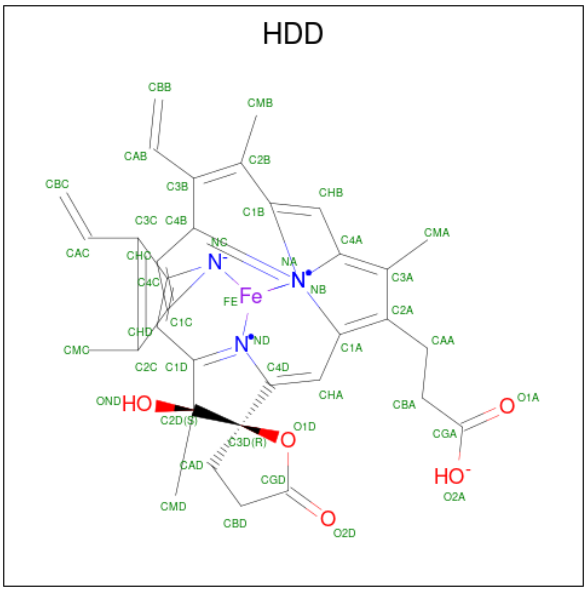
- Molecule 1 is a protein called Catalase HPII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	5	0
			5755	3652	1009	1083	11			
1	B	726	Total	C	N	O	S	0	5	0
			5757	3654	1009	1083	11			
1	C	726	Total	C	N	O	S	0	2	0
			5747	3649	1007	1080	11			
1	D	726	Total	C	N	O	S	0	9	0
			5771	3662	1013	1085	11			

There are 12 discrepancies between the modelled and reference sequences:

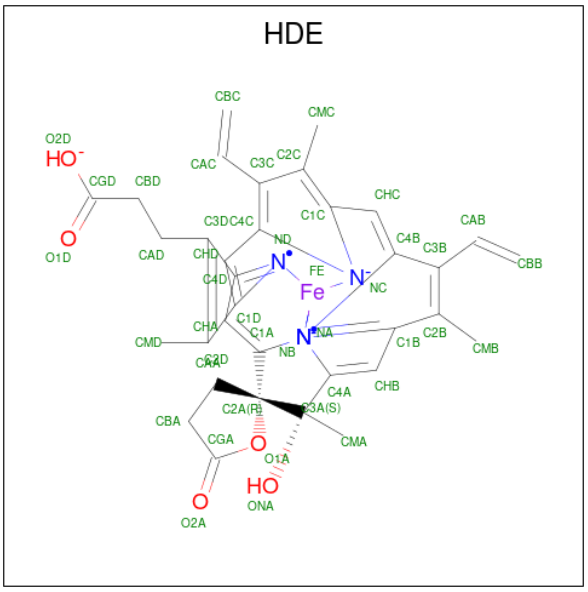
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	CYS	ILE	engineered mutation	UNP P21179
A	438	ALA	CYS	engineered mutation	UNP P21179
A	669	ALA	CYS	engineered mutation	UNP P21179
B	274	CYS	ILE	engineered mutation	UNP P21179
B	438	ALA	CYS	engineered mutation	UNP P21179
B	669	ALA	CYS	engineered mutation	UNP P21179
C	274	CYS	ILE	engineered mutation	UNP P21179
C	438	ALA	CYS	engineered mutation	UNP P21179
C	669	ALA	CYS	engineered mutation	UNP P21179
D	274	CYS	ILE	engineered mutation	UNP P21179
D	438	ALA	CYS	engineered mutation	UNP P21179
D	669	ALA	CYS	engineered mutation	UNP P21179

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



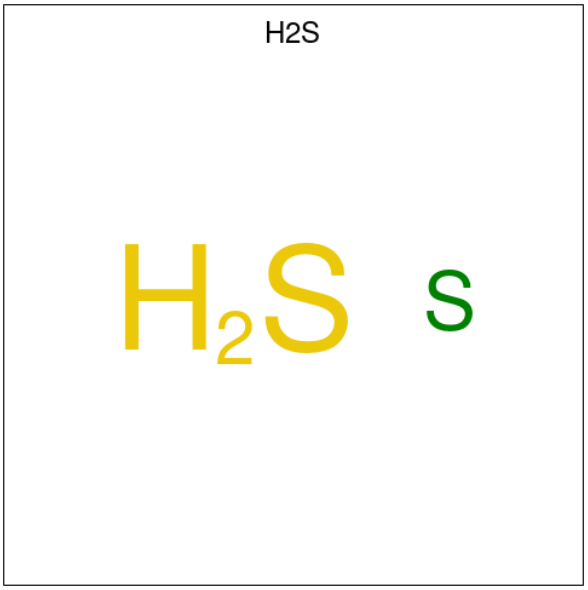
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	B	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	C	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	D	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		

- Molecule 3 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE 17R, 18S (CCD ID: HDE) (formula: $C_{34}H_{32}FeN_4O_5$).



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

- Molecule 4 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H_2S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	S	0	0
			1	1		
4	B	1	Total	S	0	0
			1	1		
4	C	1	Total	S	0	0
			1	1		
4	D	1	Total	S	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	897	Total	O	0	0
			897	897		
5	B	787	Total	O	0	0
			787	787		

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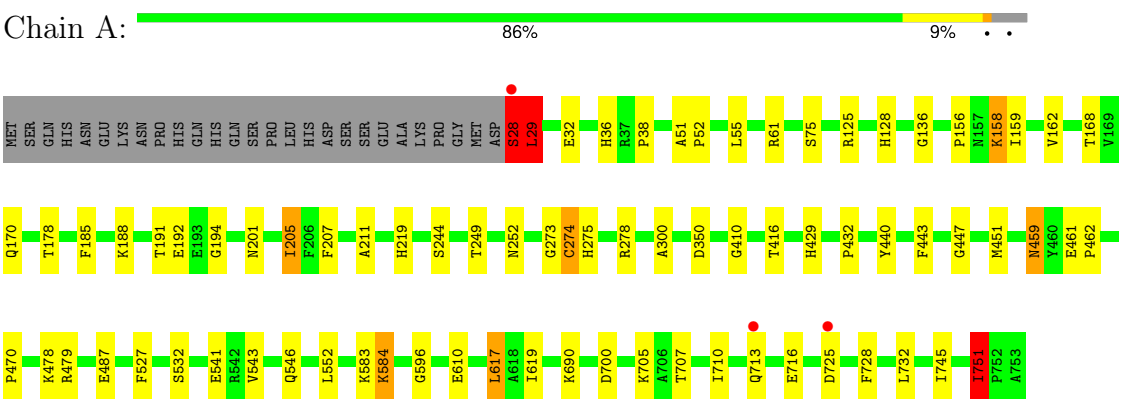
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	842	Total O 842 842	0	0
5	D	898	Total O 898 898	0	0

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.

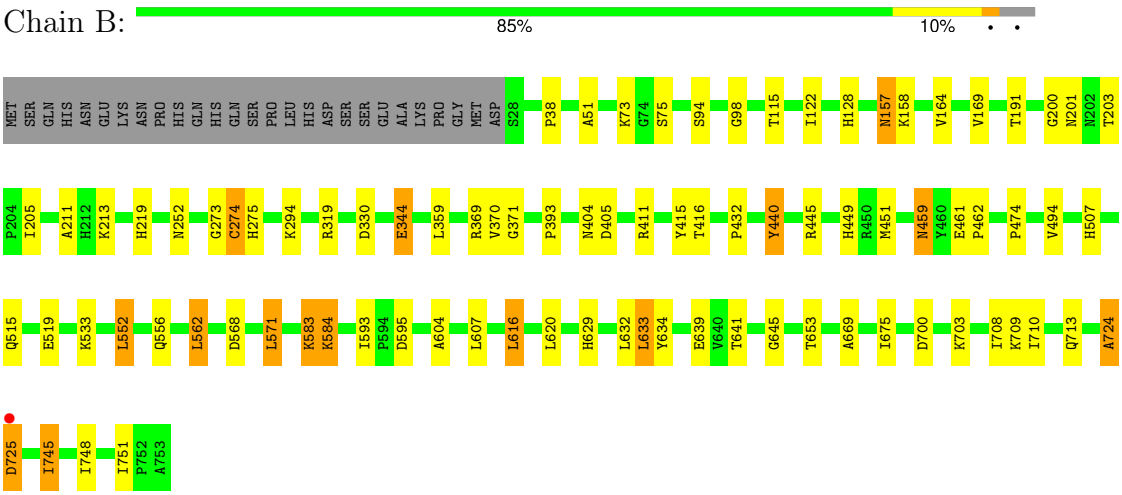
• Molecule 1: Catalase HPII

Chain A:



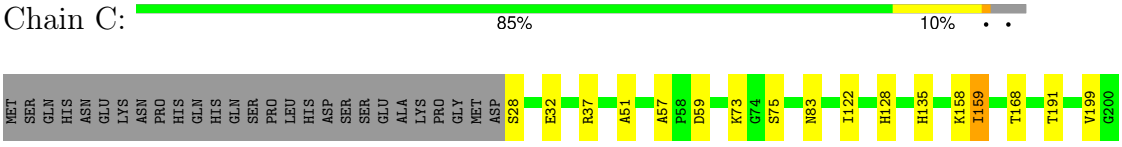
• Molecule 1: Catalase HPII

Chain B:



• Molecule 1: Catalase HPII

Chain C:

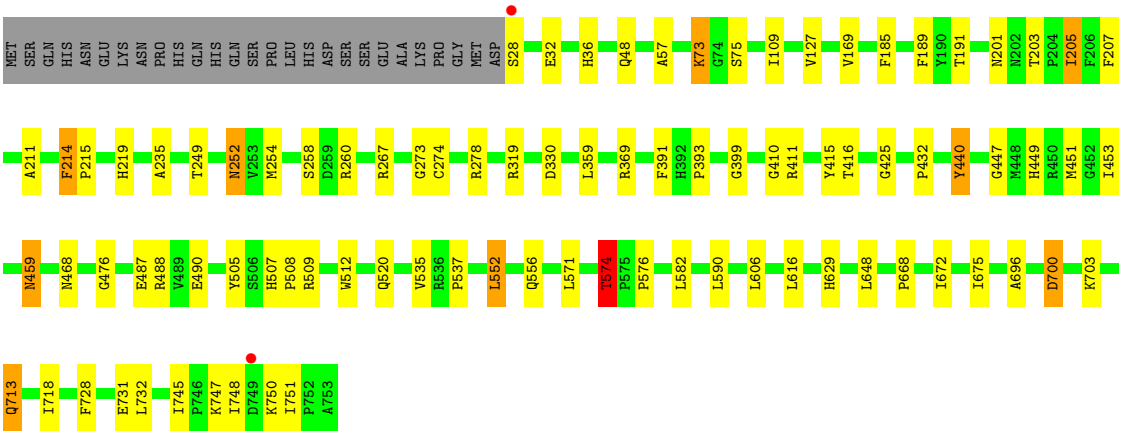




• Molecule 1: Catalase HPII

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	93.50Å 133.02Å 122.67Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	34.25 – 1.80 34.25 – 1.80	Depositor EDS
% Data completeness (in resolution range)	93.9 (34.25-1.80) 94.4 (34.25-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 1.79Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.143 , 0.190 0.143 , 0.190	Depositor DCC
R_{free} test set	12379 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	11.8	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 42.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	26810	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HDE, HDD, H2S

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	1.39	11/5932 (0.2%)	1.17	9/8064 (0.1%)
1	B	1.34	14/5931 (0.2%)	1.14	4/8062 (0.0%)
1	C	1.35	11/5908 (0.2%)	1.14	12/8033 (0.1%)
1	D	1.42	19/5966 (0.3%)	1.13	3/8109 (0.0%)
All	All	1.37	55/23737 (0.2%)	1.14	28/32268 (0.1%)

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	C	0	2

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	474	PRO	CA-C	11.83	1.58	1.51
1	C	235	ALA	CA-CB	8.04	1.62	1.52
1	A	745	ILE	CA-CB	7.68	1.57	1.54
1	A	29	LEU	N-CA	-7.34	1.35	1.46
1	D	203	THR	N-CA	7.16	1.51	1.45

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	159	ILE	CB-CG1-CD1	-8.14	96.70	113.80
1	C	725	ASP	N-CA-C	7.68	127.15	110.80
1	C	550	ILE	N-CA-C	-7.60	104.33	111.48
1	C	657	ALA	CA-C-N	6.40	126.77	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	657	ALA	C-N-CA	6.40	126.77	119.92

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	724	ALA	Peptide
1	C	725	ASP	Peptide

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	5755	0	5582	60	0
1	B	5757	0	5587	59	0
1	C	5747	0	5577	51	2
1	D	5771	0	5598	51	0
2	A	44	0	31	3	0
2	B	44	0	31	5	0
2	C	44	0	30	10	0
2	D	44	0	31	3	0
3	A	44	0	36	7	0
3	B	44	0	36	11	0
3	C	44	0	36	10	0
3	D	44	0	36	11	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	1	0
4	D	1	0	0	0	0
5	A	897	0	0	16	2
5	B	787	0	0	13	1
5	C	842	0	0	21	0
5	D	898	0	0	21	2
All	All	26810	0	22611	246	4

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 5.

The worst 5 of 246 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:716:GLU:HG2	5:A:3090:HOH:O	1.31	1.28
1:C:578:ASP:HB3	5:C:2919:HOH:O	1.32	1.28
1:B:416:THR:HG21	5:D:2464:HOH:O	1.43	1.18
1:A:29:LEU:HD22	5:C:2405:HOH:O	1.48	1.12
3:C:761[B]:HDE:CBC	3:C:761[B]:HDE:HMCB	1.79	1.11

All (4) 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)
5:A:3241:HOH:O	5:D:2457:HOH:O[2_646]	1.98	0.22
1:C:584:LYS:NZ	5:A:1624:HOH:O[1_554]	1.99	0.21
1:C:59:ASP:CB	5:B:3206:HOH:O[2_545]	2.11	0.09
5:D:2178:HOH:O	5:D:2976:HOH:O[1_655]	2.12	0.08

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	729/753 (97%)	707 (97%)	21 (3%)	1 (0%)	48	34
1	B	729/753 (97%)	704 (97%)	22 (3%)	3 (0%)	30	19
1	C	726/753 (96%)	709 (98%)	16 (2%)	1 (0%)	48	34
1	D	733/753 (97%)	714 (97%)	18 (2%)	1 (0%)	48	34
All	All	2917/3012 (97%)	2834 (97%)	77 (3%)	6 (0%)	43	31

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	725	ASP

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Mol	Chain	Res	Type
1	B	584	LYS
1	C	75	SER
1	A	75	SER
1	B	75	SER

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	614/634 (97%)	596 (97%)	18 (3%)	37	25
1	B	614/634 (97%)	594 (97%)	20 (3%)	33	21
1	C	611/634 (96%)	585 (96%)	26 (4%)	26	13
1	D	618/634 (98%)	594 (96%)	24 (4%)	28	16
All	All	2457/2536 (97%)	2369 (96%)	88 (4%)	32	18

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	707	THR
1	D	252	ASN
1	C	725	ASP
1	D	48	GLN
1	D	440	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	252	ASN
1	D	556	GLN
1	C	507	HIS
1	D	671	ASN
1	D	252	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 4 are modelled with single atom - leaving 8 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	$\#\|Z\| > 2$
3	HDE	C	761[B]	5,1	50,52,52	2.56	22 (44%)	60,89,89	2.58	25 (41%)
2	HDD	C	760[A]	5,1	49,52,52	1.96	8 (16%)	62,89,89	1.98	16 (25%)
3	HDE	D	761[B]	5,1	50,52,52	2.53	20 (40%)	60,89,89	2.52	24 (40%)
2	HDD	B	760[A]	5,1	49,52,52	1.93	11 (22%)	62,89,89	2.21	16 (25%)
2	HDD	A	760[A]	5,1	49,52,52	2.24	14 (28%)	62,89,89	2.30	21 (33%)
3	HDE	B	761[B]	5,1	50,52,52	2.51	25 (50%)	60,89,89	2.50	25 (41%)
3	HDE	A	761[B]	5,1	50,52,52	2.59	23 (46%)	60,89,89	2.16	20 (33%)
2	HDD	D	760[A]	5,1	49,52,52	2.32	11 (22%)	62,89,89	2.30	23 (37%)

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	HDE	C	761[B]	5,1	-	2/9/89/89	0/1/9/9
2	HDD	C	760[A]	5,1	1/1/8/14	4/9/89/89	0/1/9/9
3	HDE	D	761[B]	5,1	-	2/9/89/89	0/1/9/9
2	HDD	B	760[A]	5,1	1/1/8/14	2/9/89/89	0/1/9/9
2	HDD	A	760[A]	5,1	1/1/8/14	6/9/89/89	0/1/9/9
3	HDE	B	761[B]	5,1	-	2/9/89/89	0/1/9/9
3	HDE	A	761[B]	5,1	-	2/9/89/89	0/1/9/9
2	HDD	D	760[A]	5,1	1/1/8/14	6/9/89/89	0/1/9/9

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	760[A]	HDD	FE-ND	9.88	2.25	1.94
2	A	760[A]	HDD	C1D-ND	8.49	1.40	1.35
2	C	760[A]	HDD	C1D-ND	7.24	1.40	1.35
2	C	760[A]	HDD	FE-ND	6.77	2.15	1.94
3	C	761[B]	HDE	C3B-C2B	6.76	1.50	1.37

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	760[A]	HDD	O1D-CGD-O2D	9.48	128.79	120.81
2	A	760[A]	HDD	O1D-CGD-CBD	-8.46	102.46	110.17
2	B	760[A]	HDD	O1D-CGD-CBD	-7.51	103.33	110.17
2	D	760[A]	HDD	O1D-CGD-O2D	6.74	126.49	120.81
3	C	761[B]	HDE	C2D-C1D-ND	6.68	117.52	109.84

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	760[A]	HDD	NC
2	B	760[A]	HDD	NC
2	C	760[A]	HDD	NC
2	D	760[A]	HDD	NC

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	760[A]	HDD	C2B-C3B-CAB-CBB
2	D	760[A]	HDD	C2B-C3B-CAB-CBB
2	D	760[A]	HDD	C4B-C3B-CAB-CBB

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	760[A]	HDD	C2C-C3C-CAC-CBC
2	A	760[A]	HDD	C4B-C3B-CAB-CBB

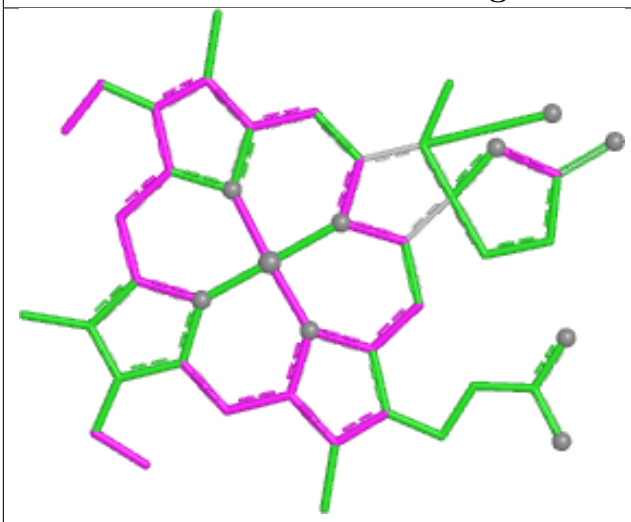
There are no ring outliers.

8 monomers are involved in 60 short contacts:

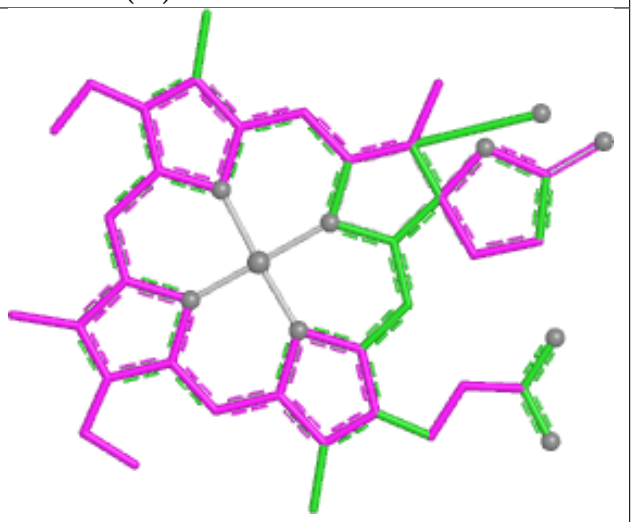
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	761[B]	HDE	10	0
2	C	760[A]	HDD	10	0
3	D	761[B]	HDE	11	0
2	B	760[A]	HDD	5	0
2	A	760[A]	HDD	3	0
3	B	761[B]	HDE	11	0
3	A	761[B]	HDE	7	0
2	D	760[A]	HDD	3	0

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 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.

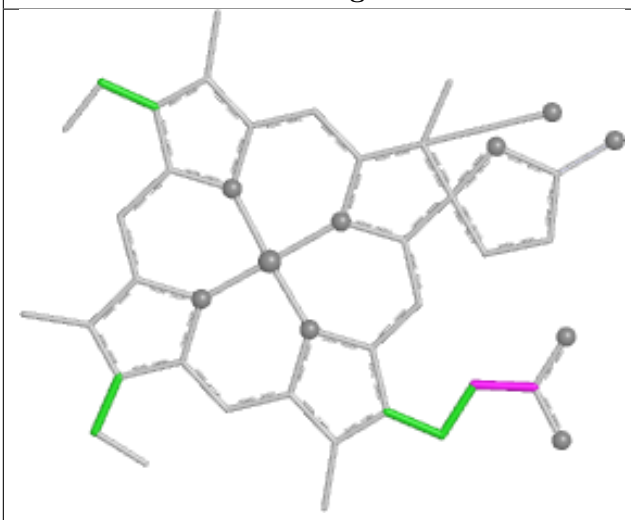
Ligand HDE C 761 (B)



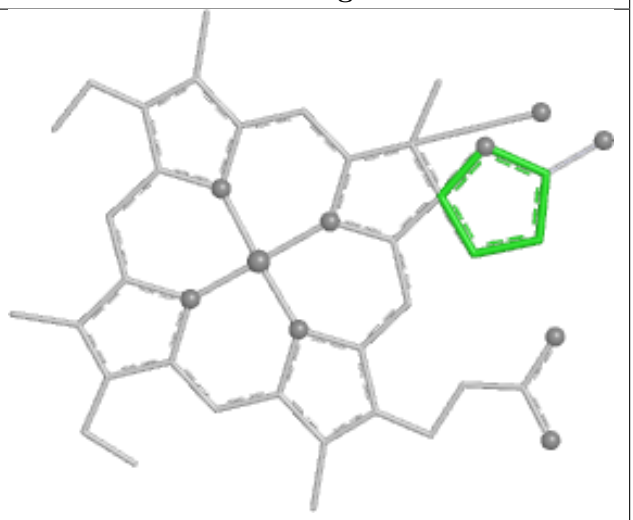
Bond lengths



Bond angles

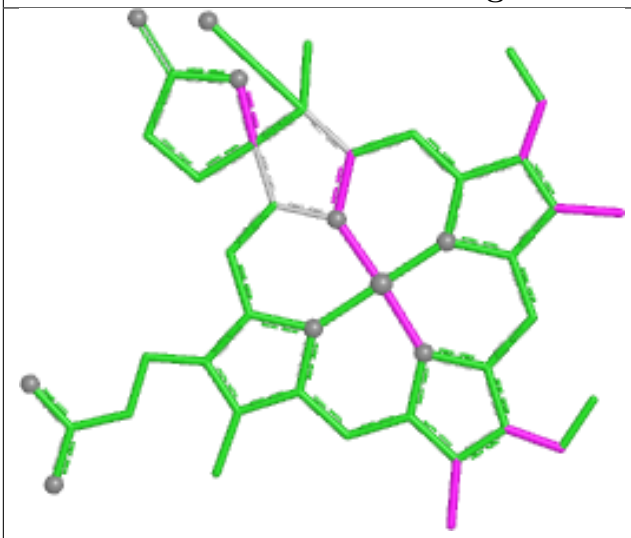


Torsions

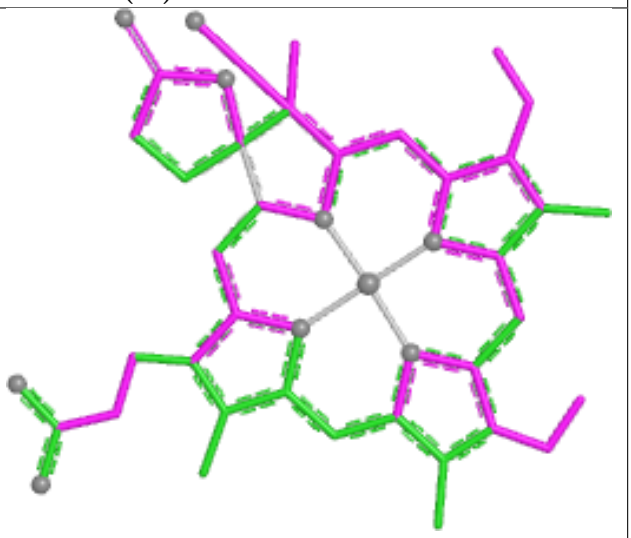


Rings

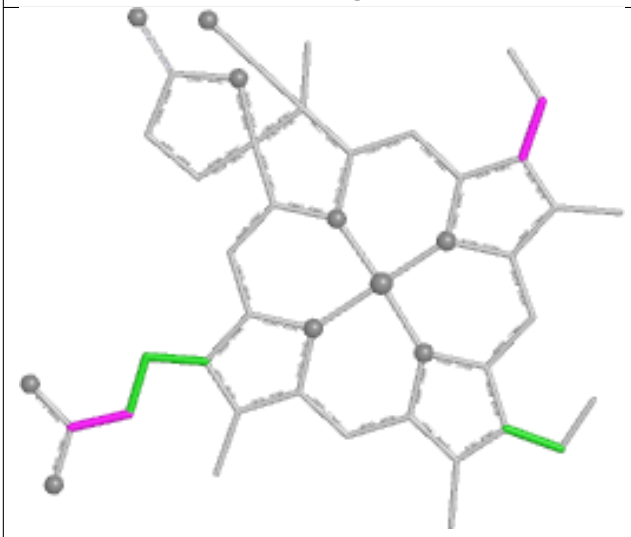
Ligand HDD C 760 (A)



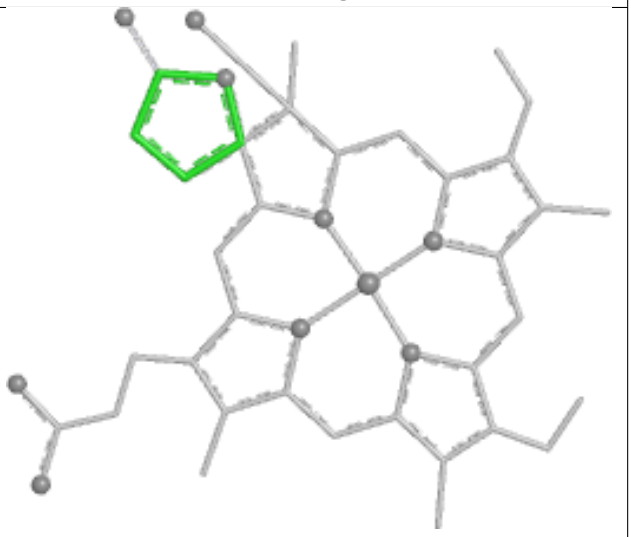
Bond lengths



Bond angles

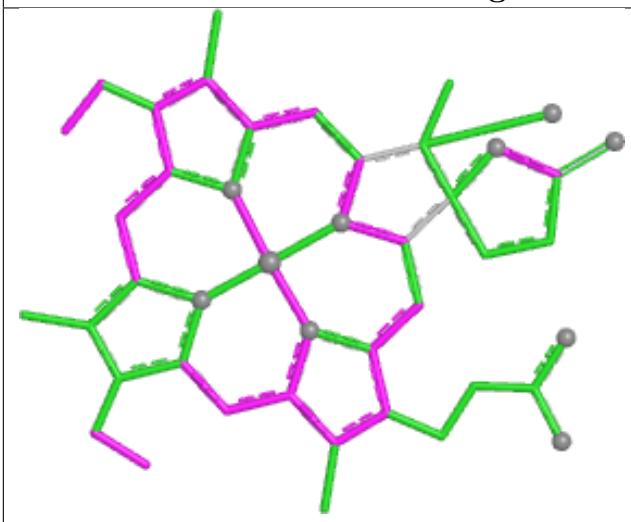


Torsions

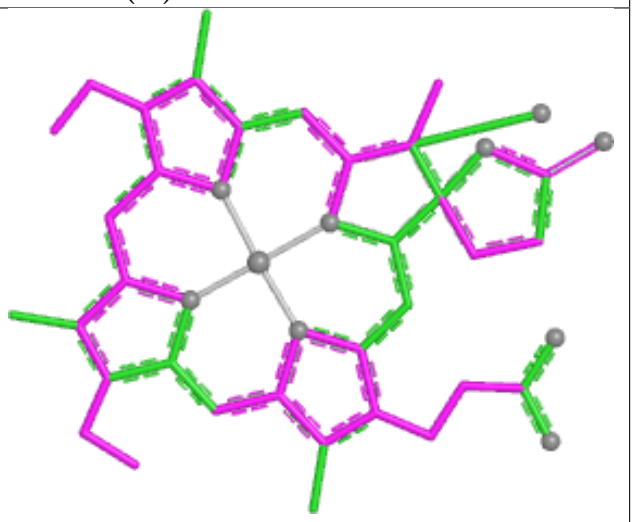


Rings

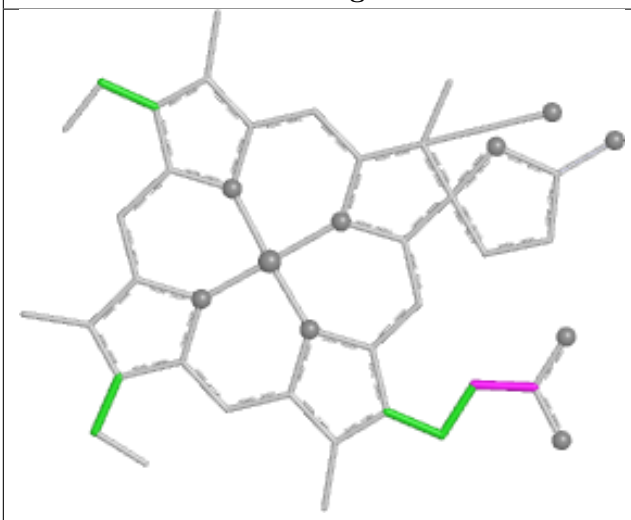
Ligand HDE D 761 (B)



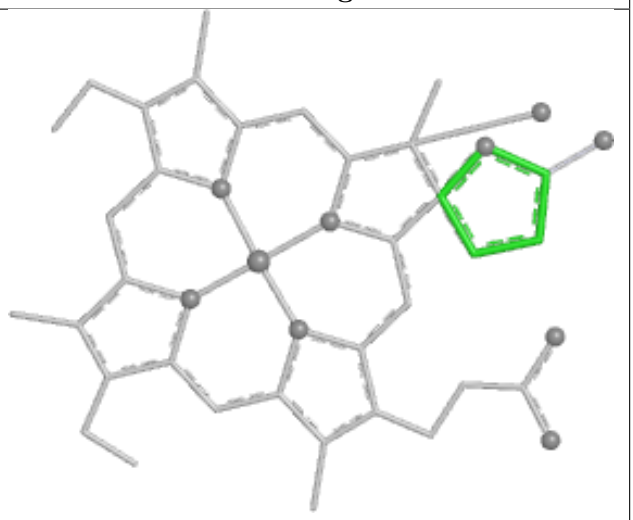
Bond lengths



Bond angles

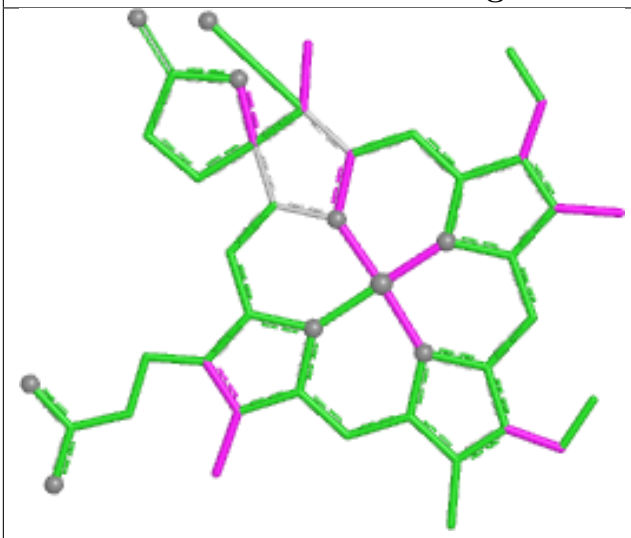


Torsions

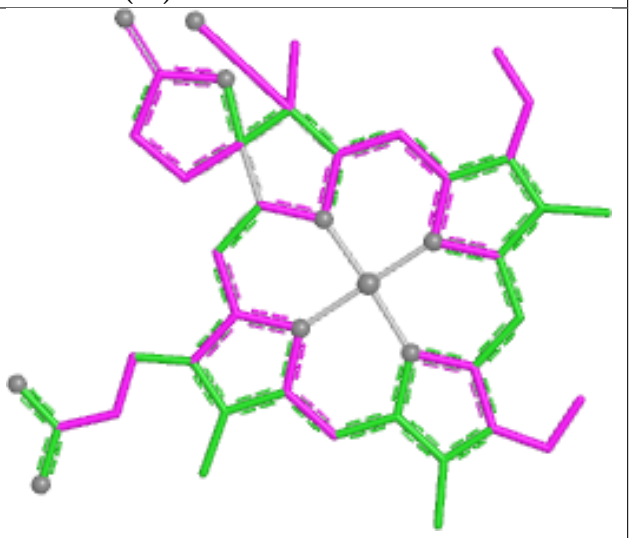


Rings

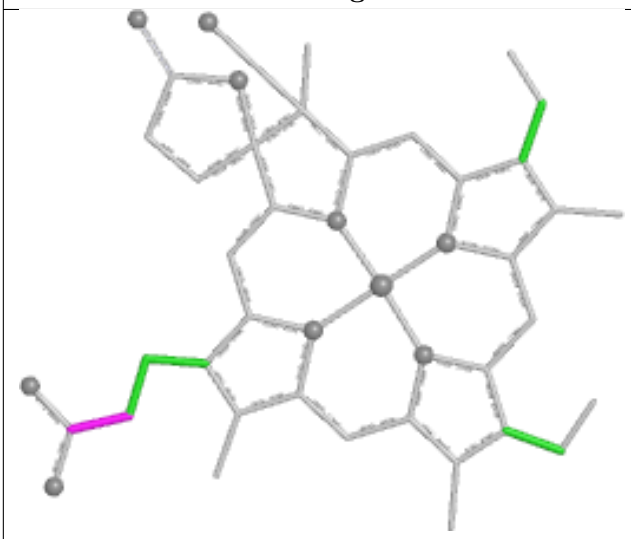
Ligand HDD B 760 (A)



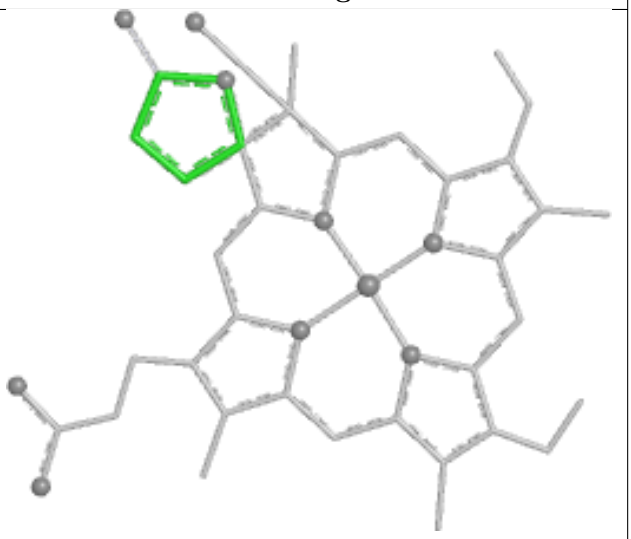
Bond lengths



Bond angles

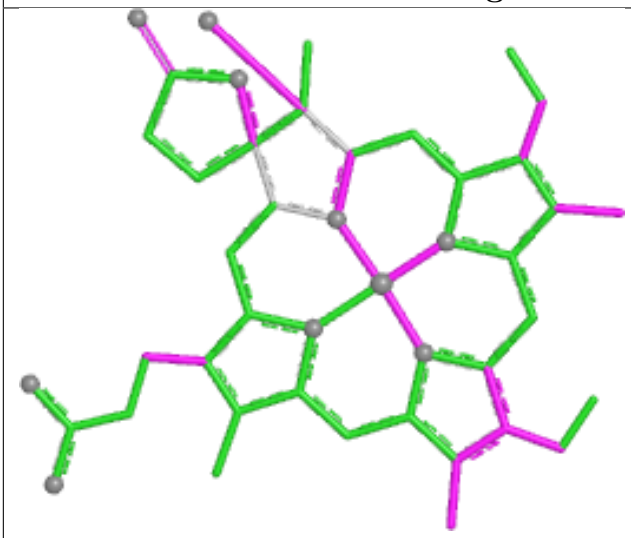


Torsions

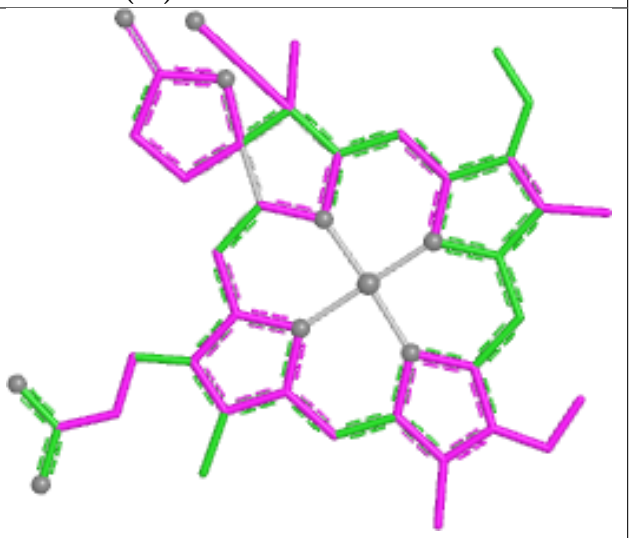


Rings

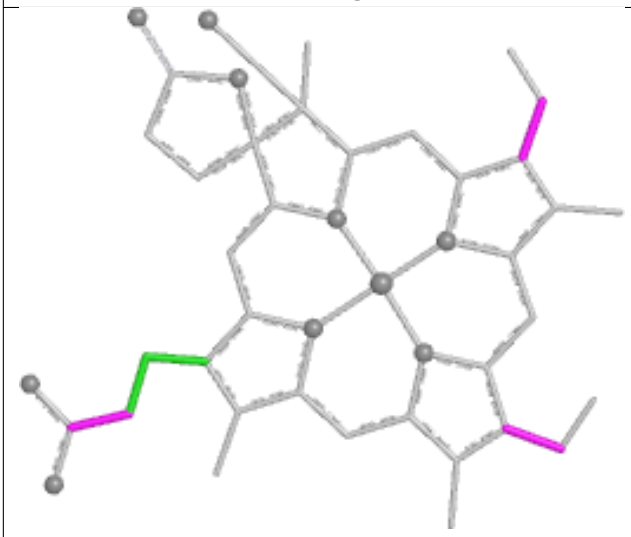
Ligand HDD A 760 (A)



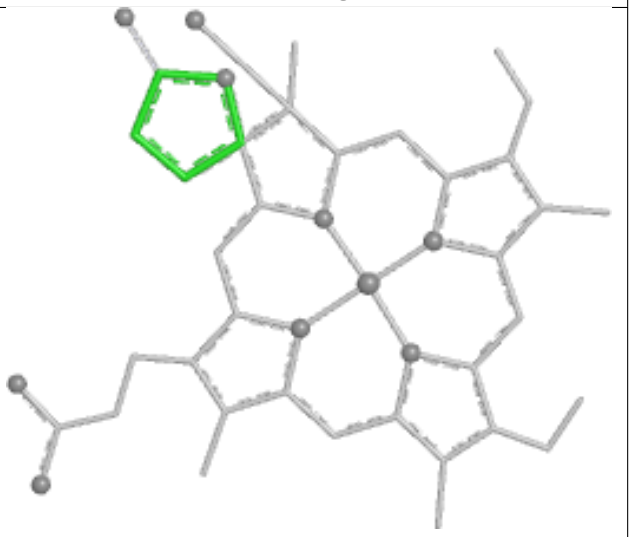
Bond lengths



Bond angles

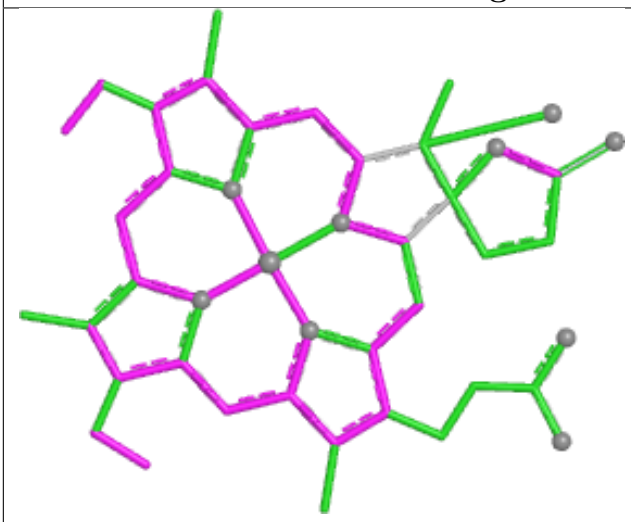


Torsions



Rings

Ligand HDE B 761 (B)



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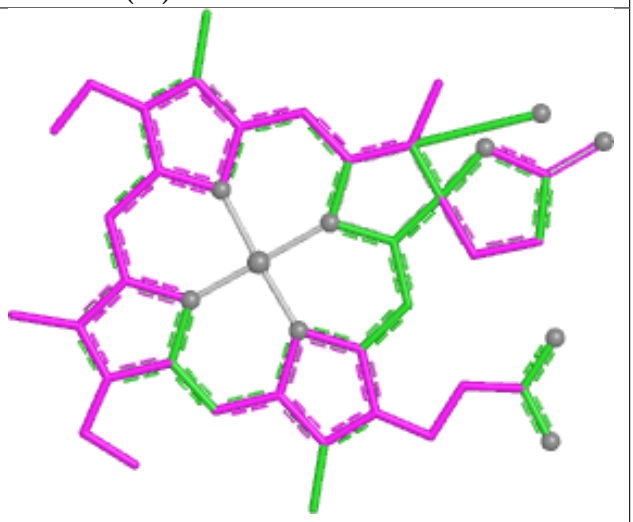
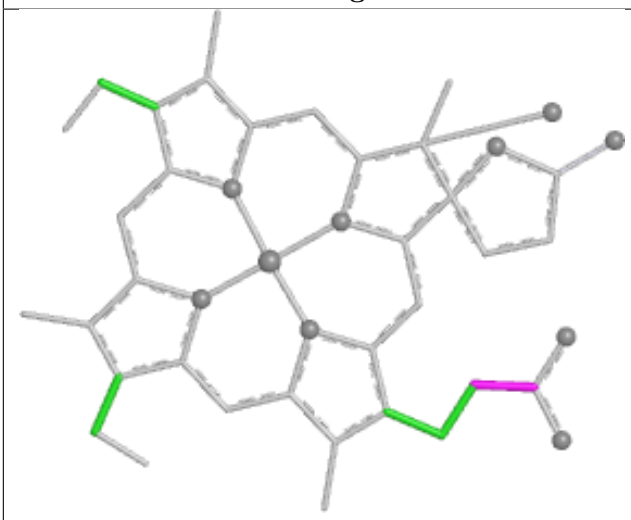
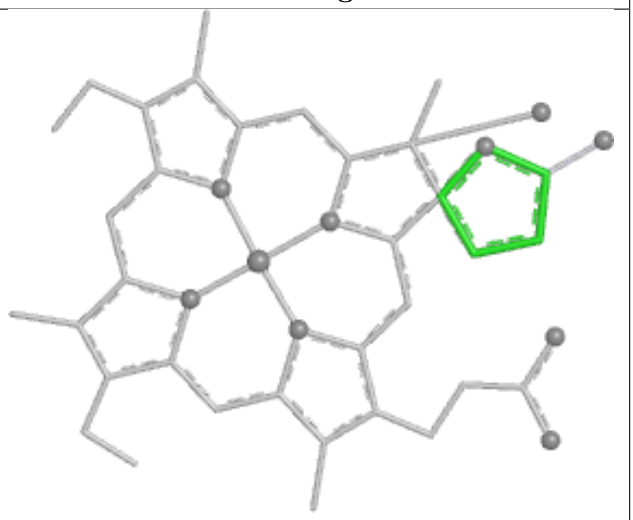


Bond angles

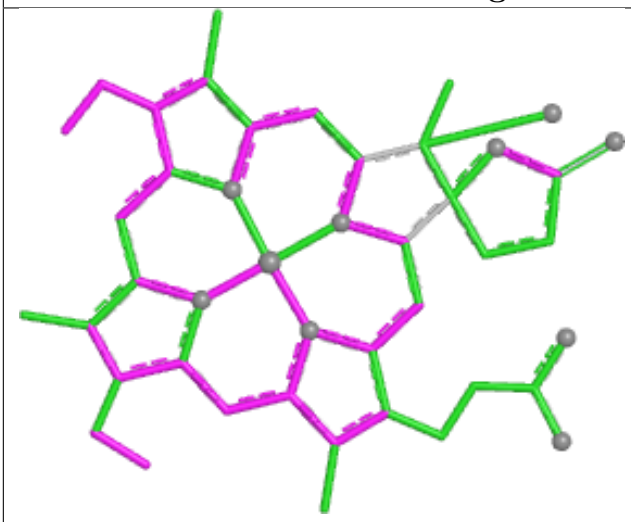


Torsions

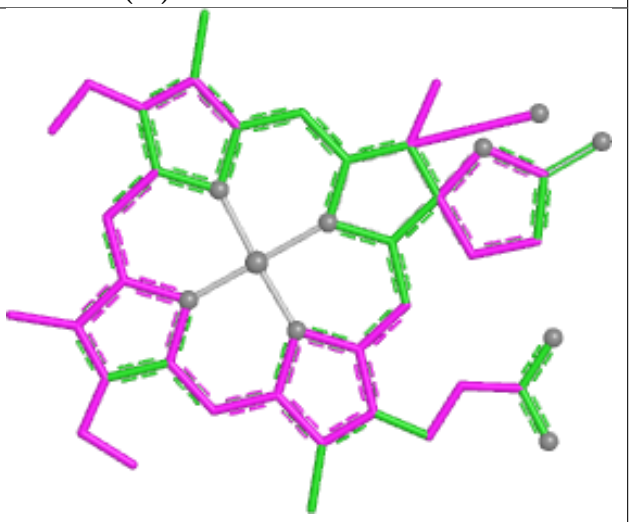


Rings

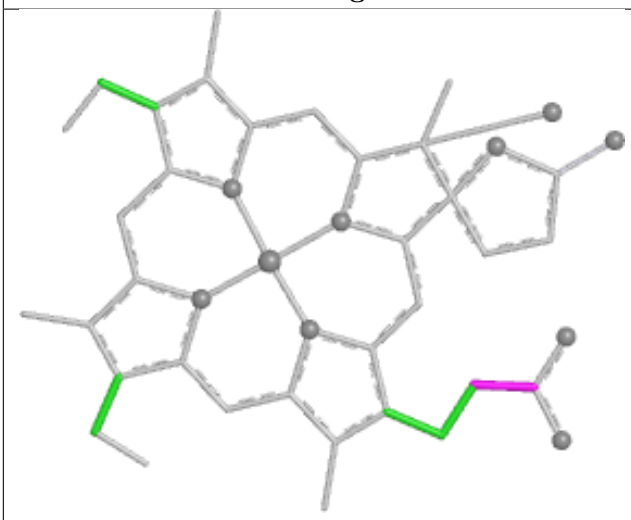
Ligand HDE A 761 (B)



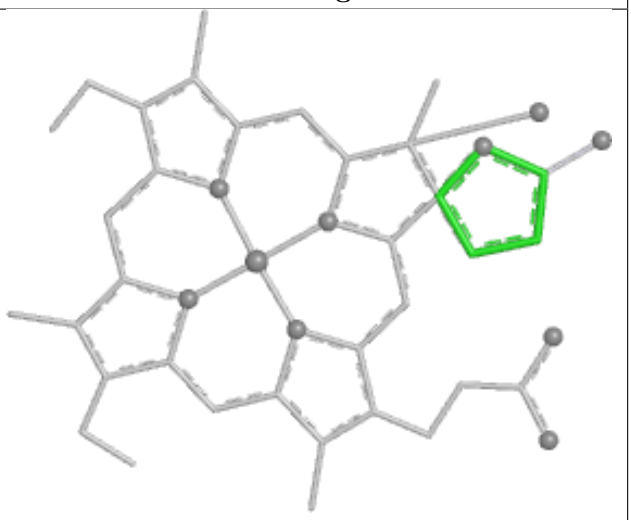
Bond lengths



Bond angles

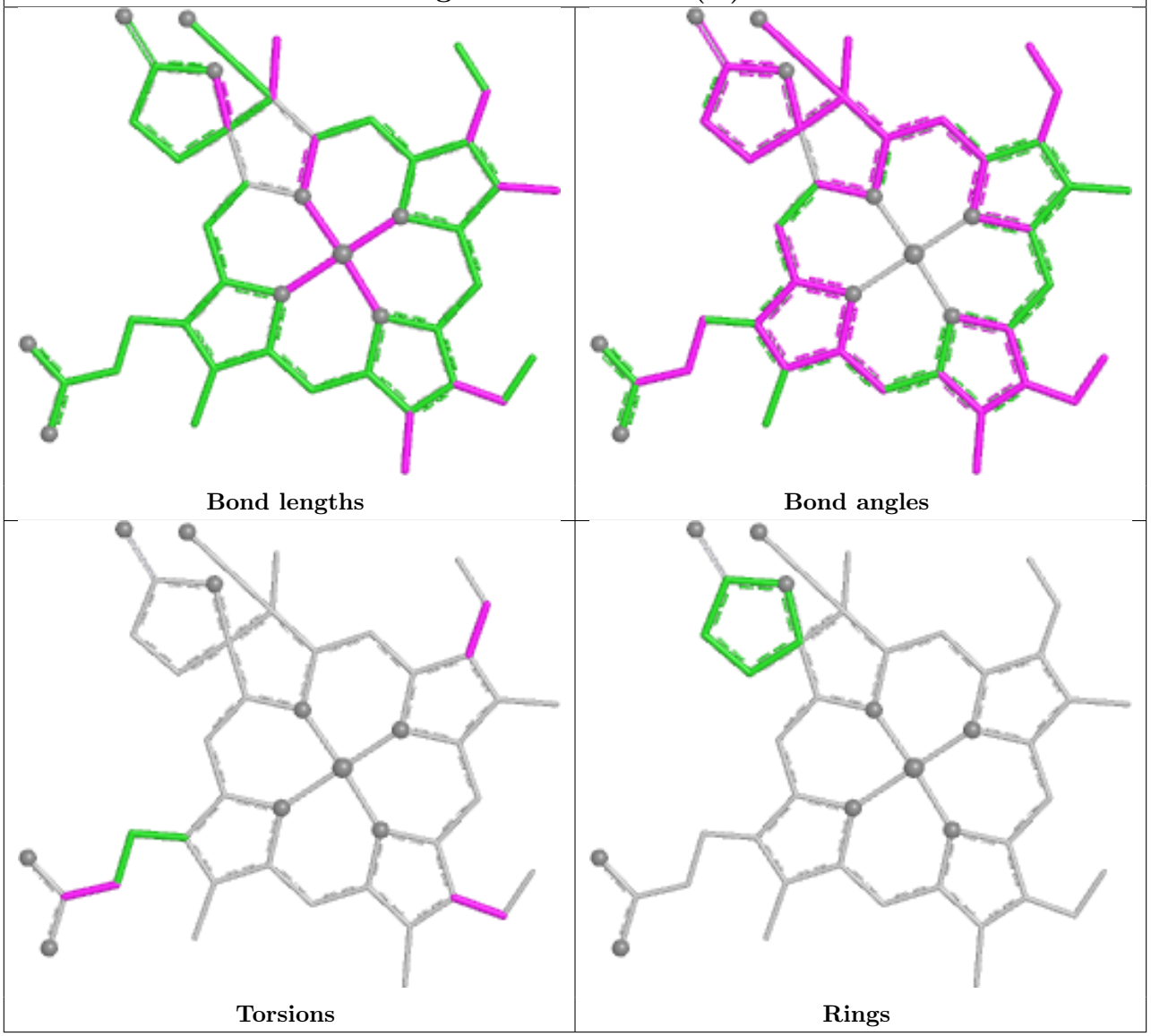


Torsions



Rings

Ligand HDD D 760 (A)



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	726/753 (96%)	-0.81	3 (0%)	88	89	3, 10, 28, 45	7 (0%)
1	B	726/753 (96%)	-0.68	1 (0%)	92	91	3, 12, 33, 47	7 (0%)
1	C	726/753 (96%)	-0.71	1 (0%)	92	91	2, 12, 32, 46	4 (0%)
1	D	726/753 (96%)	-0.80	2 (0%)	90	90	3, 10, 28, 43	10 (1%)
All	All	2904/3012 (96%)	-0.75	7 (0%)	91	91	2, 11, 31, 47	28 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	28	SER	3.7
1	A	28	SER	3.2
1	A	713	GLN	2.6
1	C	750	LYS	2.2
1	D	749	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

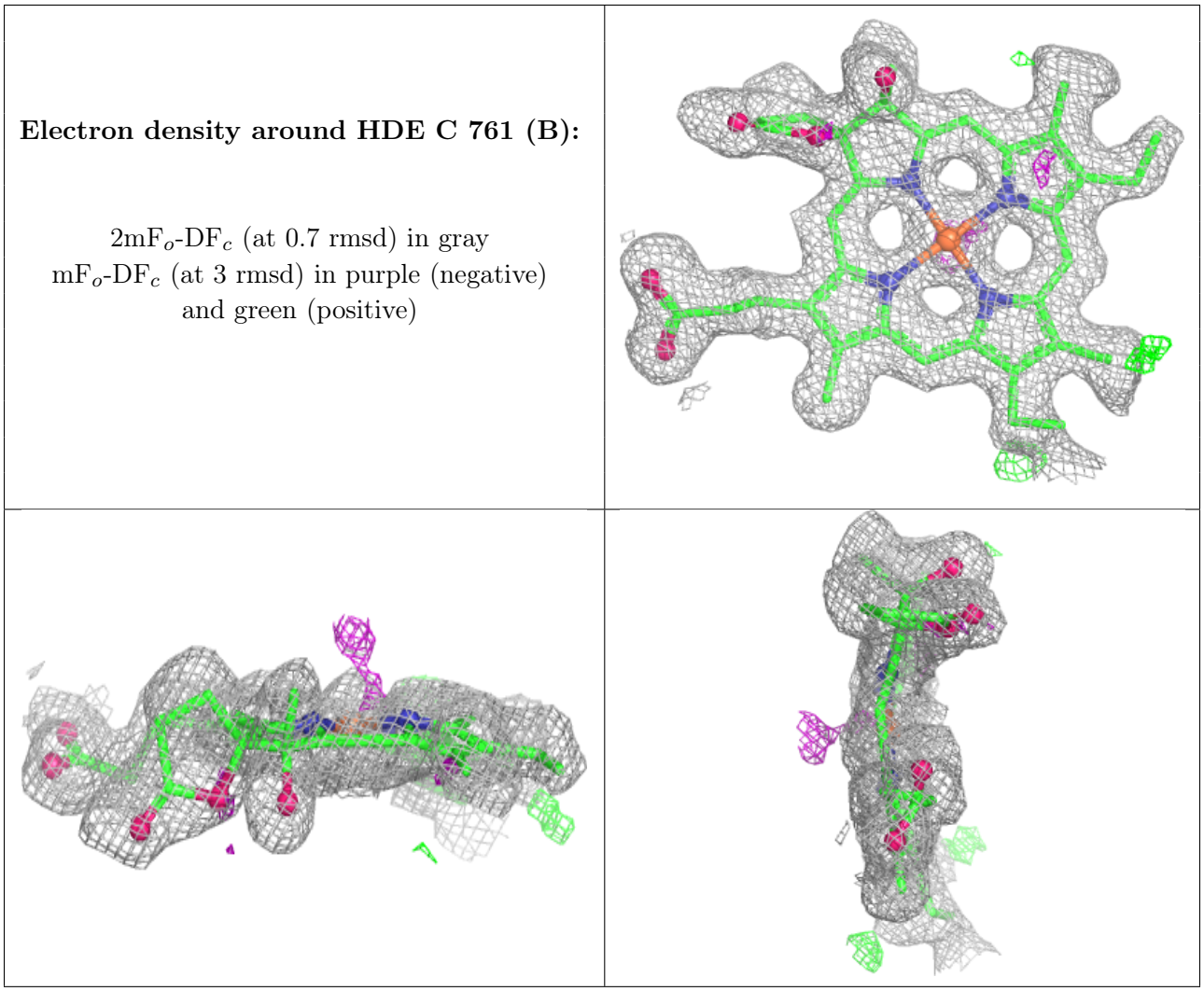
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	H2S	D	754	1/1	0.87	0.12	25,25,25,25	1
4	H2S	B	754	1/1	0.94	0.06	18,18,18,18	1
4	H2S	A	754	1/1	0.95	0.11	26,26,26,26	1
4	H2S	C	754	1/1	0.96	0.11	20,20,20,20	1
3	HDE	C	761[B]	44/44	0.98	0.06	4,10,13,16	44
3	HDE	D	761[B]	44/44	0.98	0.05	2,8,14,16	44
3	HDE	B	761[B]	44/44	0.98	0.06	3,12,15,16	44
2	HDD	C	760[A]	44/44	0.99	0.05	2,5,8,11	44
2	HDD	D	760[A]	44/44	0.99	0.04	2,3,7,15	44
3	HDE	A	761[B]	44/44	0.99	0.05	2,7,10,14	44
2	HDD	A	760[A]	44/44	0.99	0.05	2,3,9,16	44
2	HDD	B	760[A]	44/44	0.99	0.05	3,4,8,11	44

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.

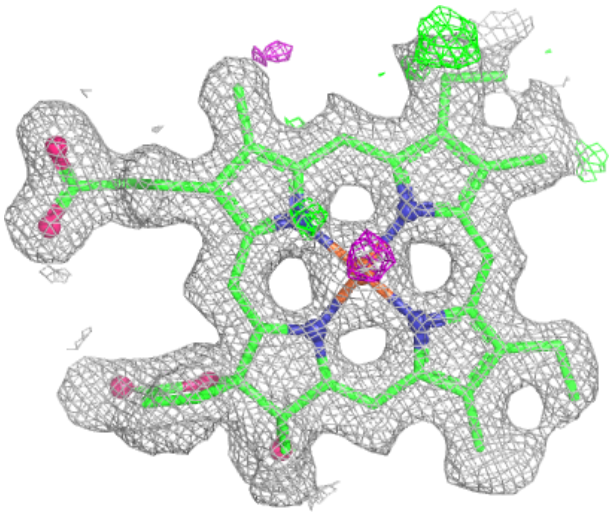
Electron density around HDE C 761 (B):

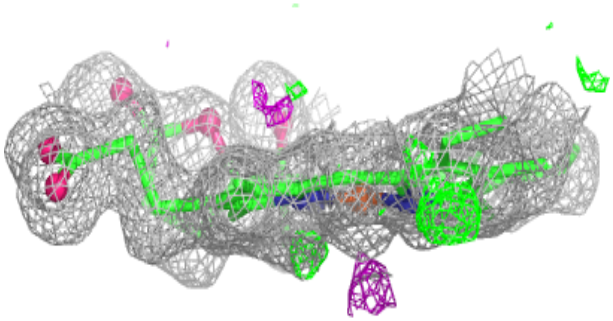
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

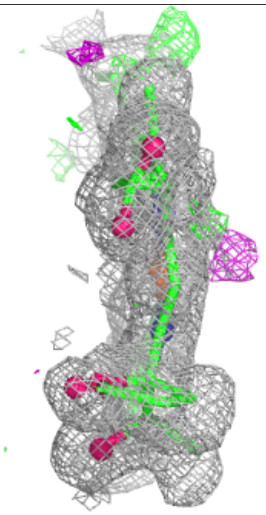


Electron density around HDE D 761 (B):

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

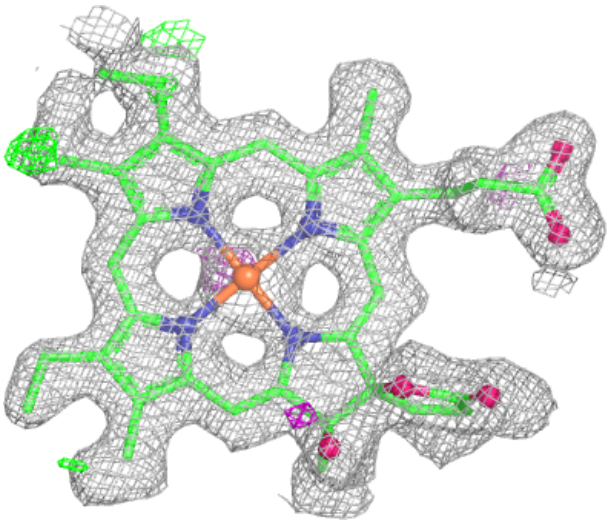


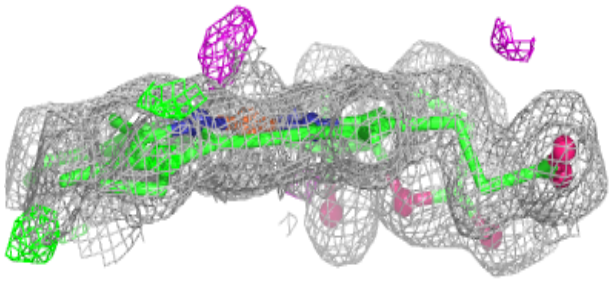


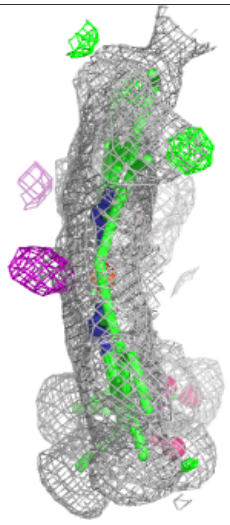


Electron density around HDE B 761 (B):

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

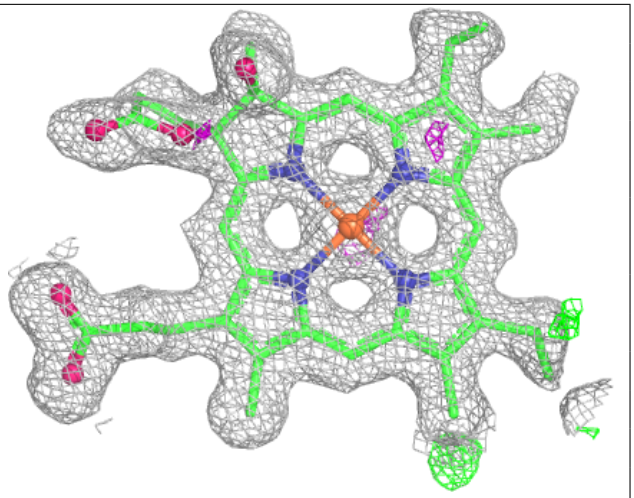


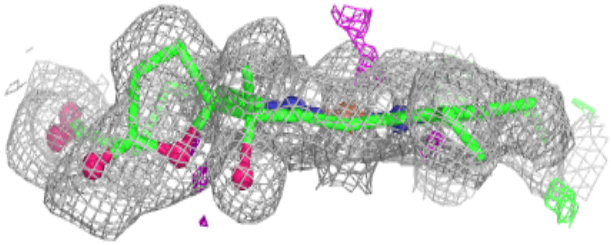


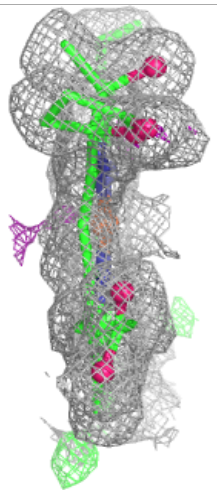


Electron density around HDD C 760 (A):

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

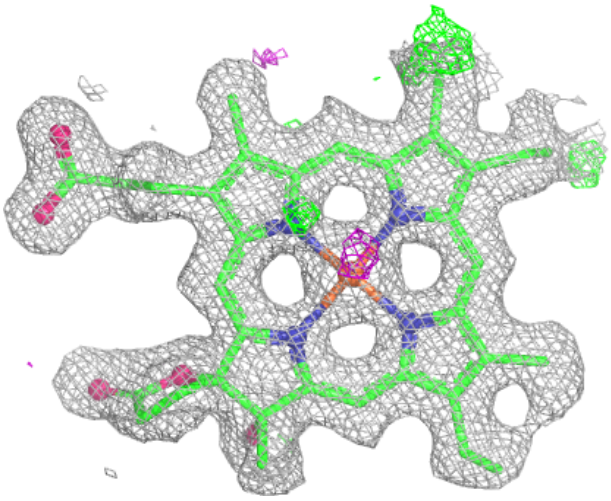


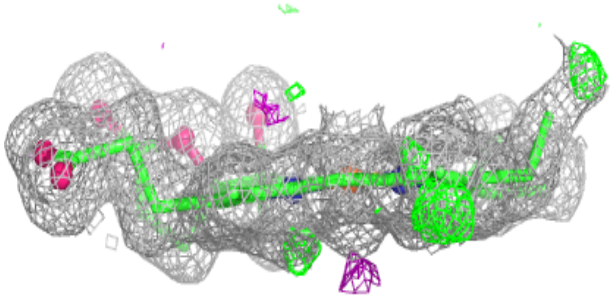


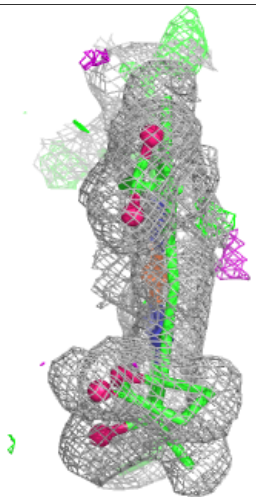


Electron density around HDD D 760 (A):

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

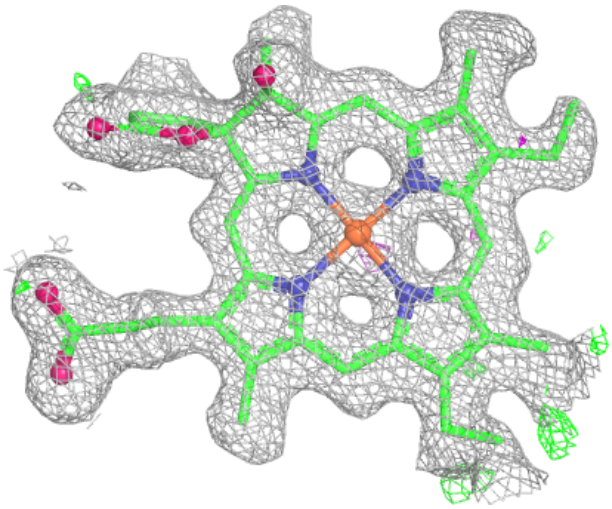


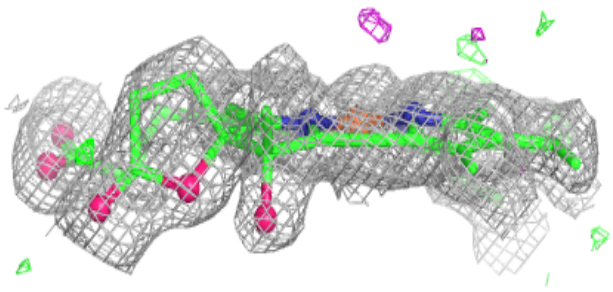


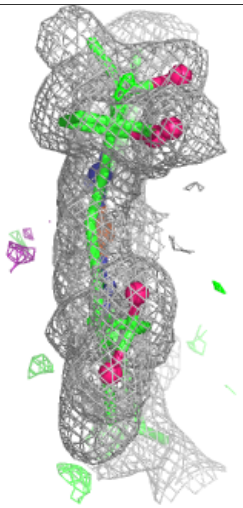


Electron density around HDE A 761 (B):

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

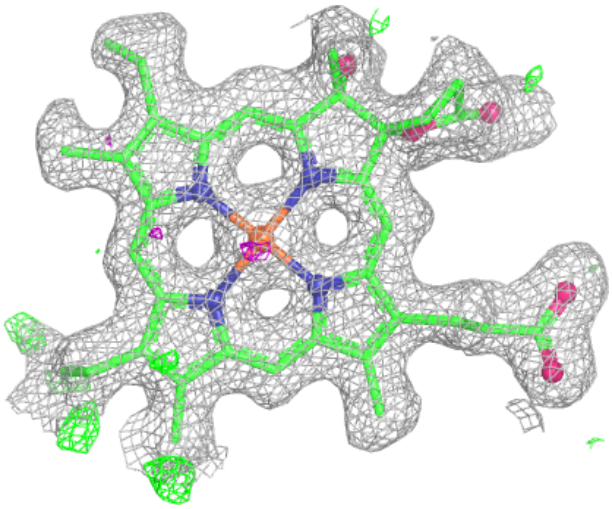


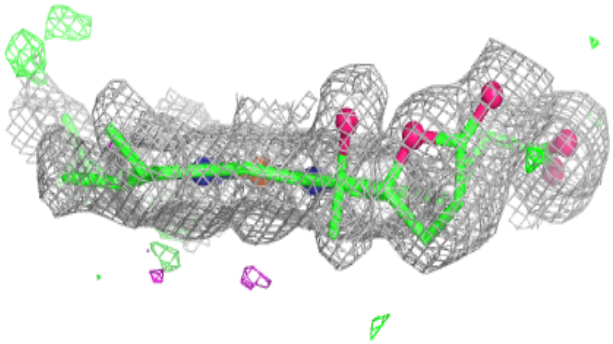


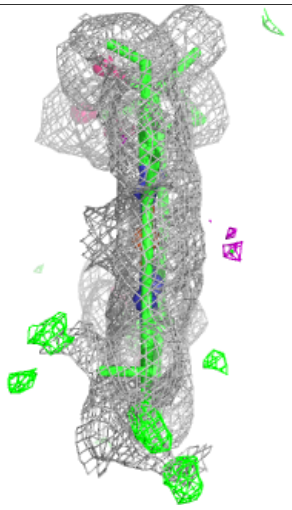


Electron density around HDD A 760 (A):

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

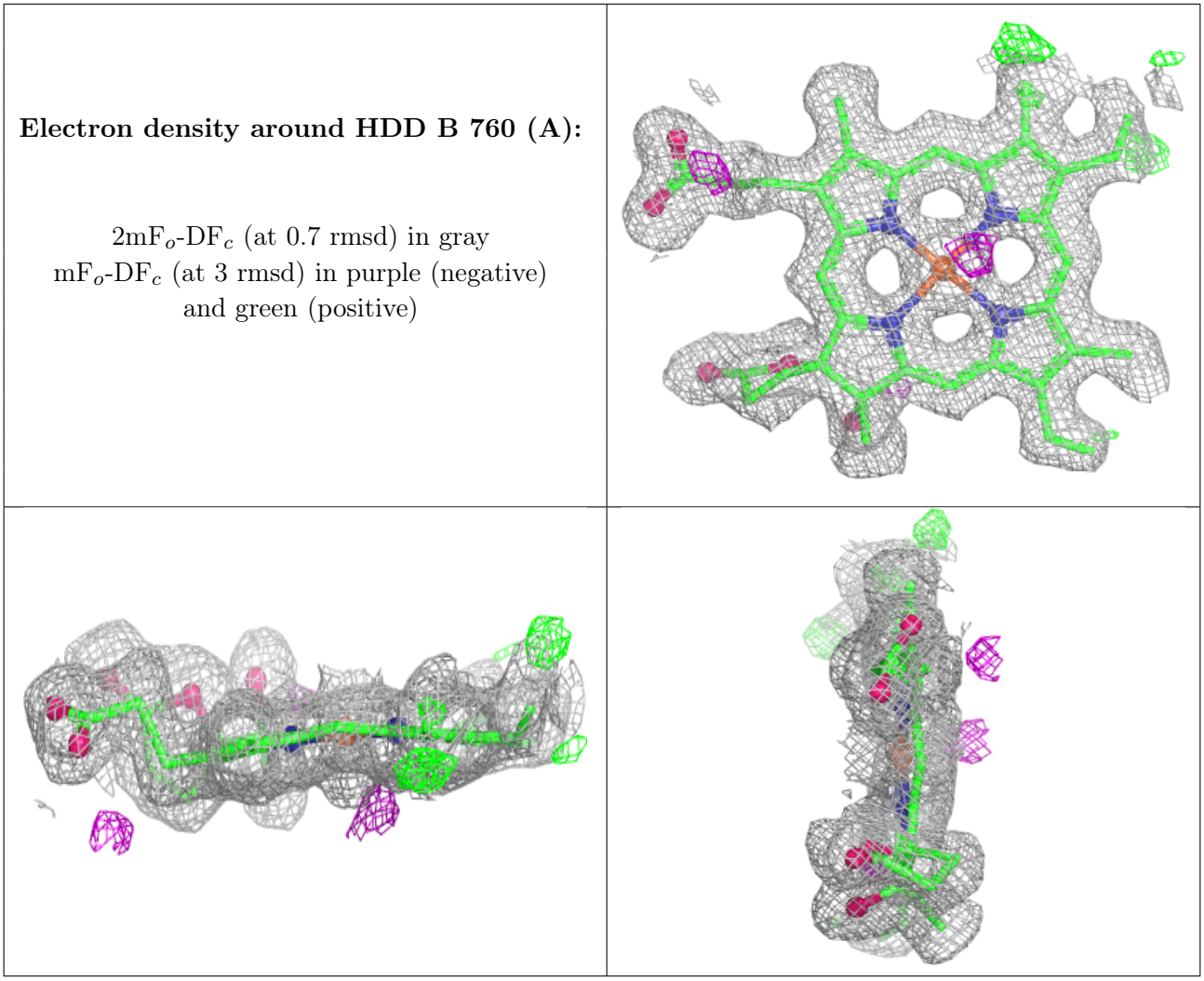






Electron density around HDD B 760 (A):

$2mF_o$-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.