



wwPDB X-ray Structure Validation Summary Report ⓘ

May 28, 2020 – 09:55 pm BST

PDB ID : 6PO0
Title : The structure of the orthorhombic (P212121) crystal form of beef liver catalase at 1.85 Å resolution
Authors : McPherson, A.
Deposited on : 2019-07-03
Resolution : 1.75 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

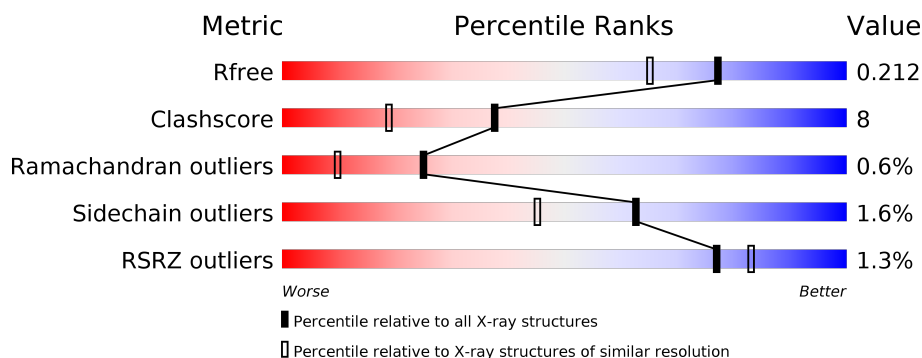
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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

Mol	Chain	Length	Quality of chain
1	A	527	<div> <div>2%</div> <div>84% 10% 5%</div> </div>
1	B	527	<div> <div>82% 12% 5%</div> </div>
1	C	527	<div> <div>2%</div> <div>80% 14% 5%</div> </div>
1	D	527	<div> <div>2%</div> <div>81% 13% 5%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33334 atoms, of which 15607 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	499	Total	C	H	N	O	S	0	1	0
			7869	2551	3846	716	741	15			
1	B	499	Total	C	H	N	O	S	0	0	0
			7859	2548	3842	715	740	14			
1	C	499	Total	C	H	N	O	S	0	2	0
			7885	2560	3854	715	742	14			
1	D	499	Total	C	H	N	O	S	0	0	0
			7858	2548	3841	715	740	14			

There are 8 discrepancies between the modelled and reference sequences:

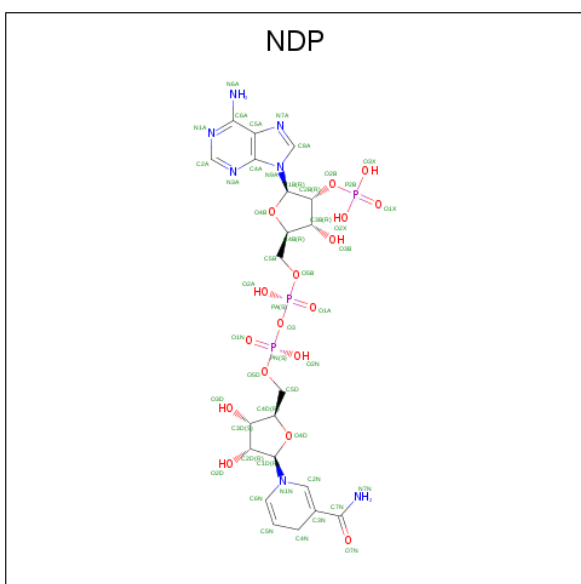
Chain	Residue	Modelled	Actual	Comment	Reference
A	212	ASP	ASN	engineered mutation	UNP P00432
A	225	ASP	ASN	engineered mutation	UNP P00432
B	212	ASP	ASN	engineered mutation	UNP P00432
B	225	ASP	ASN	engineered mutation	UNP P00432
C	212	ASP	ASN	engineered mutation	UNP P00432
C	225	ASP	ASN	engineered mutation	UNP P00432
D	212	ASP	ASN	engineered mutation	UNP P00432
D	225	ASP	ASN	engineered mutation	UNP P00432

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	B	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	C	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	D	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0

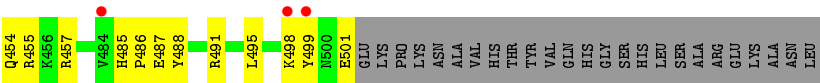
- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $\text{C}_{21}\text{H}_{30}\text{N}_7\text{O}_{17}\text{P}_3$).



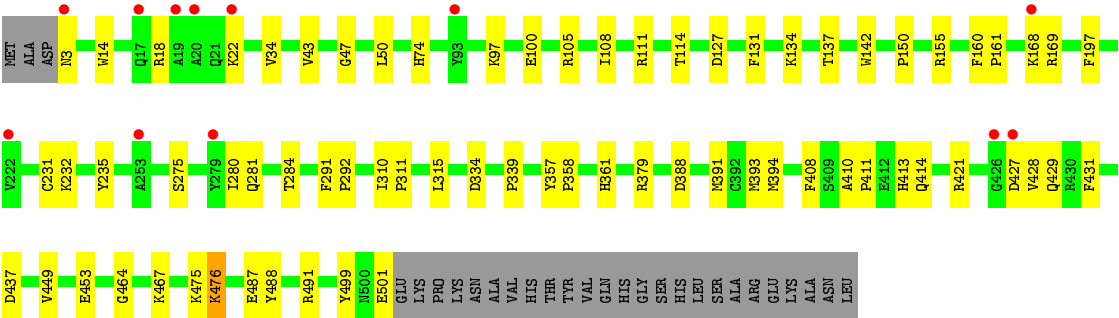
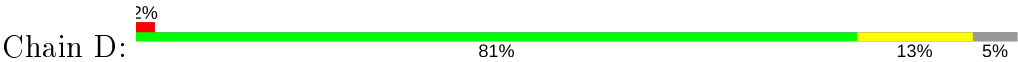
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	
			74	21	26	7	17	3	
3	B	1	Total	C	H	N	O	P	
			74	21	26	7	17	3	
3	C	1	Total	C	H	N	O	P	
			74	21	26	7	17	3	
3	D	1	Total	C	H	N	O	P	
			74	21	26	7	17	3	

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	305	Total	O		
			305	305	0	0
4	B	347	Total	O		
			347	347	0	0
4	C	365	Total	O		
			368	368	0	3
4	D	255	Total	O		
			255	255	0	0



● Molecule 1: Catalase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.98Å 140.39Å 228.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	119.57 – 1.75 119.57 – 1.75	Depositor EDS
% Data completeness (in resolution range)	74.6 (119.57-1.75) 74.6 (119.57-1.75)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.173 , 0.207 0.183 , 0.212	Depositor DCC
R_{free} test set	10179 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33334	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, NDP

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	0.65	1/4143 (0.0%)	0.75	2/5628 (0.0%)
1	B	0.67	0/4137	0.82	5/5619 (0.1%)
1	C	0.68	0/4158	0.77	0/5647
1	D	0.65	2/4137 (0.0%)	0.74	3/5619 (0.1%)
All	All	0.66	3/16575 (0.0%)	0.77	10/22513 (0.0%)

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	0	1
1	B	0	2
1	C	0	1
1	D	0	2
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	138	GLU	CD-OE1	9.89	1.36	1.25
1	D	476	LYS	C-N	-8.01	1.15	1.34
1	D	475	LYS	C-N	-7.00	1.18	1.34

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	430	ARG	NE-CZ-NH2	-14.04	113.28	120.30
1	B	430	ARG	NE-CZ-NH1	12.67	126.63	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	155	ARG	NE-CZ-NH2	-9.09	115.75	120.30
1	A	155	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	B	430	ARG	CG-CD-NE	-6.89	97.34	111.80

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	455	ARG	Sidechain
1	B	111	ARG	Sidechain
1	B	126	ARG	Sidechain
1	C	111	ARG	Sidechain
1	D	105	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4023	3846	3844	48	0
1	B	4017	3842	3839	63	0
1	C	4031	3854	3854	82	1
1	D	4017	3841	3837	65	1
2	A	43	30	30	3	0
2	B	43	30	30	2	0
2	C	43	30	30	9	0
2	D	43	30	30	2	0
3	A	48	26	26	1	0
3	B	48	26	26	5	0
3	C	48	26	26	19	0
3	D	48	26	26	14	0
4	A	305	0	0	7	0
4	B	347	0	0	12	0
4	C	368	0	0	11	0
4	D	255	0	0	8	0
All	All	17727	15607	15598	247	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 247 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:C:197[A]:PHE:CD1	3:C:602:NDP:H2A	1.55	1.41
1:C:197[A]:PHE:CE1	3:C:602:NDP:H2A	1.57	1.36
1:A:67:ARG:NH2	1:D:168:LYS:CE	1.91	1.33
1:A:67:ARG:NH2	1:D:168:LYS:HE3	1.03	1.33
1:C:197[B]:PHE:CD1	3:C:602:NDP:H2A	1.88	1.06

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)
1:C:486:PRO:HB3	1:D:22:LYS:HD3[3_645]	1.06	0.54

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	498/527 (94%)	485 (97%)	9 (2%)	4 (1%)	19	6
1	B	497/527 (94%)	481 (97%)	14 (3%)	2 (0%)	34	17
1	C	499/527 (95%)	481 (96%)	15 (3%)	3 (1%)	25	10
1	D	497/527 (94%)	480 (97%)	15 (3%)	2 (0%)	34	17
All	All	1991/2108 (94%)	1927 (97%)	53 (3%)	11 (1%)	25	10

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	437	ASP
1	A	437	ASP

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Mol	Chain	Res	Type
1	C	388	ASP
1	D	388	ASP
1	D	437	ASP

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	432/454 (95%)	426 (99%)	6 (1%)	67	52
1	B	431/454 (95%)	423 (98%)	8 (2%)	57	37
1	C	433/454 (95%)	427 (99%)	6 (1%)	67	52
1	D	431/454 (95%)	423 (98%)	8 (2%)	57	37
All	All	1727/1816 (95%)	1699 (98%)	28 (2%)	62	45

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	235	TYR
1	C	131	PHE
1	D	235	TYR
1	B	488	TYR
1	C	127	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	13	HIS
1	B	429	GLN
1	C	101	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	HEM	C	601	1,4	27,50,50	1.03	4 (14%)	17,82,82	2.44	7 (41%)
2	HEM	A	601	1	27,50,50	0.89	1 (3%)	17,82,82	1.60	6 (35%)
3	NDP	C	602	-	45,52,52	0.80	1 (2%)	53,80,80	0.81	2 (3%)
2	HEM	D	601	1	27,50,50	1.07	2 (7%)	17,82,82	1.25	1 (5%)
2	HEM	B	601	1	27,50,50	1.37	4 (14%)	17,82,82	1.69	4 (23%)
3	NDP	D	602	-	45,52,52	0.68	1 (2%)	53,80,80	0.87	2 (3%)
3	NDP	B	602	-	45,52,52	0.65	0	53,80,80	0.85	2 (3%)
3	NDP	A	602	-	45,52,52	0.75	1 (2%)	53,80,80	0.86	2 (3%)

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	HEM	C	601	1,4	-	0/6/54/54	-
2	HEM	A	601	1	-	0/6/54/54	-
3	NDP	C	602	-	-	4/30/77/77	0/5/5/5
2	HEM	D	601	1	-	0/6/54/54	-
2	HEM	B	601	1	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NDP	D	602	-	-	13/30/77/77	0/5/5/5
3	NDP	B	602	-	-	13/30/77/77	0/5/5/5
3	NDP	A	602	-	-	4/30/77/77	0/5/5/5

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	HEM	C4D-C3D	3.90	1.51	1.42
2	B	601	HEM	C3B-C2B	-3.62	1.35	1.40
3	C	602	NDP	P2B-O2B	3.19	1.65	1.59
2	D	601	HEM	C4D-C3D	3.00	1.49	1.42
3	A	602	NDP	P2B-O2B	2.92	1.64	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	HEM	C4A-C3A-C2A	5.02	110.49	107.00
2	C	601	HEM	CMA-C3A-C4A	-4.66	121.30	128.46
2	B	601	HEM	C4A-C3A-C2A	3.94	109.74	107.00
2	C	601	HEM	CAA-CBA-CGA	3.44	118.45	112.67
2	C	601	HEM	CMD-C2D-C1D	-3.04	123.79	128.46

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	602	NDP	C5B-O5B-PA-O1A
3	D	602	NDP	C5D-O5D-PN-O1N
3	D	602	NDP	C5D-O5D-PN-O2N
3	D	602	NDP	O4D-C1D-N1N-C6N
3	B	602	NDP	C5B-O5B-PA-O1A

There are no ring outliers.

8 monomers are involved in 55 short contacts:

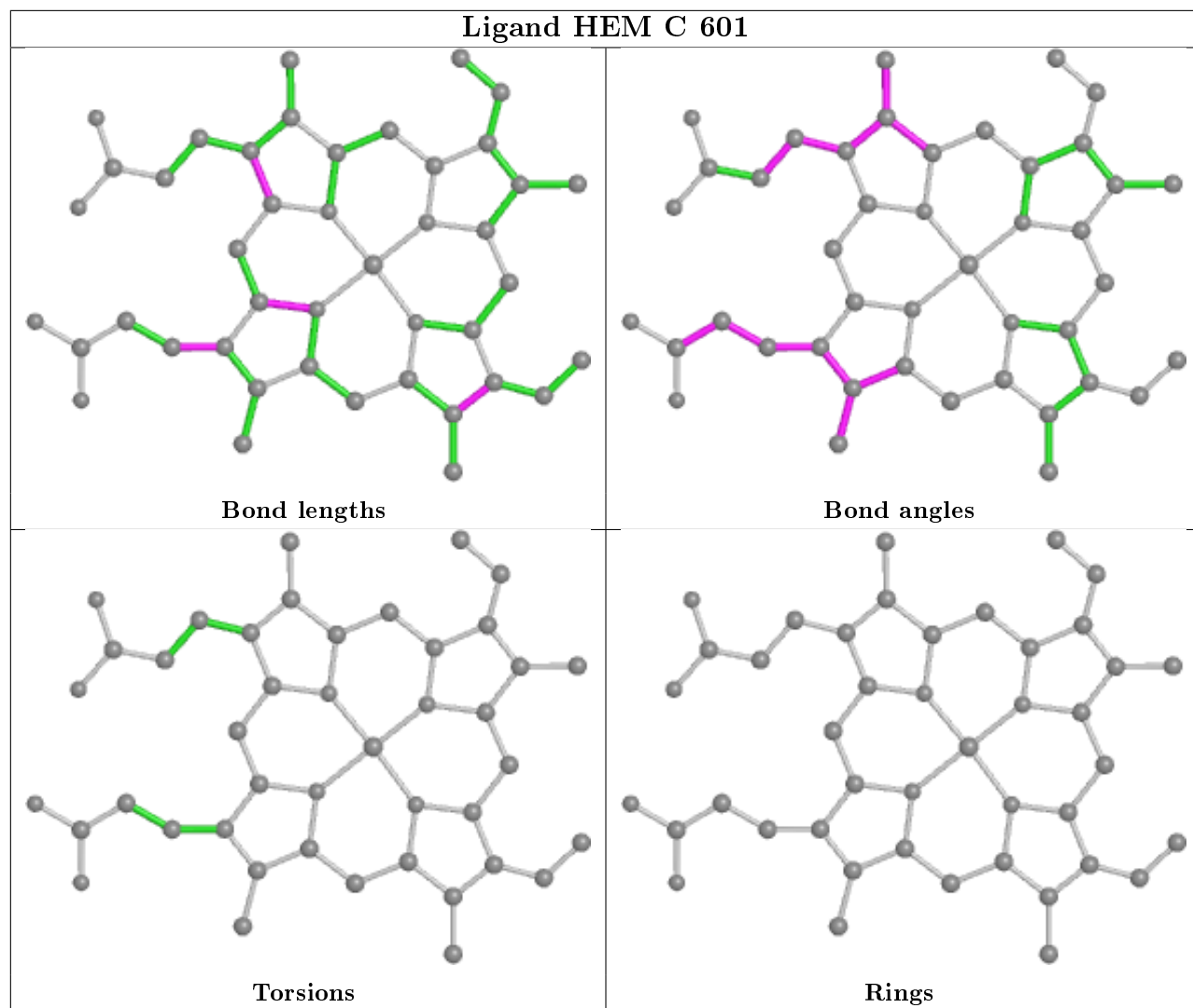
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	HEM	9	0
2	A	601	HEM	3	0
3	C	602	NDP	19	0
2	D	601	HEM	2	0

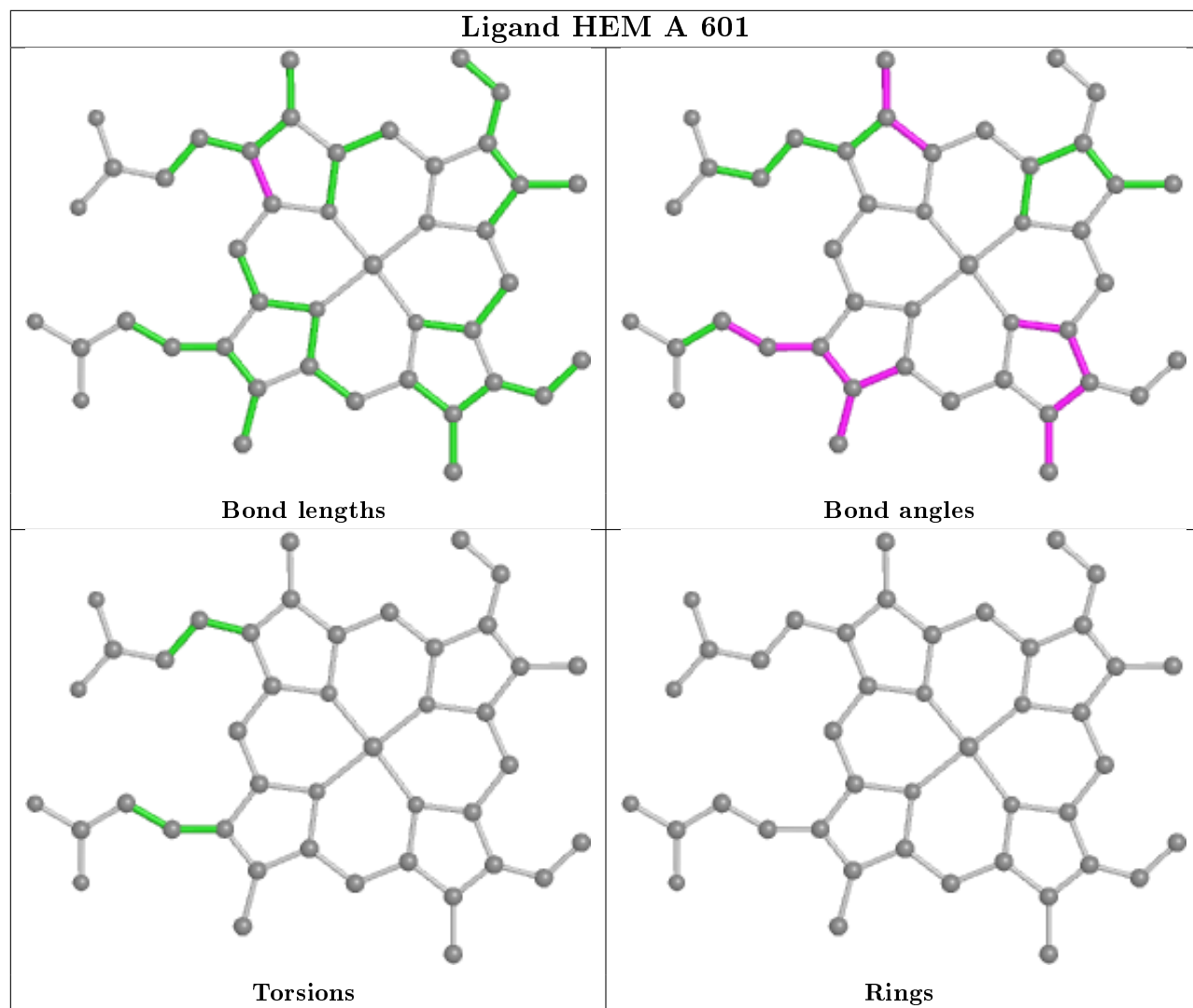
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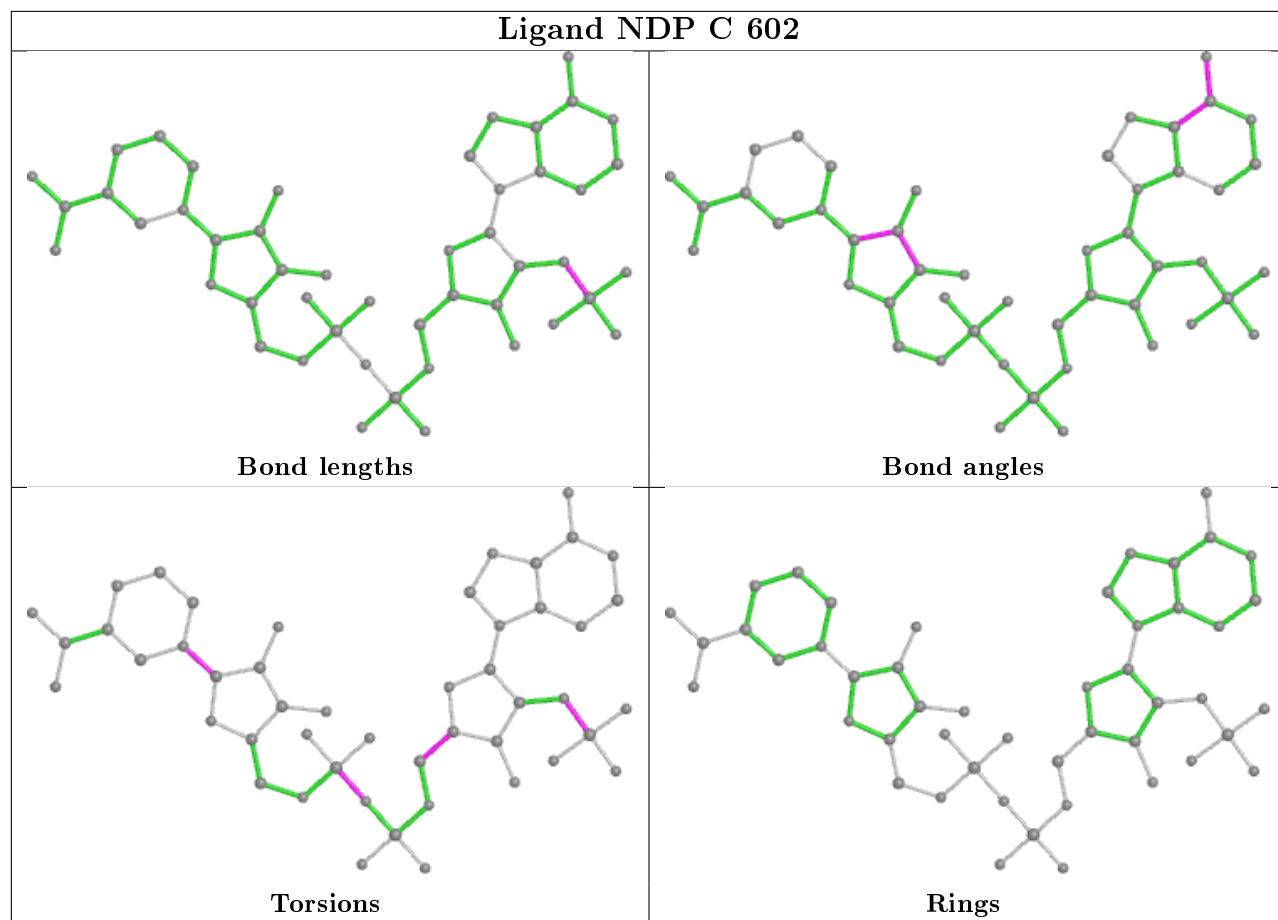
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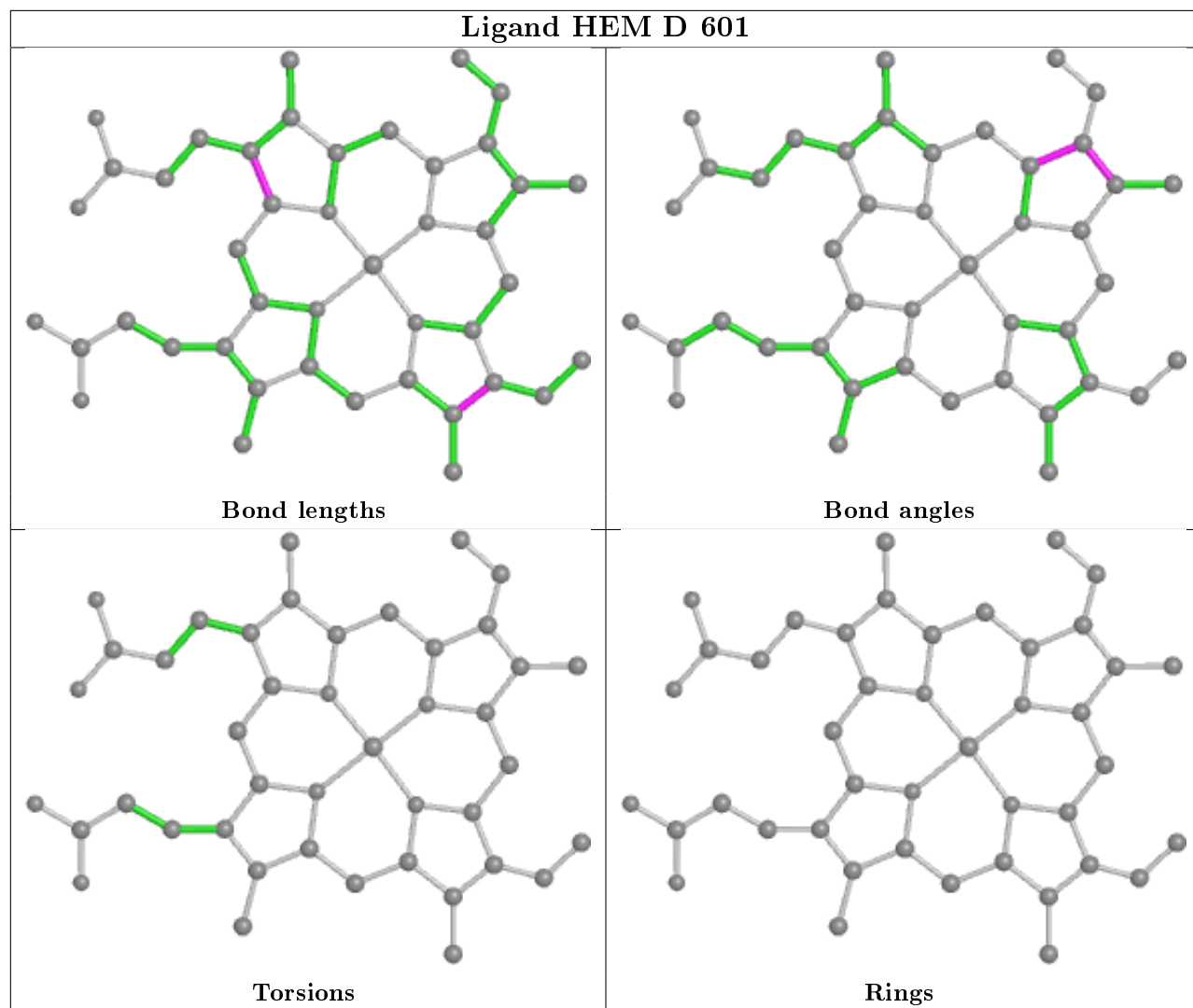
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	HEM	2	0
3	D	602	NDP	14	0
3	B	602	NDP	5	0
3	A	602	NDP	1	0

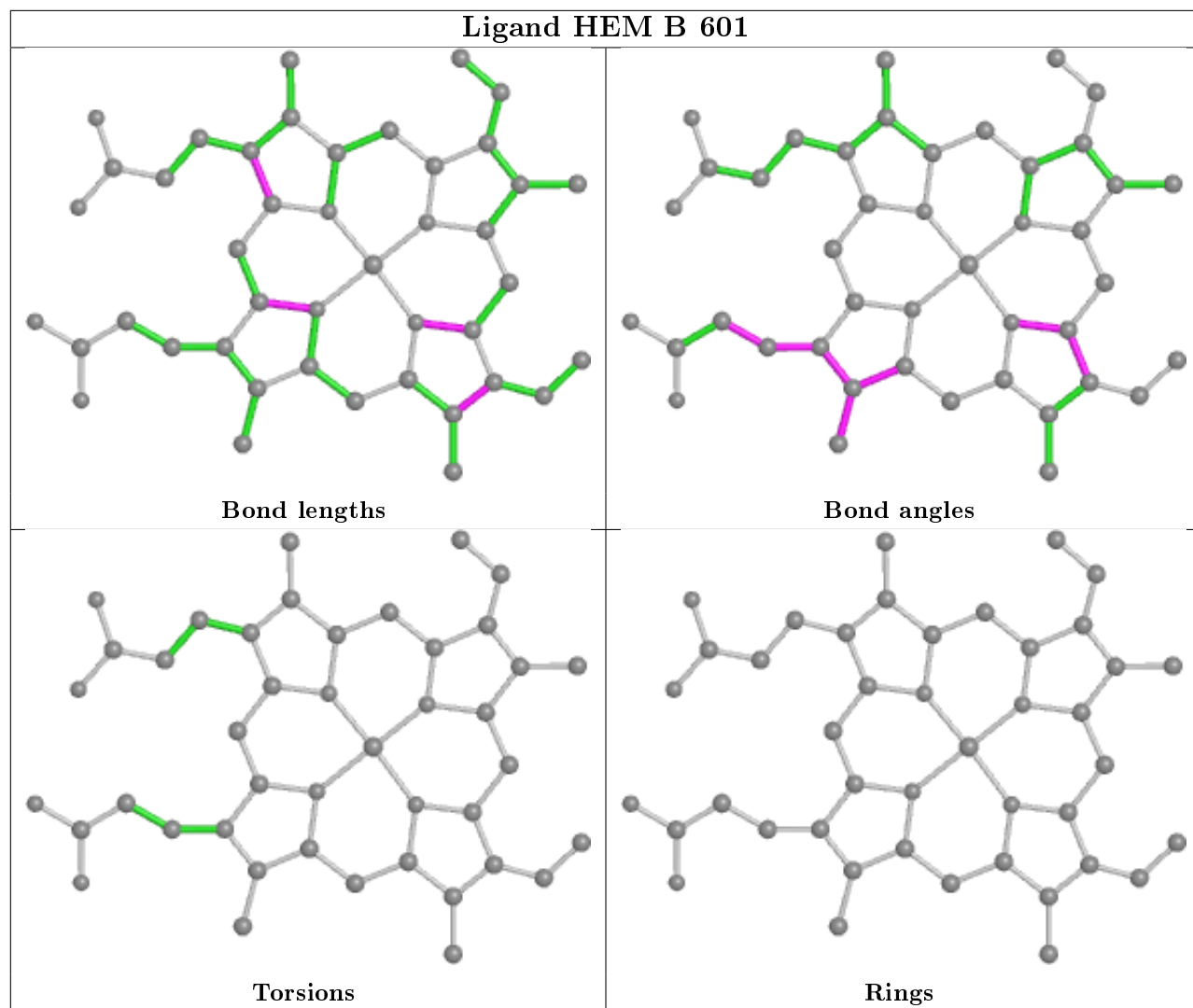
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

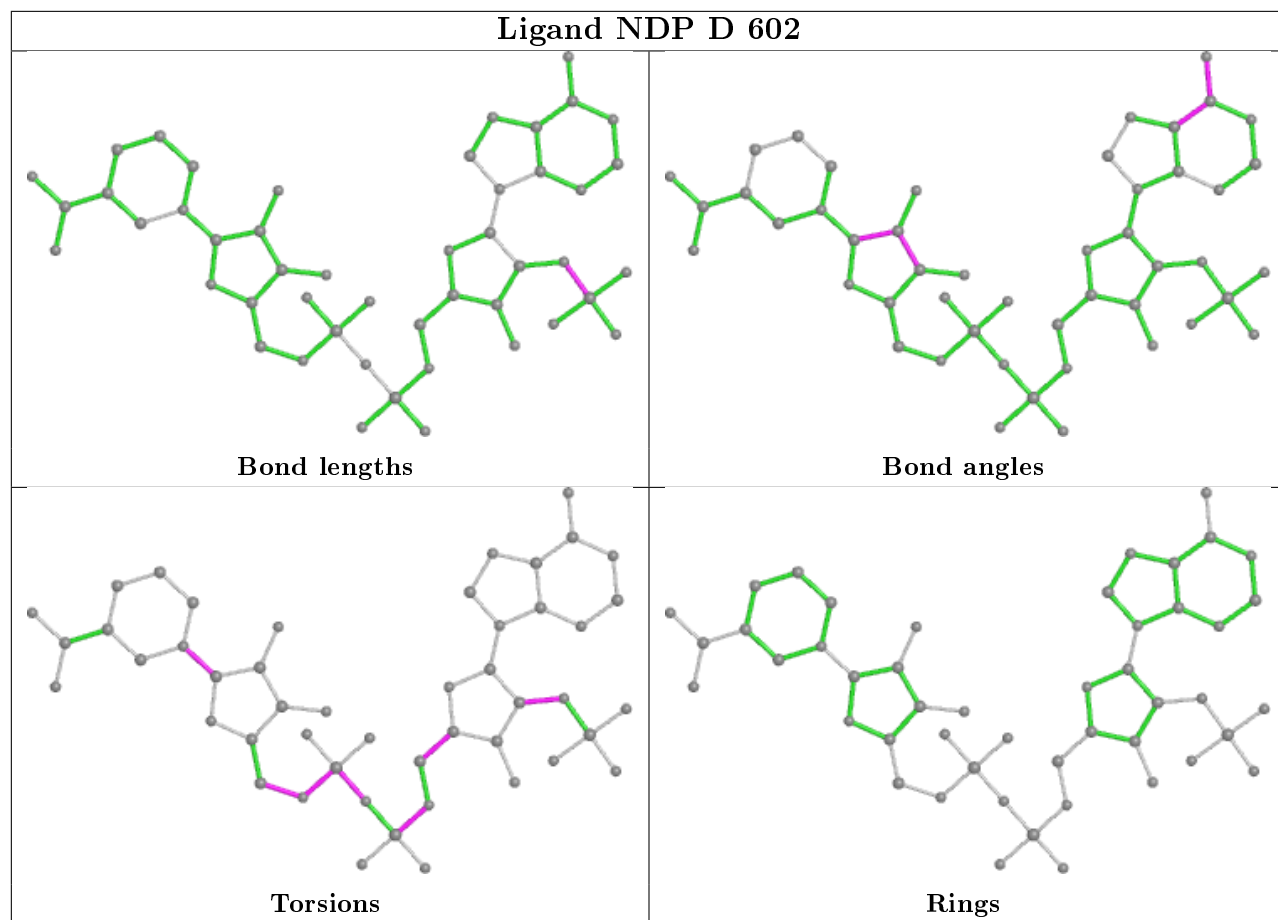


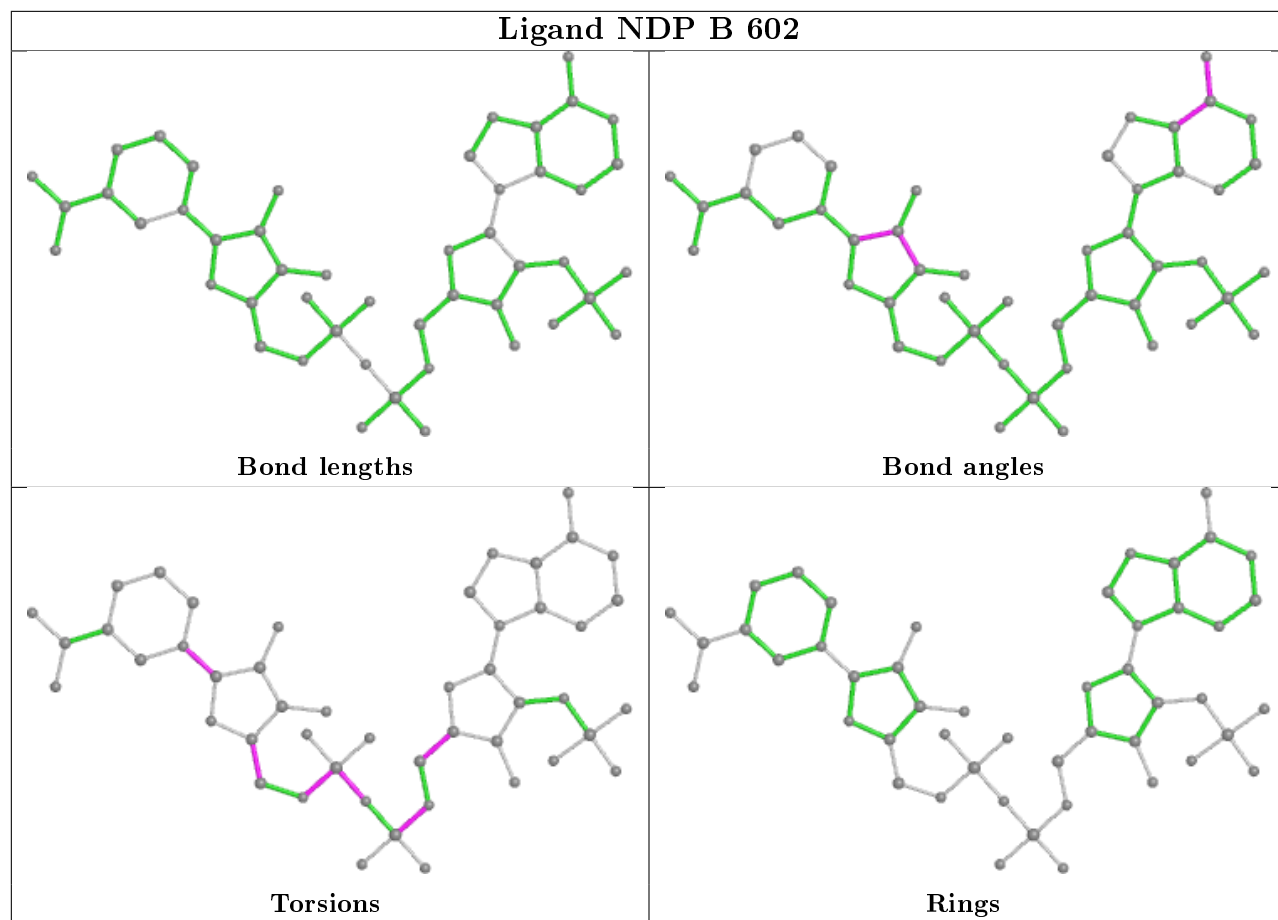


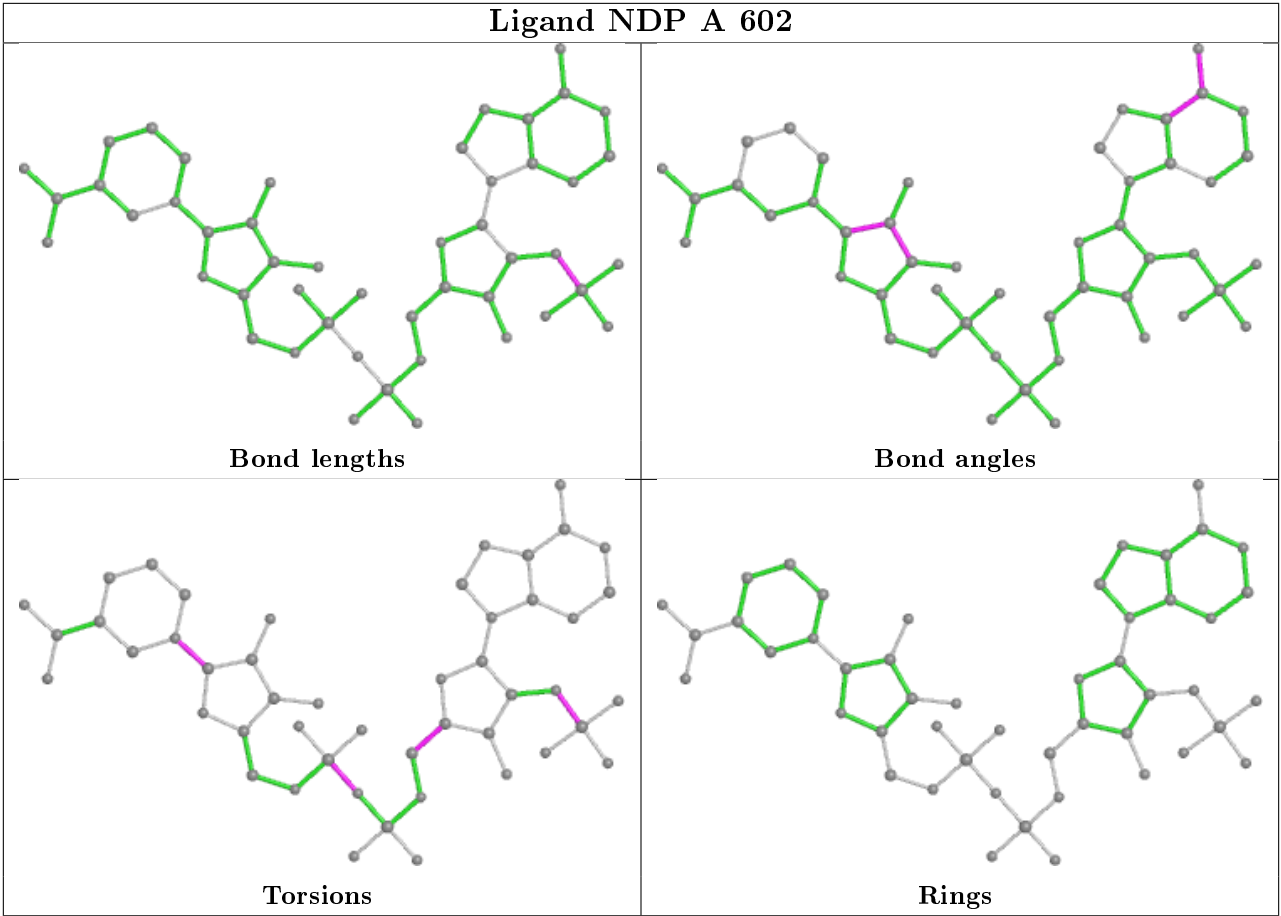












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	475:LYS	C	476:LYS	N	1.17
1	D	476:LYS	C	477:ALA	N	1.15

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	499/527 (94%)	0.03	3 (0%) 89 92	24, 41, 66, 96	0
1	B	499/527 (94%)	0.03	2 (0%) 92 94	24, 42, 67, 118	0
1	C	499/527 (94%)	0.03	8 (1%) 72 79	23, 38, 67, 109	0
1	D	499/527 (94%)	0.23	12 (2%) 59 65	26, 55, 84, 122	0
All	All	1996/2108 (94%)	0.08	25 (1%) 77 83	23, 43, 74, 122	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	197[A]	PHE	5.4
1	D	20	ALA	4.5
1	D	427	ASP	4.2
1	D	168	LYS	3.6
1	D	19	ALA	3.5

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

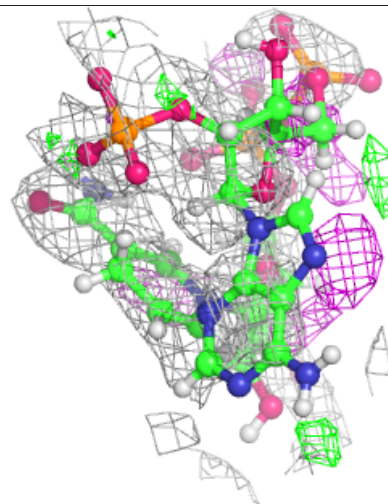
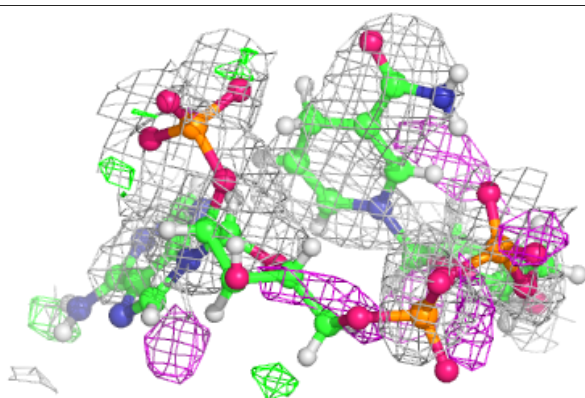
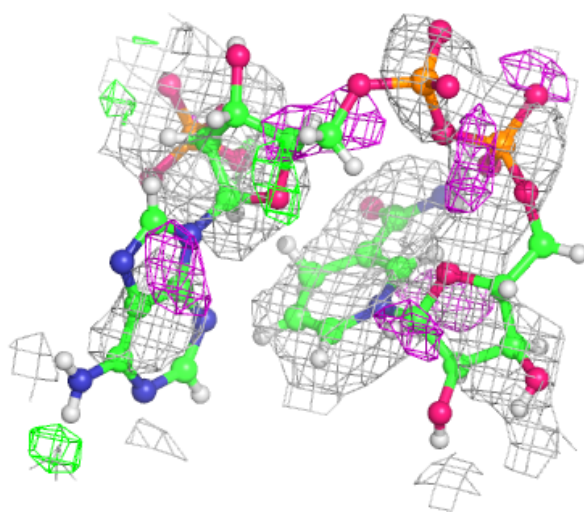
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NDP	D	602	48/48	0.71	0.35	102,133,137,139	0
3	NDP	A	602	48/48	0.83	0.24	56,86,106,113	0
3	NDP	B	602	48/48	0.93	0.12	53,70,79,92	0
3	NDP	C	602	48/48	0.96	0.10	47,55,61,64	0
2	HEM	B	601	43/43	0.98	0.11	27,30,44,46	0
2	HEM	A	601	43/43	0.98	0.11	28,33,47,48	0
2	HEM	C	601	43/43	0.99	0.10	25,34,52,55	0
2	HEM	D	601	43/43	0.99	0.10	35,45,61,64	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.

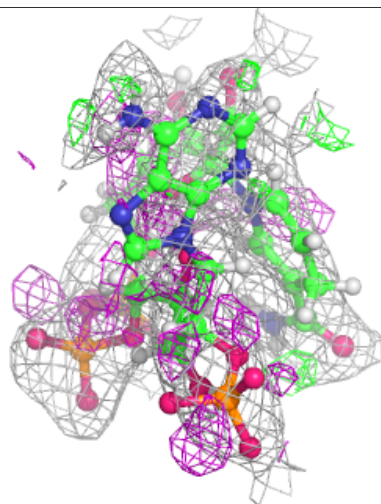
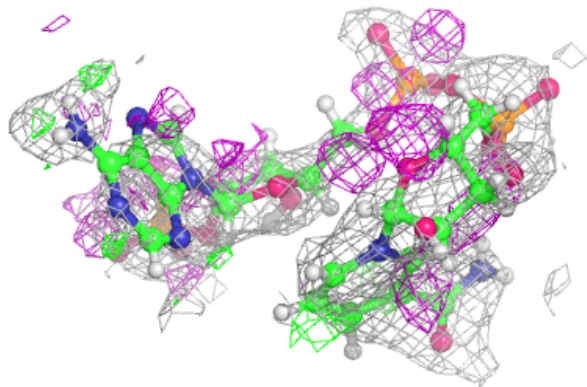
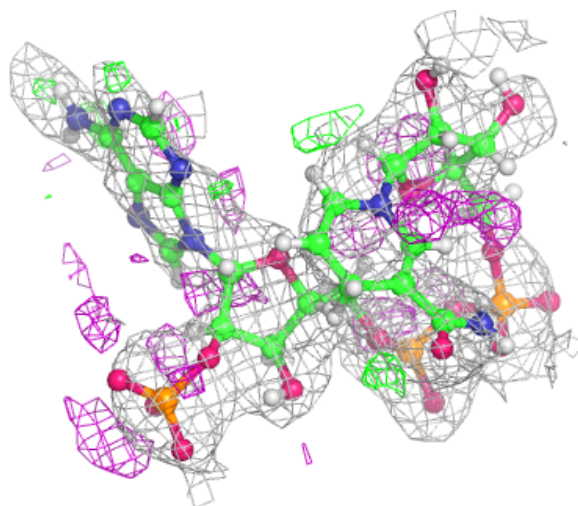
Electron density around NDP D 602:

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



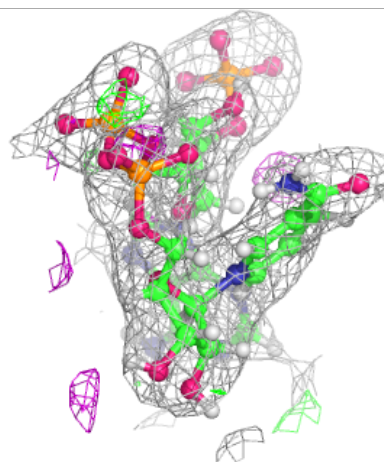
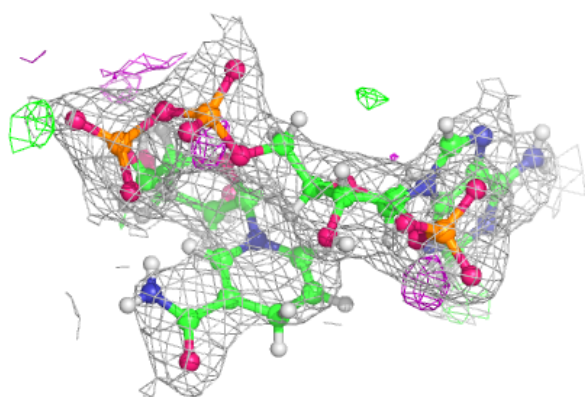
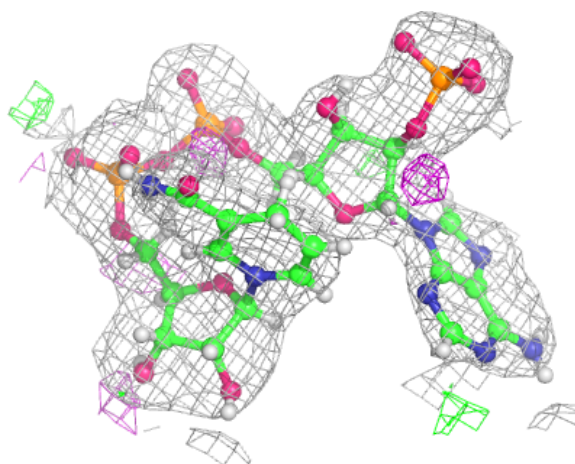
Electron density around NDP A 602:

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



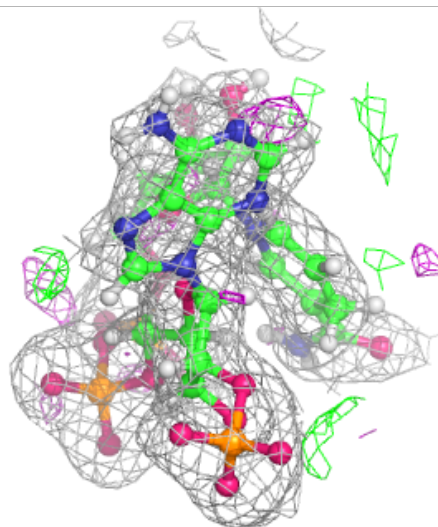
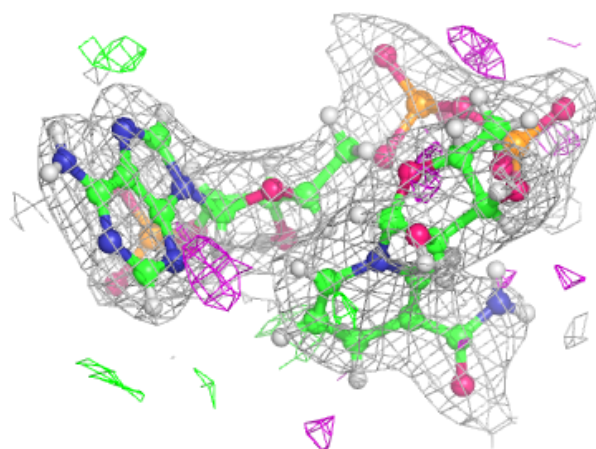
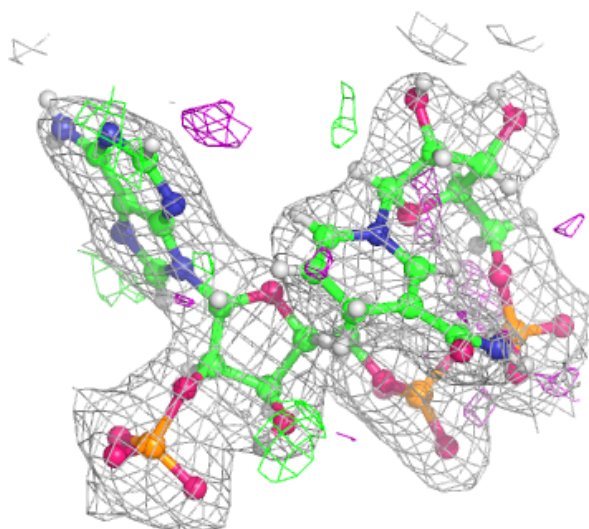
Electron density around NDP B 602:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



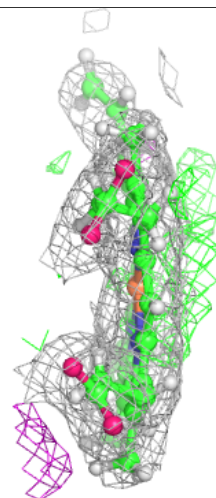
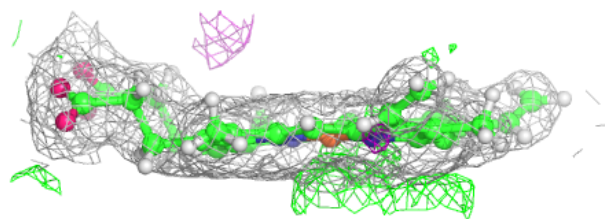
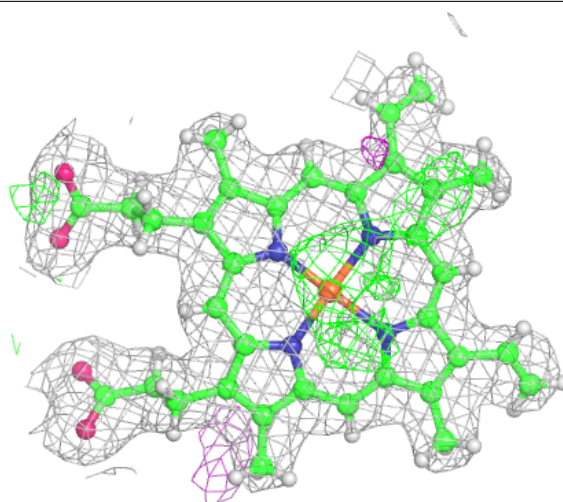
Electron density around NDP C 602:

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and green (positive)



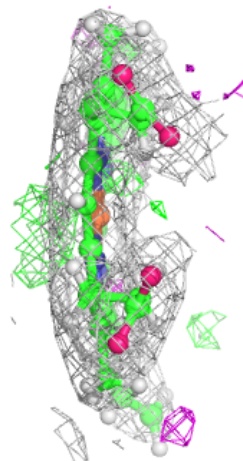
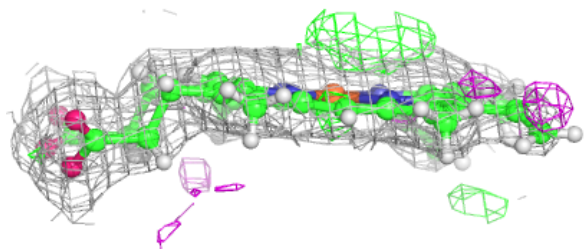
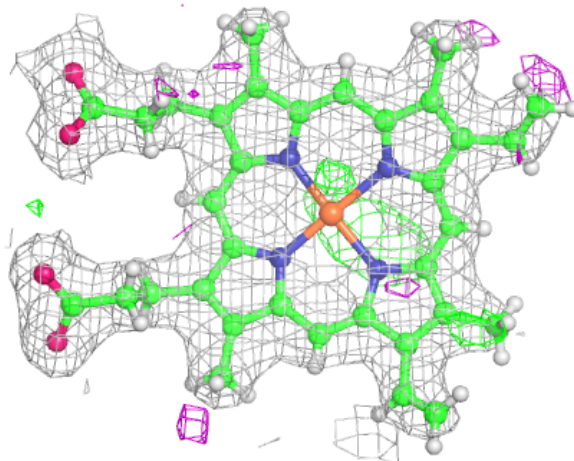
Electron density around HEM B 601:

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



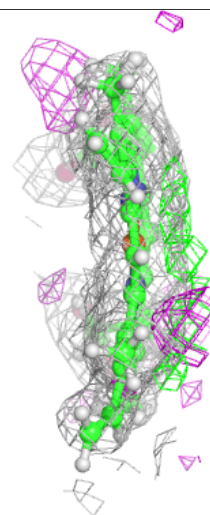
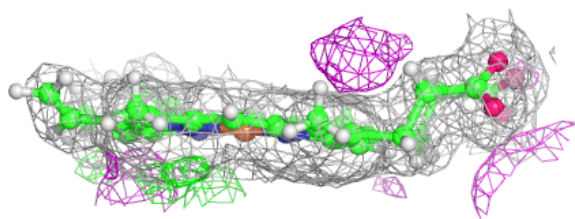
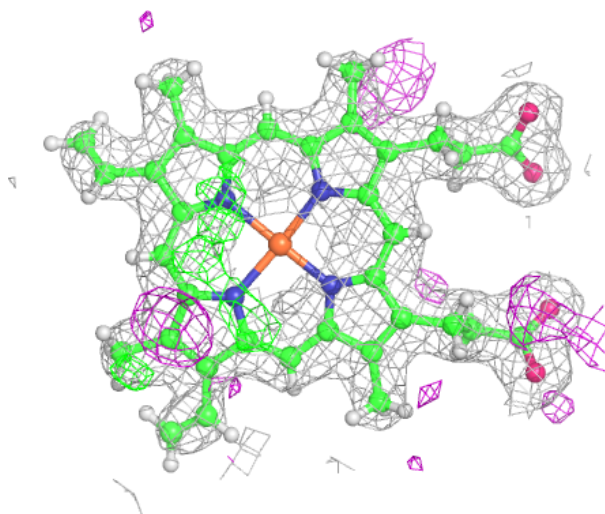
Electron density around HEM A 601:

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and green (positive)



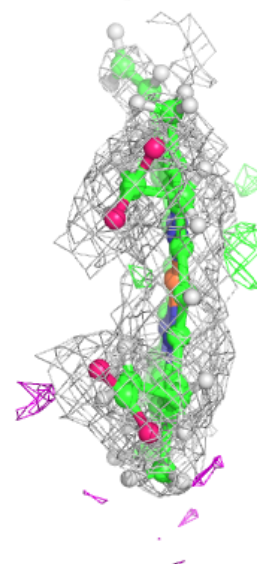
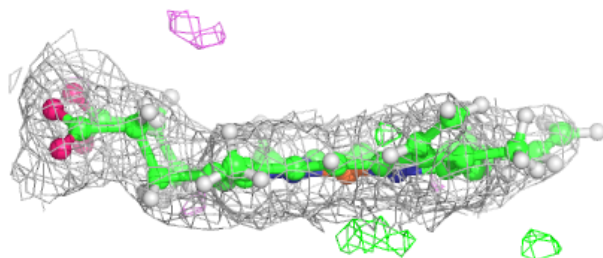
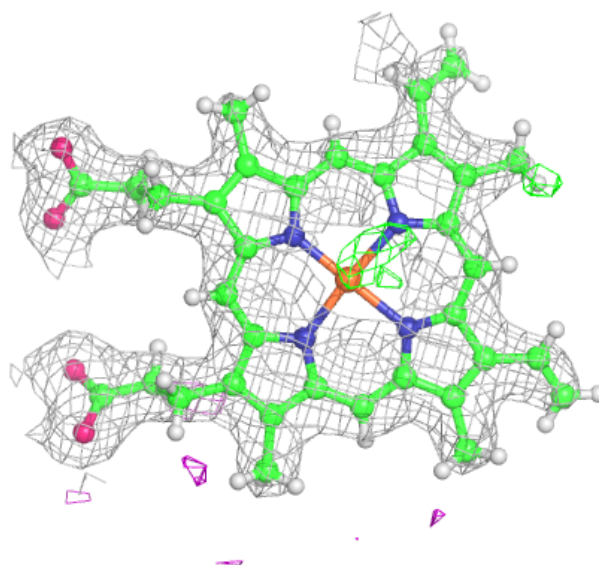
Electron density around HEM C 601:

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



Electron density around HEM D 601:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.