



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:46 AM UTC

PDB ID : 8RV0 / pdb_00008rv0
Title : Crystal structure of octaheme nitrite reductase from *Trichlorobacter ammonif-
icans* in complex with nitrite
Authors : Polyakov, K.M.; Safonova, T.N.; Osipov, E.; Popov, A.N.; Tikhonova, T.V.;
Popov, V.O.
Deposited on : 2024-01-31
Resolution : 1.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

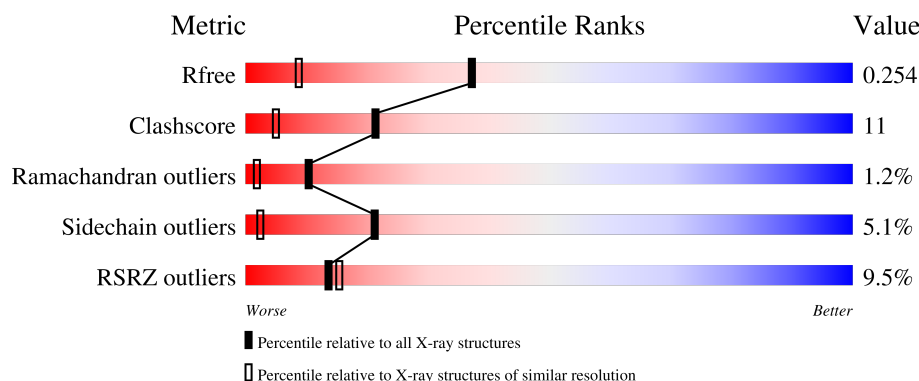
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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

Mol	Chain	Length	Quality of chain
1	Y	495	9% 75% 20% ..

2 Entry composition [i](#)

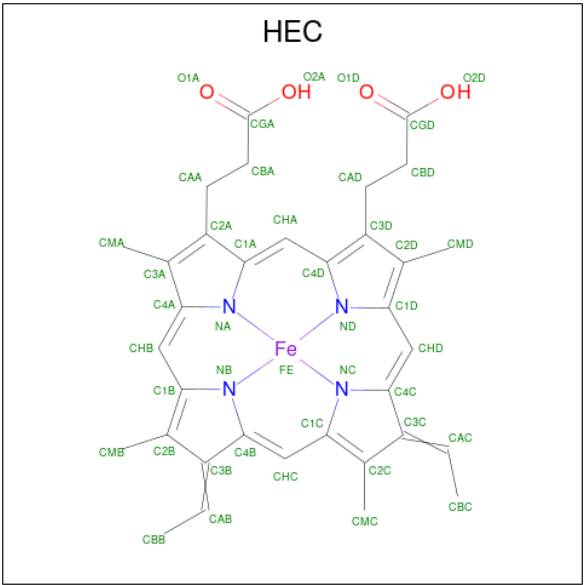
There are 6 unique types of molecules in this entry. The entry contains 4709 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Octaheme cytochrome c nitrite reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Y	495	Total	C	N	O	S	0	6	0
			3909	2445	714	721	29			

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



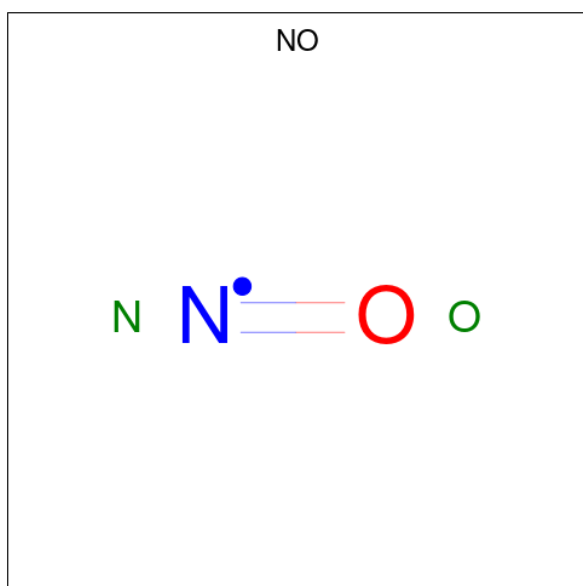
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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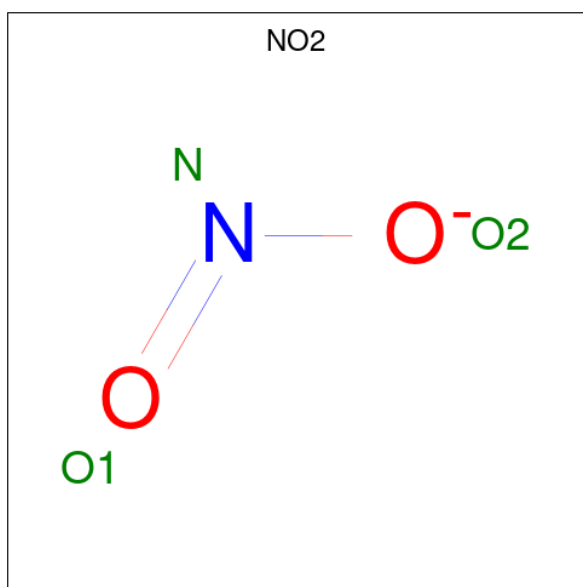
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is NITRIC OXIDE (CCD ID: NO) (formula: NO) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	Y	1	Total	N	O	0	0
			2	1	1		

- Molecule 4 is NITRITE ION (CCD ID: NO2) (formula: NO₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	Y	1	Total	N	O	0	0
			3	1	2		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	Y	1	Total	Ca	0	0
			1	1		

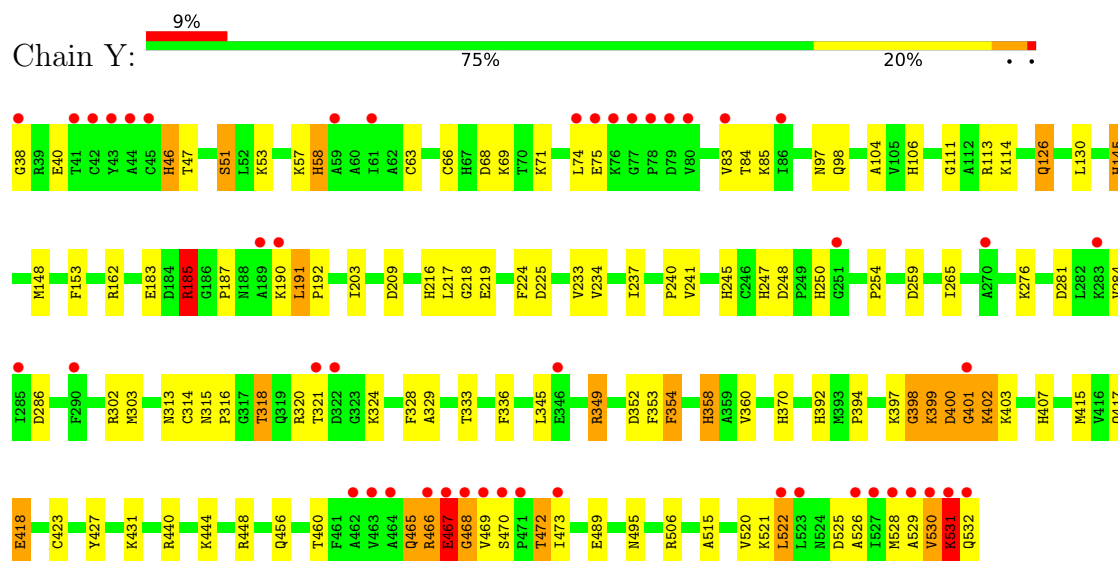
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	Y	450	Total	O	0	0
			450	450		

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: Octaheme cytochrome c nitrite reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	114.44Å 114.44Å 65.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.60 – 1.55 49.60 – 1.55	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.60-1.55) 98.8 (49.60-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.203 , 0.255 (Not available) , 0.254	Depositor DCC
R_{free} test set	3361 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	16.6	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 34.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.037 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4709	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEC, NO2, NO, CA

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	Y	1.08	8/4033 (0.2%)	1.62	41/5431 (0.8%)

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	Y	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Y	358	HIS	CE1-NE2	11.32	1.43	1.32
1	Y	245	HIS	CG-ND1	5.80	1.44	1.38
1	Y	392	HIS	CE1-NE2	5.66	1.38	1.32
1	Y	407	HIS	CE1-NE2	5.64	1.38	1.32
1	Y	46	HIS	CE1-NE2	5.51	1.38	1.32
1	Y	247	HIS	CE1-NE2	5.47	1.38	1.32
1	Y	145	HIS	CE1-NE2	5.33	1.37	1.32
1	Y	38	GLY	N-CA	5.07	1.53	1.45

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	219	GLU	CB-CG-CD	9.07	128.02	112.60
1	Y	399	LYS	CB-CA-C	-8.86	106.35	116.54
1	Y	254	PRO	CB-CA-C	7.92	121.74	111.21
1	Y	336	PHE	CA-CB-CG	7.76	121.56	113.80
1	Y	51	SER	N-CA-CB	7.69	121.43	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	40	GLU	CB-CG-CD	6.50	123.65	112.60
1	Y	126	GLN	CB-CG-CD	-6.47	101.61	112.60
1	Y	84	THR	CA-CB-OG1	-6.39	100.01	109.60
1	Y	460	THR	CA-CB-OG1	-6.32	100.12	109.60
1	Y	47	THR	CA-CB-OG1	-6.22	100.27	109.60
1	Y	113	ARG	CB-CA-C	6.16	120.79	111.80
1	Y	74	LEU	CA-C-N	6.04	128.62	120.65
1	Y	74	LEU	C-N-CA	6.04	128.62	120.65
1	Y	187	PRO	CA-C-N	-6.01	113.17	122.49
1	Y	187	PRO	C-N-CA	-6.01	113.17	122.49
1	Y	472	THR	CA-C-N	5.96	128.28	120.60
1	Y	472	THR	C-N-CA	5.96	128.28	120.60
1	Y	58	HIS	CE1-NE2-CD2	-5.81	103.19	109.00
1	Y	448	ARG	CB-CG-CD	5.77	124.57	111.30
1	Y	185	ARG	CG-CD-NE	5.73	124.61	112.00
1	Y	84	THR	CA-C-N	-5.72	113.42	121.72
1	Y	84	THR	C-N-CA	-5.72	113.42	121.72
1	Y	515	ALA	N-CA-CB	5.70	118.28	110.01
1	Y	104	ALA	CA-C-N	-5.63	115.70	122.90
1	Y	104	ALA	C-N-CA	-5.63	115.70	122.90
1	Y	506	ARG	CG-CD-NE	-5.61	99.66	112.00
1	Y	209	ASP	N-CA-C	5.45	117.98	111.71
1	Y	423	CYS	CB-CA-C	5.40	118.46	109.56
1	Y	489	GLU	CB-CG-CD	5.32	121.64	112.60
1	Y	259	ASP	N-CA-CB	5.30	117.64	109.91
1	Y	248	ASP	O-C-N	-5.25	116.03	121.28
1	Y	531	LYS	CA-C-N	5.21	131.07	121.70
1	Y	531	LYS	C-N-CA	5.21	131.07	121.70
1	Y	162	ARG	CG-CD-NE	-5.14	100.69	112.00
1	Y	329	ALA	N-CA-C	-5.10	106.16	112.38
1	Y	318	THR	CA-CB-OG1	-5.08	101.98	109.60
1	Y	315	ASN	N-CA-C	-5.07	103.66	108.22
1	Y	354	PHE	CA-CB-CG	5.06	118.86	113.80
1	Y	302	ARG	N-CA-CB	5.04	117.44	109.94
1	Y	284	VAL	CB-CA-C	5.02	117.67	111.15
1	Y	392	HIS	CE1-NE2-CD2	-5.01	103.99	109.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Y	398	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	Y	467	GLU	Peptide

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	Y	3909	0	3816	88	0
2	Y	344	0	240	11	0
3	Y	2	0	0	0	0
4	Y	3	0	0	1	0
5	Y	1	0	0	0	0
6	Y	450	0	0	11	0
All	All	4709	0	4056	91	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 11.

All (91) 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)
2:Y:601:HEC:HBA1	6:Y:919:HOH:O	1.49	1.12
1:Y:531:LYS:HD2	1:Y:531:LYS:H	1.17	1.08
1:Y:402:LYS:HA	1:Y:402:LYS:CE	1.85	1.07
1:Y:399:LYS:HD2	1:Y:402:LYS:CB	1.91	0.99
1:Y:183:GLU:OE2	1:Y:185:ARG:NH2	1.94	0.99
1:Y:402:LYS:HA	1:Y:402:LYS:HE2	1.39	0.98
1:Y:399:LYS:CD	1:Y:402:LYS:HB2	1.94	0.98
1:Y:399:LYS:HD2	1:Y:402:LYS:HB2	0.97	0.94
1:Y:400:ASP:OD2	1:Y:401:GLY:N	2.07	0.87
1:Y:328:PHE:CE1	6:Y:1009:HOH:O	2.27	0.86
1:Y:415[A]:MET:HG2	1:Y:418:GLU:HG2	1.59	0.83
1:Y:402:LYS:HA	1:Y:402:LYS:NZ	1.97	0.79
1:Y:328:PHE:HE1	6:Y:1009:HOH:O	1.64	0.78
1:Y:402:LYS:HE2	1:Y:402:LYS:CA	2.16	0.73
1:Y:456:GLN:OE1	6:Y:701:HOH:O	2.05	0.73
1:Y:531:LYS:HD2	1:Y:531:LYS:N	2.00	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:417[B]:GLN:HG3	6:Y:894:HOH:O	1.91	0.71
1:Y:402:LYS:CE	1:Y:402:LYS:CA	2.69	0.69
1:Y:265:ILE:HD13	1:Y:303[A]:MET:CE	2.21	0.69
1:Y:265:ILE:CD1	1:Y:303[A]:MET:HE2	2.24	0.67
1:Y:531:LYS:H	1:Y:531:LYS:CD	2.03	0.63
1:Y:495:ASN:HB3	2:Y:607:HEC:HAA1	1.80	0.63
1:Y:465:GLN:O	1:Y:467:GLU:N	2.36	0.59
1:Y:265:ILE:CD1	1:Y:303[A]:MET:CE	2.80	0.59
1:Y:58:HIS:CE1	2:Y:603:HEC:NB	2.72	0.58
1:Y:265:ILE:HD11	1:Y:303[A]:MET:HE2	1.85	0.57
1:Y:525:ASP:O	1:Y:528:MET:HE3	2.05	0.56
1:Y:316:PRO:HD3	1:Y:328:PHE:CZ	2.41	0.56
1:Y:153:PHE:CE2	1:Y:234:VAL:HB	2.42	0.55
1:Y:57:LYS:HG2	6:Y:879:HOH:O	2.06	0.54
1:Y:66:CYS:HB2	2:Y:602:HEC:C4C	2.37	0.54
1:Y:46:HIS:CE1	2:Y:601:HEC:ND	2.75	0.54
1:Y:218:GLY:O	1:Y:225:ASP:HB2	2.08	0.54
1:Y:456:GLN:HG2	1:Y:520:VAL:HG21	1.90	0.53
1:Y:53:LYS:HD3	2:Y:602:HEC:HBB2	1.89	0.53
1:Y:106:HIS:HE1	6:Y:848:HOH:O	1.92	0.52
1:Y:465:GLN:O	1:Y:468:GLY:HA2	2.10	0.51
1:Y:216:HIS:CD2	1:Y:217:LEU:HG	2.46	0.51
1:Y:265:ILE:HD13	1:Y:303[A]:MET:HE1	1.93	0.51
1:Y:473:ILE:HG21	1:Y:526:ALA:HB2	1.93	0.50
1:Y:68:ASP:O	1:Y:69:LYS:HB2	2.10	0.50
1:Y:203:ILE:HD12	1:Y:203:ILE:N	2.26	0.50
1:Y:400:ASP:CG	1:Y:401:GLY:N	2.70	0.49
1:Y:240:PRO:O	1:Y:241:VAL:C	2.56	0.49
1:Y:126:GLN:HG3	1:Y:130:LEU:HD12	1.94	0.48
1:Y:320:ARG:HB2	1:Y:352:ASP:OD1	2.14	0.48
1:Y:399:LYS:HG3	1:Y:400:ASP:OD2	2.14	0.48
1:Y:97:ASN:HD21	1:Y:399:LYS:HE3	1.79	0.48
1:Y:358:HIS:CE1	1:Y:360:VAL:HB	2.49	0.48
1:Y:83:VAL:HA	6:Y:704:HOH:O	2.13	0.47
1:Y:398:GLY:C	1:Y:399:LYS:HG2	2.40	0.47
1:Y:530:VAL:CG1	1:Y:531:LYS:HE2	2.44	0.47
1:Y:427:TYR:CE1	1:Y:431:LYS:HE2	2.49	0.47
1:Y:398:GLY:C	1:Y:399:LYS:CG	2.88	0.46
1:Y:529:ALA:HA	1:Y:532:GLN:HB2	1.96	0.46
1:Y:440:ARG:HB3	1:Y:444:LYS:HE2	1.98	0.46
1:Y:318:THR:HB	1:Y:354:PHE:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:415[A]:MET:CG	1:Y:418:GLU:HG2	2.40	0.45
1:Y:145:HIS:CD2	2:Y:606:HEC:ND	2.84	0.45
1:Y:370:HIS:NE2	4:Y:610:NO2:O1	2.35	0.45
1:Y:314:CYS:HA	1:Y:333:THR:O	2.17	0.45
2:Y:608:HEC:HBC3	2:Y:608:HEC:HMC1	1.98	0.45
1:Y:97:ASN:ND2	1:Y:399:LYS:HE3	2.32	0.45
1:Y:522:LEU:C	1:Y:522:LEU:HD12	2.41	0.45
1:Y:111:GLY:O	1:Y:114:LYS:HE3	2.17	0.45
2:Y:606:HEC:HMA2	2:Y:607:HEC:HBA1	1.99	0.44
1:Y:185:ARG:HH21	1:Y:185:ARG:HG2	1.83	0.43
1:Y:399:LYS:HD3	1:Y:400:ASP:OD2	2.18	0.43
1:Y:399:LYS:CD	1:Y:400:ASP:OD2	2.66	0.43
1:Y:530:VAL:HG12	1:Y:531:LYS:N	2.34	0.43
1:Y:345:LEU:O	1:Y:349:ARG:HG3	2.18	0.43
1:Y:465:GLN:O	1:Y:466:ARG:C	2.62	0.43
1:Y:530:VAL:C	1:Y:532:GLN:H	2.26	0.42
1:Y:418:GLU:HB3	6:Y:969:HOH:O	2.19	0.42
1:Y:394:PRO:HB2	1:Y:418:GLU:HB2	2.00	0.42
1:Y:250:HIS:CE1	2:Y:602:HEC:NA	2.86	0.42
1:Y:286:ASP:OD1	1:Y:286:ASP:C	2.62	0.42
1:Y:145:HIS:O	1:Y:148:MET:HG2	2.20	0.42
1:Y:473:ILE:HG21	1:Y:526:ALA:CB	2.49	0.42
1:Y:191:LEU:CD2	1:Y:192:PRO:HD2	2.50	0.41
1:Y:63:CYS:HB2	6:Y:1080:HOH:O	2.20	0.41
1:Y:98:GLN:HG2	2:Y:605:HEC:C4A	2.50	0.41
1:Y:321:THR:HG23	1:Y:352:ASP:OD1	2.20	0.41
1:Y:203:ILE:N	1:Y:203:ILE:CD1	2.83	0.41
1:Y:399:LYS:HG3	1:Y:401:GLY:H	1.85	0.41
1:Y:191:LEU:HD23	1:Y:192:PRO:HD2	2.02	0.41
1:Y:281:ASP:C	1:Y:281:ASP:OD1	2.62	0.41
1:Y:216:HIS:HB3	6:Y:847:HOH:O	2.20	0.40
1:Y:224:PHE:CD1	1:Y:233:VAL:HG22	2.56	0.40
1:Y:203:ILE:HG21	1:Y:237:ILE:CD1	2.52	0.40
1:Y:313:ASN:ND2	1:Y:353:PHE:CZ	2.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	499/495 (101%)	462 (93%)	31 (6%)	6 (1%)	10	2

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Y	466	ARG
1	Y	468	GLY
1	Y	465	GLN
1	Y	400	ASP
1	Y	401	GLY
1	Y	530	VAL

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	Y	420/414 (101%)	399 (95%)	21 (5%)	22	2

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Y	51	SER
1	Y	71	LYS
1	Y	75	GLU
1	Y	85	LYS
1	Y	185	ARG

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Mol	Chain	Res	Type
1	Y	190	LYS
1	Y	191	LEU
1	Y	276	LYS
1	Y	324	LYS
1	Y	349	ARG
1	Y	397	LYS
1	Y	402	LYS
1	Y	403	LYS
1	Y	418	GLU
1	Y	467	GLU
1	Y	469	VAL
1	Y	470	SER
1	Y	472	THR
1	Y	521	LYS
1	Y	522	LEU
1	Y	531	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	97	ASN
1	Y	106	HIS
1	Y	126	GLN
1	Y	213	GLN
1	Y	216	HIS
1	Y	414	GLN
1	Y	476	GLN
1	Y	524	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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	HEC	Y	605	1	46,50,50	2.48	17 (36%)	58,82,82	2.57	22 (37%)
3	NO	Y	609	4,2	0,1,1	-	-	-	-	-
2	HEC	Y	601	1	46,50,50	2.64	18 (39%)	58,82,82	3.99	31 (53%)
2	HEC	Y	607	1	46,50,50	2.44	22 (47%)	58,82,82	2.83	28 (48%)
2	HEC	Y	602	1	46,50,50	2.98	23 (50%)	58,82,82	4.42	31 (53%)
2	HEC	Y	608	1	46,50,50	2.75	22 (47%)	58,82,82	2.62	22 (37%)
4	NO2	Y	610	2,3	1,2,2	0.61	0	0,1,1	-	-
2	HEC	Y	606	1	46,50,50	2.22	14 (30%)	58,82,82	2.26	14 (24%)
2	HEC	Y	603	1	46,50,50	2.43	21 (45%)	58,82,82	2.55	23 (39%)
2	HEC	Y	604	4,1,3	46,50,50	2.51	21 (45%)	58,82,82	2.18	21 (36%)

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	HEC	Y	605	1	-	6/14/54/54	-
2	HEC	Y	601	1	-	10/14/54/54	-
2	HEC	Y	607	1	-	7/14/54/54	-
2	HEC	Y	602	1	-	8/14/54/54	-
2	HEC	Y	608	1	-	6/14/54/54	-
2	HEC	Y	606	1	-	5/14/54/54	-
2	HEC	Y	603	1	-	6/14/54/54	-
2	HEC	Y	604	4,1,3	-	6/14/54/54	-

All (158) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	601	HEC	C4D-ND	-8.98	1.22	1.39
2	Y	602	HEC	C3B-C4B	7.69	1.59	1.46
2	Y	608	HEC	CAC-C3C	6.96	1.57	1.35
2	Y	602	HEC	CHC-C1C	6.01	1.52	1.39
2	Y	606	HEC	CAC-C3C	5.76	1.53	1.35
2	Y	608	HEC	CHB-C4A	5.73	1.49	1.38
2	Y	605	HEC	C4D-ND	-5.71	1.28	1.39
2	Y	604	HEC	CAB-C3B	5.39	1.52	1.35
2	Y	607	HEC	CAC-C3C	5.37	1.52	1.35
2	Y	602	HEC	CHA-C1A	5.29	1.48	1.38
2	Y	608	HEC	CHA-C4D	5.28	1.51	1.39
2	Y	602	HEC	CHB-C4A	5.15	1.48	1.38
2	Y	602	HEC	CAB-C3B	5.11	1.51	1.35
2	Y	603	HEC	CHD-C4C	5.06	1.48	1.38
2	Y	608	HEC	C4D-ND	-4.99	1.30	1.39
2	Y	604	HEC	C1C-NC	-4.99	1.30	1.39
2	Y	606	HEC	CHB-C4A	4.96	1.48	1.38
2	Y	605	HEC	C1B-NB	-4.92	1.30	1.39
2	Y	601	HEC	CHB-C4A	4.91	1.48	1.38
2	Y	605	HEC	CHB-C1B	4.89	1.50	1.39
2	Y	601	HEC	CAC-C3C	4.88	1.50	1.35
2	Y	604	HEC	CAC-C3C	4.87	1.50	1.35
2	Y	608	HEC	C1A-NA	-4.81	1.30	1.39
2	Y	601	HEC	C2A-C3A	4.72	1.47	1.36
2	Y	607	HEC	CAB-C3B	4.71	1.50	1.35
2	Y	604	HEC	CHB-C4A	4.70	1.47	1.38
2	Y	602	HEC	C1A-NA	-4.65	1.30	1.39
2	Y	605	HEC	CAB-C3B	4.56	1.49	1.35
2	Y	603	HEC	CAC-C3C	4.52	1.49	1.35
2	Y	602	HEC	C4A-C3A	4.52	1.54	1.45
2	Y	604	HEC	CHD-C4C	4.50	1.47	1.38
2	Y	605	HEC	CHD-C4C	4.46	1.47	1.38
2	Y	602	HEC	CHC-C4B	4.46	1.47	1.38
2	Y	603	HEC	C4A-NA	-4.44	1.31	1.39
2	Y	606	HEC	CHD-C4C	4.39	1.47	1.38
2	Y	604	HEC	CHC-C1C	4.35	1.49	1.39
2	Y	607	HEC	CHA-C4D	4.34	1.49	1.39
2	Y	606	HEC	CHB-C1B	4.32	1.49	1.39
2	Y	603	HEC	CAB-C3B	4.30	1.49	1.35
2	Y	601	HEC	CHB-C1B	4.29	1.49	1.39
2	Y	601	HEC	CHA-C4D	4.21	1.48	1.39
2	Y	605	HEC	CAC-C3C	4.15	1.48	1.35
2	Y	601	HEC	CHC-C4B	4.14	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	603	HEC	CHD-C1D	4.13	1.48	1.39
2	Y	605	HEC	C1D-ND	-4.12	1.31	1.39
2	Y	602	HEC	C1D-ND	-4.10	1.31	1.39
2	Y	607	HEC	C4D-ND	-4.07	1.31	1.39
2	Y	603	HEC	CHA-C4D	4.07	1.48	1.39
2	Y	607	HEC	C4B-NB	-4.05	1.32	1.39
2	Y	606	HEC	CAB-C3B	3.94	1.47	1.35
2	Y	607	HEC	C1C-NC	-3.91	1.32	1.39
2	Y	608	HEC	CHA-C1A	3.89	1.46	1.38
2	Y	608	HEC	C4A-NA	-3.88	1.32	1.39
2	Y	607	HEC	C2A-C3A	3.86	1.45	1.36
2	Y	604	HEC	CHA-C1A	3.85	1.45	1.38
2	Y	608	HEC	CHD-C4C	3.85	1.45	1.38
2	Y	603	HEC	C3D-C2D	3.84	1.48	1.38
2	Y	608	HEC	CAB-C3B	3.78	1.47	1.35
2	Y	601	HEC	CHD-C1D	3.68	1.47	1.39
2	Y	608	HEC	C4B-NB	-3.63	1.32	1.39
2	Y	605	HEC	CHA-C1A	3.60	1.45	1.38
2	Y	604	HEC	C2A-C3A	3.59	1.44	1.36
2	Y	606	HEC	C1A-NA	-3.58	1.32	1.39
2	Y	608	HEC	C1B-NB	-3.58	1.32	1.39
2	Y	605	HEC	CHB-C4A	3.56	1.45	1.38
2	Y	608	HEC	CBA-CGA	3.55	1.58	1.50
2	Y	608	HEC	CHC-C1C	3.53	1.47	1.39
2	Y	602	HEC	C4C-NC	-3.52	1.33	1.39
2	Y	603	HEC	C1A-NA	-3.51	1.33	1.39
2	Y	607	HEC	C1D-ND	-3.48	1.33	1.39
2	Y	602	HEC	CMC-C2C	-3.48	1.43	1.50
2	Y	601	HEC	CAB-C3B	3.46	1.46	1.35
2	Y	605	HEC	C2A-C3A	3.36	1.44	1.36
2	Y	602	HEC	C4B-NB	-3.35	1.33	1.39
2	Y	603	HEC	CHC-C1C	3.34	1.46	1.39
2	Y	603	HEC	C1C-NC	-3.32	1.33	1.39
2	Y	602	HEC	CAC-C3C	3.32	1.45	1.35
2	Y	604	HEC	C1A-NA	-3.32	1.33	1.39
2	Y	604	HEC	C3B-C4B	-3.31	1.40	1.46
2	Y	602	HEC	O1A-CGA	3.25	1.32	1.22
2	Y	608	HEC	CHB-C1B	3.23	1.46	1.39
2	Y	606	HEC	C1B-NB	-3.23	1.33	1.39
2	Y	604	HEC	C4A-NA	-3.22	1.33	1.39
2	Y	603	HEC	CHA-C1A	3.21	1.44	1.38
2	Y	602	HEC	C1C-NC	-3.17	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	602	HEC	O1D-CGD	3.15	1.32	1.22
2	Y	606	HEC	C4A-C3A	-3.15	1.39	1.45
2	Y	605	HEC	C4A-NA	-3.12	1.33	1.39
2	Y	603	HEC	C2A-C3A	3.12	1.43	1.36
2	Y	605	HEC	C4B-NB	-3.09	1.33	1.39
2	Y	603	HEC	CHB-C4A	3.07	1.44	1.38
2	Y	601	HEC	C1C-NC	-3.04	1.33	1.39
2	Y	602	HEC	C3D-C2D	3.04	1.46	1.38
2	Y	607	HEC	C1B-NB	-3.03	1.33	1.39
2	Y	604	HEC	CHD-C1D	3.02	1.46	1.39
2	Y	607	HEC	C4A-NA	-3.02	1.33	1.39
2	Y	607	HEC	CBD-CGD	2.98	1.57	1.50
2	Y	607	HEC	C1A-NA	-2.90	1.34	1.39
2	Y	602	HEC	C3C-C2C	2.89	1.50	1.41
2	Y	602	HEC	C4D-ND	-2.87	1.34	1.39
2	Y	602	HEC	CBD-CGD	2.87	1.57	1.50
2	Y	601	HEC	C4A-C3A	2.85	1.51	1.45
2	Y	601	HEC	C3B-C2B	2.78	1.50	1.41
2	Y	608	HEC	C2A-C3A	2.77	1.42	1.36
2	Y	606	HEC	CHA-C1A	2.76	1.43	1.38
2	Y	604	HEC	C4C-NC	-2.76	1.34	1.39
2	Y	607	HEC	C1B-C2B	2.73	1.49	1.43
2	Y	603	HEC	C4B-NB	-2.72	1.34	1.39
2	Y	607	HEC	CHB-C4A	2.71	1.43	1.38
2	Y	606	HEC	C4D-ND	-2.71	1.34	1.39
2	Y	608	HEC	CBA-CAA	2.69	1.61	1.51
2	Y	601	HEC	C1A-NA	-2.69	1.34	1.39
2	Y	605	HEC	C1C-NC	-2.67	1.34	1.39
2	Y	606	HEC	C1C-NC	-2.60	1.34	1.39
2	Y	603	HEC	C4D-ND	-2.59	1.34	1.39
2	Y	607	HEC	CHD-C4C	2.56	1.43	1.38
2	Y	608	HEC	C3D-C2D	2.55	1.45	1.38
2	Y	607	HEC	C1D-C2D	2.53	1.49	1.43
2	Y	607	HEC	O2D-CGD	-2.52	1.22	1.30
2	Y	602	HEC	C3C-C4C	-2.52	1.41	1.46
2	Y	603	HEC	CHB-C1B	2.50	1.45	1.39
2	Y	604	HEC	CHA-C4D	2.49	1.45	1.39
2	Y	605	HEC	C3C-C4C	-2.46	1.41	1.46
2	Y	608	HEC	C1B-C2B	-2.44	1.37	1.43
2	Y	603	HEC	C1D-C2D	2.43	1.48	1.43
2	Y	603	HEC	C3B-C2B	2.42	1.49	1.41
2	Y	606	HEC	C4B-NB	-2.41	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	607	HEC	CMC-C2C	2.41	1.55	1.50
2	Y	607	HEC	CHD-C1D	2.40	1.44	1.39
2	Y	604	HEC	CBD-CAD	2.38	1.60	1.51
2	Y	603	HEC	C1B-C2B	2.36	1.48	1.43
2	Y	608	HEC	CHD-C1D	2.31	1.44	1.39
2	Y	604	HEC	C4B-NB	-2.29	1.35	1.39
2	Y	607	HEC	O1A-CGA	2.28	1.29	1.22
2	Y	605	HEC	CHC-C1C	2.25	1.44	1.39
2	Y	606	HEC	CBA-CAA	2.24	1.59	1.51
2	Y	602	HEC	C1B-C2B	2.23	1.48	1.43
2	Y	604	HEC	CBD-CGD	2.22	1.55	1.50
2	Y	607	HEC	CBA-CGA	-2.20	1.45	1.50
2	Y	604	HEC	C1D-ND	-2.18	1.35	1.39
2	Y	607	HEC	C3D-C2D	2.15	1.44	1.38
2	Y	601	HEC	C1C-C2C	2.15	1.48	1.43
2	Y	601	HEC	C4C-NC	-2.15	1.35	1.39
2	Y	604	HEC	C4D-C3D	2.15	1.48	1.44
2	Y	608	HEC	O2D-CGD	-2.14	1.23	1.30
2	Y	605	HEC	CBA-CGA	2.14	1.55	1.50
2	Y	603	HEC	CBD-CGD	2.14	1.55	1.50
2	Y	601	HEC	C1A-C2A	2.10	1.48	1.45
2	Y	602	HEC	CMB-C2B	2.09	1.55	1.50
2	Y	604	HEC	C1B-C2B	2.07	1.48	1.43
2	Y	604	HEC	C4D-ND	-2.07	1.35	1.39
2	Y	606	HEC	C3C-C2C	2.07	1.48	1.41
2	Y	601	HEC	C3B-C4B	-2.06	1.42	1.46
2	Y	601	HEC	CHA-C1A	2.06	1.42	1.38
2	Y	603	HEC	O1A-CGA	2.04	1.28	1.22
2	Y	608	HEC	C4C-NC	-2.03	1.35	1.39
2	Y	608	HEC	CBC-CAC	2.02	1.57	1.49
2	Y	605	HEC	C4C-NC	-2.00	1.35	1.39

All (192) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	602	HEC	C2A-C1A-NA	15.94	125.70	110.32
2	Y	607	HEC	CBB-CAB-C3B	-10.82	105.81	127.43
2	Y	601	HEC	CBB-CAB-C3B	-10.46	106.53	127.43
2	Y	602	HEC	C4A-NA-C1A	-10.13	89.30	105.82
2	Y	602	HEC	CHB-C4A-C3A	-9.96	104.77	125.49
2	Y	608	HEC	CBB-CAB-C3B	-9.83	107.79	127.43
2	Y	601	HEC	C3D-C4D-ND	9.58	120.78	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	606	HEC	CBB-CAB-C3B	-9.11	109.22	127.43
2	Y	601	HEC	C1D-C2D-C3D	-8.76	96.78	106.82
2	Y	602	HEC	C4A-C3A-C2A	-8.39	94.52	106.97
2	Y	603	HEC	CBB-CAB-C3B	-8.01	111.43	127.43
2	Y	602	HEC	CBB-CAB-C3B	-7.87	111.71	127.43
2	Y	601	HEC	C2A-C1A-NA	7.84	117.89	110.32
2	Y	601	HEC	CMD-C2D-C1D	7.63	137.04	125.42
2	Y	604	HEC	CBB-CAB-C3B	-7.49	112.46	127.43
2	Y	602	HEC	C3A-C4A-NA	7.44	123.40	109.64
2	Y	607	HEC	C3D-C4D-ND	7.31	118.27	110.15
2	Y	605	HEC	CBB-CAB-C3B	-7.21	113.03	127.43
2	Y	602	HEC	CMA-C3A-C4A	6.93	136.94	124.73
2	Y	601	HEC	C2D-C1D-ND	6.93	121.25	110.14
2	Y	601	HEC	CHD-C4C-NC	-6.91	116.92	124.45
2	Y	605	HEC	CBC-CAC-C3C	-6.82	113.81	127.43
2	Y	602	HEC	CHB-C4A-NA	6.77	131.83	124.45
2	Y	602	HEC	CHA-C1A-NA	-6.63	117.24	124.45
2	Y	606	HEC	CBC-CAC-C3C	-6.61	114.23	127.43
2	Y	602	HEC	CBC-CAC-C3C	-6.54	114.37	127.43
2	Y	608	HEC	CBA-CAA-C2A	-6.05	95.81	112.53
2	Y	605	HEC	C3D-C4D-ND	5.77	116.55	110.15
2	Y	601	HEC	C1A-C2A-C3A	-5.63	99.69	107.11
2	Y	607	HEC	CBC-CAC-C3C	-5.62	116.20	127.43
2	Y	601	HEC	C4D-ND-C1D	-5.59	96.70	105.82
2	Y	608	HEC	CBC-CAC-C3C	-5.43	116.58	127.43
2	Y	601	HEC	CHC-C1C-C2C	-5.34	111.92	127.43
2	Y	602	HEC	CHA-C4D-C3D	-5.33	113.64	125.30
2	Y	601	HEC	CHD-C1D-C2D	-5.30	112.04	127.43
2	Y	602	HEC	CHA-C1A-C2A	-5.18	116.69	124.86
2	Y	602	HEC	CHD-C4C-C3C	-5.11	116.59	125.21
2	Y	608	HEC	C1D-C2D-C3D	-5.02	101.07	106.82
2	Y	601	HEC	CBA-CAA-C2A	4.99	126.34	112.53
2	Y	601	HEC	CHC-C4B-C3B	-4.96	116.85	125.21
2	Y	603	HEC	CBC-CAC-C3C	-4.90	117.65	127.43
2	Y	607	HEC	CMA-C3A-C4A	4.89	133.34	124.73
2	Y	602	HEC	CHD-C4C-NC	4.80	129.68	124.45
2	Y	607	HEC	C2A-C1A-NA	4.79	114.94	110.32
2	Y	603	HEC	C2B-C1B-NB	4.76	117.77	110.14
2	Y	605	HEC	CMC-C2C-C1C	4.75	132.66	125.42
2	Y	602	HEC	CHA-C4D-ND	4.69	132.36	123.86
2	Y	601	HEC	C2C-C1C-NC	4.67	117.63	110.14
2	Y	601	HEC	CAD-CBD-CGD	-4.67	101.28	113.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	602	HEC	C4D-CHA-C1A	-4.61	110.43	124.66
2	Y	603	HEC	C3D-C4D-ND	4.59	115.24	110.15
2	Y	601	HEC	CHC-C4B-NB	4.56	129.42	124.45
2	Y	605	HEC	C2A-C1A-NA	4.54	114.70	110.32
2	Y	605	HEC	CMD-C2D-C1D	4.48	132.24	125.42
2	Y	608	HEC	CHB-C4A-NA	4.44	129.29	124.45
2	Y	603	HEC	CBD-CAD-C3D	-4.31	100.61	112.53
2	Y	605	HEC	C1A-C2A-C3A	-4.30	101.44	107.11
2	Y	603	HEC	CMB-C2B-C1B	4.23	131.86	125.42
2	Y	601	HEC	CHA-C4D-C3D	-4.18	116.14	125.30
2	Y	601	HEC	CAA-C2A-C1A	4.16	133.30	124.85
2	Y	603	HEC	C4A-C3A-C2A	-4.13	100.85	106.97
2	Y	604	HEC	CHD-C4C-NC	4.09	128.91	124.45
2	Y	608	HEC	CMD-C2D-C1D	4.08	131.63	125.42
2	Y	603	HEC	CAD-CBD-CGD	-4.05	102.92	113.67
2	Y	603	HEC	CAA-CBA-CGA	-3.98	103.10	113.67
2	Y	602	HEC	CHC-C4B-NB	3.98	128.79	124.45
2	Y	601	HEC	C2B-C1B-NB	3.94	116.46	110.14
2	Y	606	HEC	O2A-CGA-O1A	-3.92	113.26	123.33
2	Y	604	HEC	C4A-C3A-C2A	-3.91	101.17	106.97
2	Y	608	HEC	CMA-C3A-C4A	3.86	131.53	124.73
2	Y	607	HEC	C4D-C3D-C2D	-3.85	100.92	106.87
2	Y	605	HEC	C1D-C2D-C3D	-3.83	102.42	106.82
2	Y	606	HEC	C2A-C1A-NA	3.81	114.00	110.32
2	Y	603	HEC	C3A-C4A-NA	3.79	116.65	109.64
2	Y	602	HEC	C2B-C1B-NB	3.77	116.19	110.14
2	Y	605	HEC	CAA-C2A-C1A	3.65	132.27	124.85
2	Y	601	HEC	CHC-C1C-NC	3.63	130.43	123.86
2	Y	603	HEC	C2A-C1A-NA	3.58	113.78	110.32
2	Y	604	HEC	C3A-C4A-NA	3.58	116.26	109.64
2	Y	608	HEC	C4A-NA-C1A	3.55	111.61	105.82
2	Y	604	HEC	CHA-C1A-C2A	-3.53	119.28	124.86
2	Y	607	HEC	C1D-C2D-C3D	-3.53	102.78	106.82
2	Y	608	HEC	CAD-CBD-CGD	-3.49	104.42	113.67
2	Y	602	HEC	C4D-C3D-C2D	-3.47	101.49	106.87
2	Y	603	HEC	C2C-C1C-NC	3.45	115.68	110.14
2	Y	607	HEC	CMD-C2D-C1D	3.45	130.68	125.42
2	Y	601	HEC	CMB-C2B-C1B	3.44	130.65	125.42
2	Y	604	HEC	CBC-CAC-C3C	-3.36	120.72	127.43
2	Y	605	HEC	CAD-CBD-CGD	-3.35	104.79	113.67
2	Y	607	HEC	C2D-C1D-ND	3.34	115.49	110.14
2	Y	608	HEC	CHC-C4B-NB	3.33	128.08	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	604	HEC	CHD-C4C-C3C	-3.32	119.61	125.21
2	Y	606	HEC	CBA-CAA-C2A	-3.32	103.36	112.53
2	Y	605	HEC	C2C-C1C-NC	3.29	115.41	110.14
2	Y	604	HEC	CHA-C1A-NA	3.25	128.00	124.45
2	Y	606	HEC	O2A-CGA-CBA	3.21	124.15	114.00
2	Y	605	HEC	CHA-C4D-C3D	-3.18	118.33	125.30
2	Y	608	HEC	O2A-CGA-CBA	3.18	124.06	114.00
2	Y	604	HEC	CHD-C1D-C2D	-3.18	118.19	127.43
2	Y	602	HEC	CAA-C2A-C3A	-3.17	121.93	127.87
2	Y	607	HEC	C4A-C3A-C2A	-3.16	102.28	106.97
2	Y	601	HEC	CAA-CBA-CGA	-3.16	105.30	113.67
2	Y	607	HEC	CHD-C4C-NC	-3.14	121.03	124.45
2	Y	607	HEC	O1D-CGD-CBD	-3.14	113.14	123.09
2	Y	604	HEC	CHD-C1D-ND	3.13	129.53	123.86
2	Y	607	HEC	C3A-C4A-NA	3.11	115.38	109.64
2	Y	604	HEC	CMB-C2B-C1B	3.10	130.15	125.42
2	Y	602	HEC	CAA-C2A-C1A	3.10	131.16	124.85
2	Y	605	HEC	C4D-C3D-C2D	-3.09	102.08	106.87
2	Y	603	HEC	CHC-C1C-C2C	-3.09	118.47	127.43
2	Y	606	HEC	CHB-C4A-C3A	-3.08	119.07	125.49
2	Y	605	HEC	CMA-C3A-C4A	3.07	130.14	124.73
2	Y	601	HEC	CBD-CAD-C3D	3.07	121.02	112.53
2	Y	601	HEC	CHD-C4C-C3C	3.04	130.34	125.21
2	Y	607	HEC	CHA-C4D-C3D	-3.04	118.64	125.30
2	Y	601	HEC	C1C-CHC-C4B	-3.03	115.30	124.66
2	Y	606	HEC	C1A-C2A-C3A	-3.02	103.13	107.11
2	Y	601	HEC	CHB-C1B-C2B	-3.01	118.68	127.43
2	Y	607	HEC	CMC-C2C-C1C	-2.99	120.86	125.42
2	Y	603	HEC	CHD-C4C-C3C	-2.99	120.16	125.21
2	Y	602	HEC	C3D-C4D-ND	2.99	113.47	110.15
2	Y	602	HEC	CMC-C2C-C3C	2.97	133.53	126.55
2	Y	608	HEC	O1A-CGA-CBA	-2.95	113.74	123.09
2	Y	605	HEC	CAD-C3D-C2D	2.95	133.68	127.07
2	Y	607	HEC	CAD-C3D-C4D	2.94	130.68	124.94
2	Y	607	HEC	O1A-CGA-CBA	-2.94	113.77	123.09
2	Y	602	HEC	CAD-C3D-C2D	2.93	133.64	127.07
2	Y	604	HEC	C4D-C3D-C2D	-2.93	102.34	106.87
2	Y	601	HEC	CHA-C1A-C2A	-2.93	120.24	124.86
2	Y	607	HEC	CHC-C4B-C3B	-2.93	120.28	125.21
2	Y	601	HEC	CMC-C2C-C3C	2.93	133.43	126.55
2	Y	603	HEC	CHB-C4A-C3A	-2.88	119.50	125.49
2	Y	603	HEC	C1D-C2D-C3D	-2.85	103.55	106.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	604	HEC	CHB-C4A-C3A	-2.82	119.62	125.49
2	Y	608	HEC	CBD-CAD-C3D	2.80	120.28	112.53
2	Y	601	HEC	O2D-CGD-CBD	2.75	122.69	114.00
2	Y	608	HEC	C2B-C1B-NB	2.70	114.47	110.14
2	Y	607	HEC	O2A-CGA-CBA	2.65	122.39	114.00
2	Y	602	HEC	O1A-CGA-CBA	2.65	131.49	123.09
2	Y	606	HEC	CHD-C1D-ND	2.62	128.61	123.86
2	Y	603	HEC	C4D-C3D-C2D	-2.62	102.82	106.87
2	Y	605	HEC	O2D-CGD-CBD	2.61	122.26	114.00
2	Y	608	HEC	C1B-CHB-C4A	-2.61	116.60	124.66
2	Y	603	HEC	CHD-C4C-NC	2.61	127.29	124.45
2	Y	604	HEC	CMA-C3A-C4A	2.60	129.31	124.73
2	Y	606	HEC	CAD-C3D-C4D	2.58	129.98	124.94
2	Y	604	HEC	CAD-C3D-C4D	2.56	129.94	124.94
2	Y	606	HEC	C2C-C1C-NC	2.54	114.22	110.14
2	Y	605	HEC	C2D-C1D-ND	2.53	114.20	110.14
2	Y	605	HEC	CBD-CAD-C3D	-2.53	105.54	112.53
2	Y	607	HEC	CMB-C2B-C3B	2.52	132.48	126.55
2	Y	608	HEC	CHB-C1B-C2B	-2.50	120.16	127.43
2	Y	602	HEC	CBD-CAD-C3D	2.50	119.44	112.53
2	Y	602	HEC	O2A-CGA-O1A	-2.48	116.94	123.33
2	Y	604	HEC	CHB-C1B-NB	2.43	128.28	123.86
2	Y	607	HEC	CMC-C2C-C3C	2.43	132.27	126.55
2	Y	603	HEC	CHA-C4D-C3D	-2.43	119.98	125.30
2	Y	606	HEC	CAA-C2A-C1A	2.42	129.76	124.85
2	Y	607	HEC	C1A-C2A-C3A	-2.41	103.93	107.11
2	Y	603	HEC	CHC-C4B-C3B	-2.40	121.16	125.21
2	Y	604	HEC	CHC-C4B-NB	-2.40	121.84	124.45
2	Y	607	HEC	C4D-ND-C1D	-2.40	101.91	105.82
2	Y	601	HEC	CHA-C1A-NA	-2.39	121.85	124.45
2	Y	607	HEC	CHA-C1A-C2A	-2.38	121.10	124.86
2	Y	605	HEC	C3A-C4A-NA	2.38	114.04	109.64
2	Y	604	HEC	CMD-C2D-C1D	2.35	129.00	125.42
2	Y	601	HEC	CAD-C3D-C2D	2.34	132.32	127.07
2	Y	608	HEC	CAD-C3D-C4D	2.34	129.51	124.94
2	Y	604	HEC	C3D-C4D-ND	2.34	112.74	110.15
2	Y	606	HEC	CMD-C2D-C3D	2.33	130.57	125.62
2	Y	608	HEC	CAA-CBA-CGA	2.33	119.84	113.67
2	Y	607	HEC	CHD-C1D-C2D	-2.32	120.69	127.43
2	Y	605	HEC	O2D-CGD-O1D	-2.31	117.38	123.33
2	Y	603	HEC	CMA-C3A-C4A	2.31	128.79	124.73
2	Y	608	HEC	C3D-C4D-ND	2.28	112.68	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	602	HEC	CAD-CBD-CGD	2.24	119.61	113.67
2	Y	602	HEC	CHC-C4B-C3B	-2.24	121.43	125.21
2	Y	604	HEC	C2C-C1C-NC	2.17	113.61	110.14
2	Y	603	HEC	CHB-C1B-C2B	-2.15	121.19	127.43
2	Y	604	HEC	CHC-C1C-C2C	-2.15	121.20	127.43
2	Y	608	HEC	CHD-C1D-C2D	-2.14	121.21	127.43
2	Y	602	HEC	O1D-CGD-CBD	-2.13	116.35	123.09
2	Y	607	HEC	O2D-CGD-CBD	2.09	120.61	114.00
2	Y	602	HEC	CHD-C1D-C2D	-2.08	121.39	127.43
2	Y	603	HEC	C4B-NB-C1B	-2.07	102.44	105.82
2	Y	608	HEC	C1A-C2A-C3A	-2.07	104.39	107.11
2	Y	608	HEC	C2D-C1D-ND	2.02	113.39	110.14
2	Y	607	HEC	C2B-C1B-NB	2.02	113.38	110.14
2	Y	605	HEC	CHD-C4C-C3C	-2.02	121.81	125.21
2	Y	605	HEC	CHB-C1B-C2B	-2.01	121.58	127.43
2	Y	607	HEC	CHB-C4A-C3A	-2.00	121.32	125.49
2	Y	606	HEC	CMA-C3A-C4A	2.00	128.26	124.73

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Y	601	HEC	C2B-C3B-CAB-CBB
2	Y	601	HEC	C4B-C3B-CAB-CBB
2	Y	601	HEC	C2C-C3C-CAC-CBC
2	Y	601	HEC	C4C-C3C-CAC-CBC
2	Y	601	HEC	C2D-C3D-CAD-CBD
2	Y	602	HEC	C2B-C3B-CAB-CBB
2	Y	602	HEC	C4B-C3B-CAB-CBB
2	Y	602	HEC	C2C-C3C-CAC-CBC
2	Y	602	HEC	C4C-C3C-CAC-CBC
2	Y	603	HEC	C2B-C3B-CAB-CBB
2	Y	603	HEC	C4B-C3B-CAB-CBB
2	Y	603	HEC	C2C-C3C-CAC-CBC
2	Y	603	HEC	C4C-C3C-CAC-CBC
2	Y	604	HEC	C2B-C3B-CAB-CBB
2	Y	604	HEC	C4B-C3B-CAB-CBB
2	Y	604	HEC	C2C-C3C-CAC-CBC
2	Y	604	HEC	C4C-C3C-CAC-CBC
2	Y	605	HEC	C2B-C3B-CAB-CBB
2	Y	605	HEC	C4B-C3B-CAB-CBB
2	Y	605	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	Y	605	HEC	C4C-C3C-CAC-CBC
2	Y	606	HEC	C2B-C3B-CAB-CBB
2	Y	606	HEC	C4B-C3B-CAB-CBB
2	Y	606	HEC	C2C-C3C-CAC-CBC
2	Y	606	HEC	C4C-C3C-CAC-CBC
2	Y	607	HEC	C2B-C3B-CAB-CBB
2	Y	607	HEC	C4B-C3B-CAB-CBB
2	Y	607	HEC	C2C-C3C-CAC-CBC
2	Y	607	HEC	C4C-C3C-CAC-CBC
2	Y	608	HEC	C2B-C3B-CAB-CBB
2	Y	608	HEC	C2C-C3C-CAC-CBC
2	Y	608	HEC	C4C-C3C-CAC-CBC
2	Y	601	HEC	C4D-C3D-CAD-CBD
2	Y	608	HEC	C4B-C3B-CAB-CBB
2	Y	604	HEC	CAA-CBA-CGA-O1A
2	Y	604	HEC	CAA-CBA-CGA-O2A
2	Y	608	HEC	CAD-CBD-CGD-O1D
2	Y	602	HEC	CAA-CBA-CGA-O1A
2	Y	607	HEC	CAA-CBA-CGA-O2A
2	Y	602	HEC	CAA-CBA-CGA-O2A
2	Y	601	HEC	CAD-CBD-CGD-O2D
2	Y	608	HEC	CAD-CBD-CGD-O2D
2	Y	602	HEC	C3D-CAD-CBD-CGD
2	Y	607	HEC	CAA-CBA-CGA-O1A
2	Y	601	HEC	CAD-CBD-CGD-O1D
2	Y	605	HEC	CAA-CBA-CGA-O2A
2	Y	605	HEC	CAA-CBA-CGA-O1A
2	Y	603	HEC	CAD-CBD-CGD-O1D
2	Y	602	HEC	CAD-CBD-CGD-O1D
2	Y	601	HEC	CAA-CBA-CGA-O1A
2	Y	603	HEC	CAD-CBD-CGD-O2D
2	Y	606	HEC	CAA-CBA-CGA-O1A
2	Y	601	HEC	C3A-C2A-CAA-CBA
2	Y	607	HEC	C2A-CAA-CBA-CGA

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Y	605	HEC	1	0
2	Y	601	HEC	2	0
2	Y	607	HEC	2	0

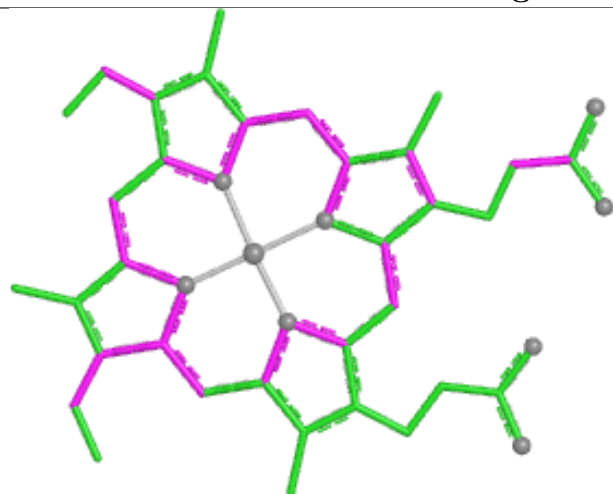
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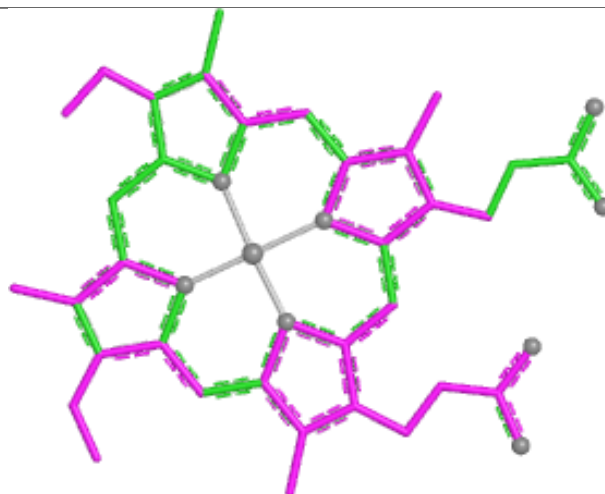
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Y	602	HEC	3	0
2	Y	608	HEC	1	0
4	Y	610	NO2	1	0
2	Y	606	HEC	2	0
2	Y	603	HEC	1	0

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.

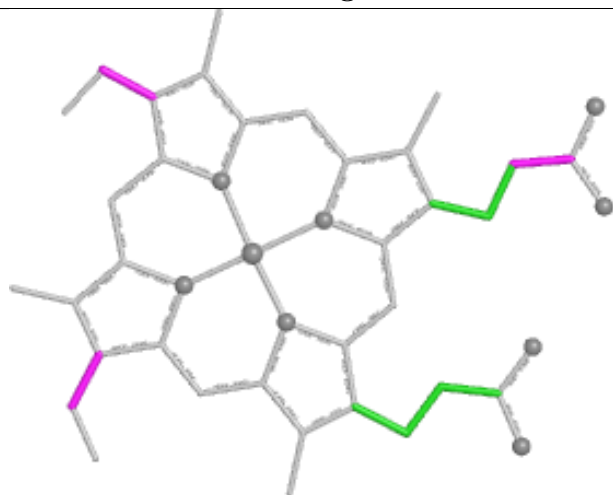
Ligand HEC Y 605



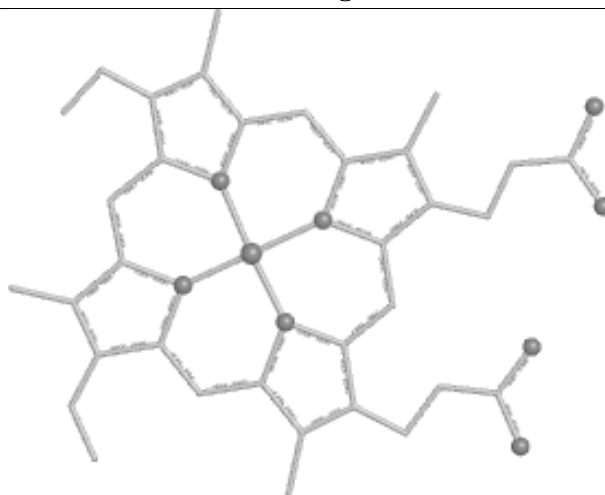
Bond lengths



Bond angles

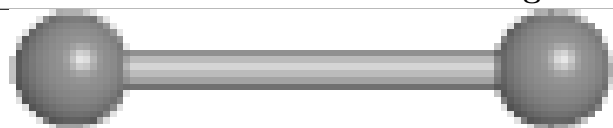


Torsions

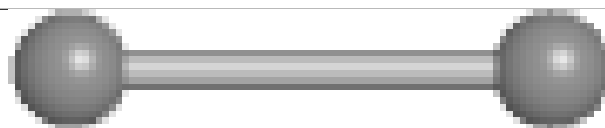


Rings

Ligand NO Y 609



Bond lengths



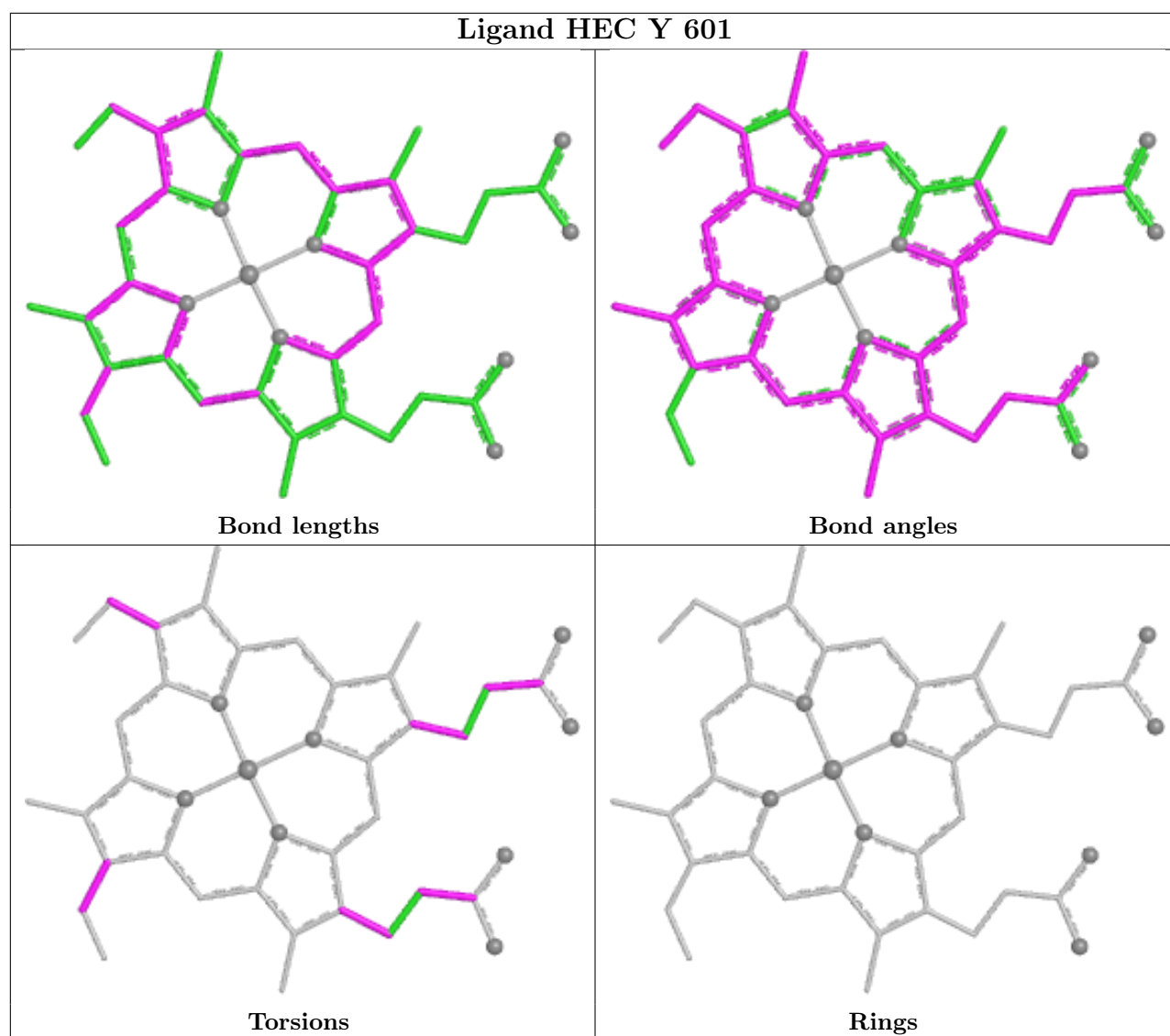
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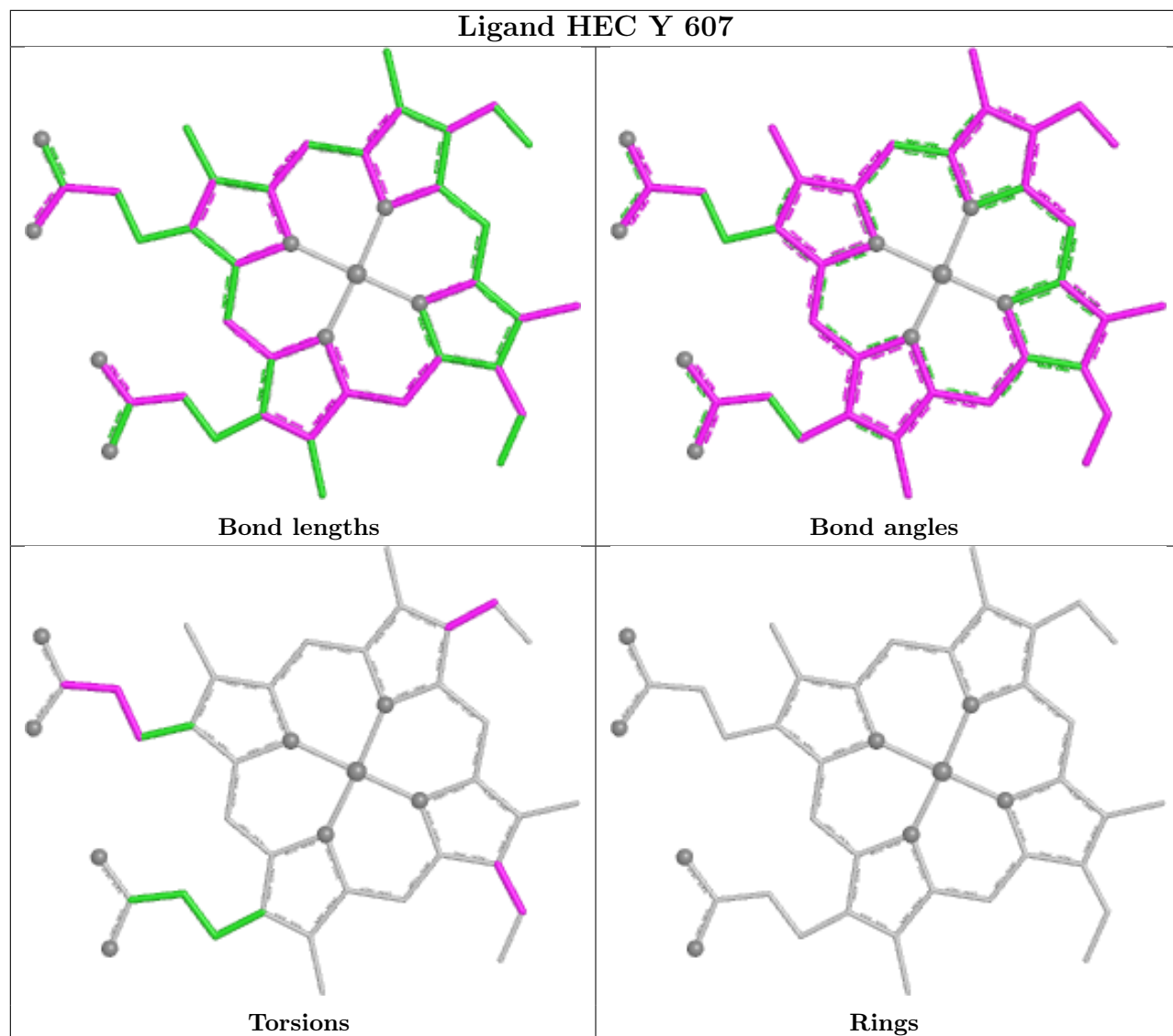


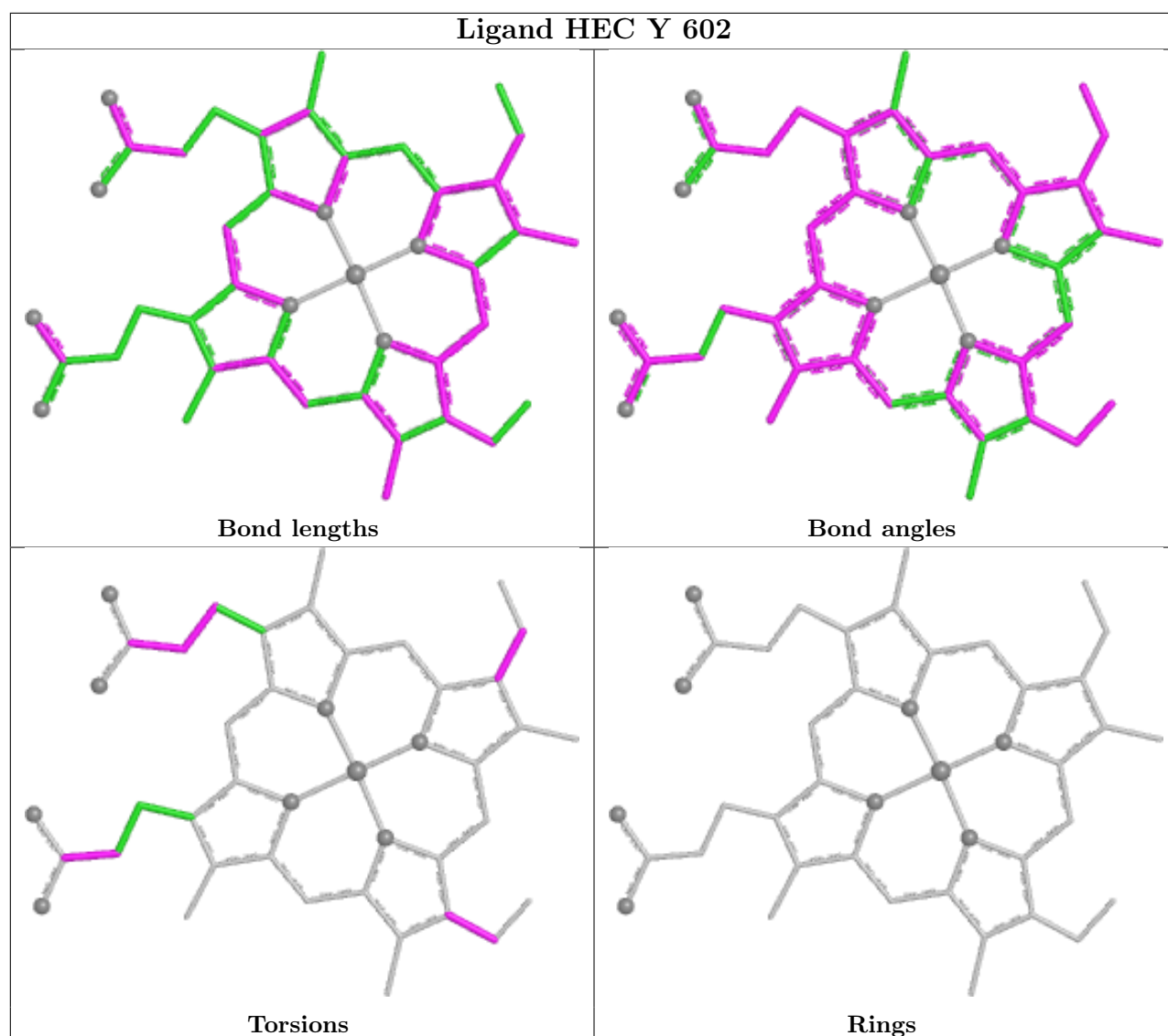
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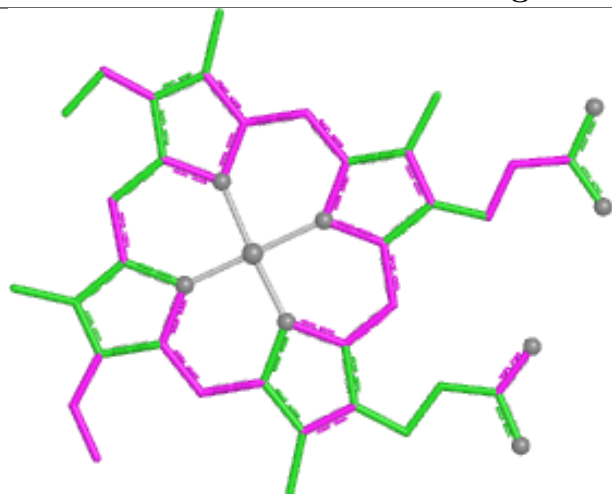
Rings



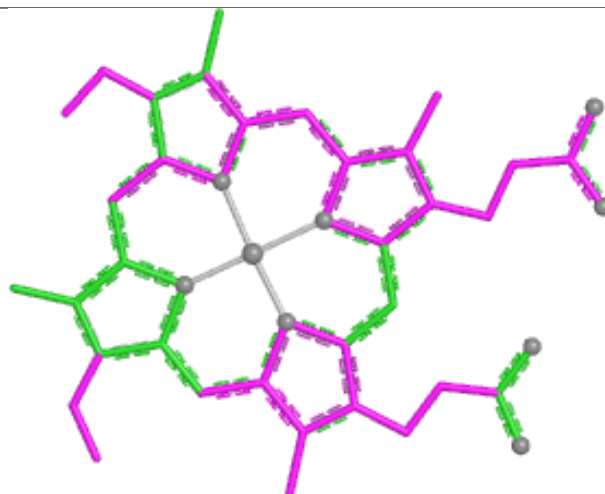




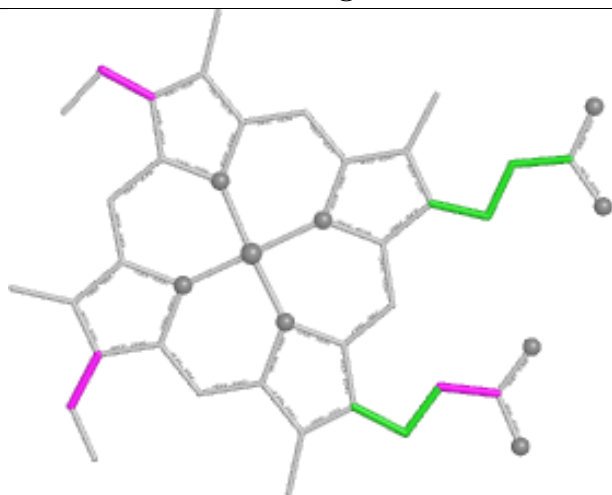
Ligand HEC Y 608



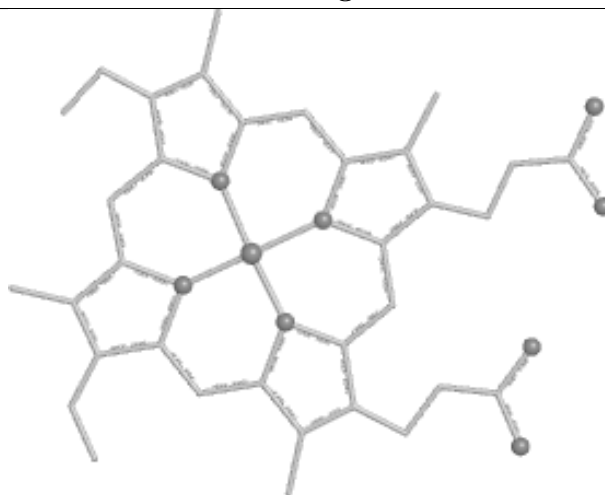
Bond lengths



Bond angles

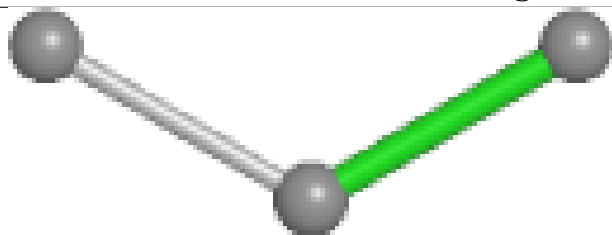


Torsions

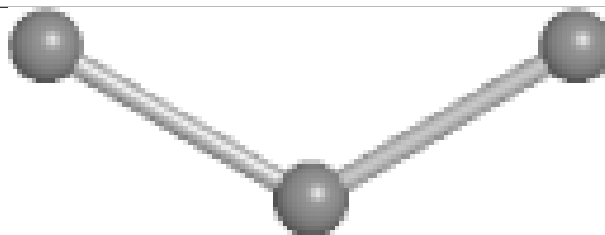


Rings

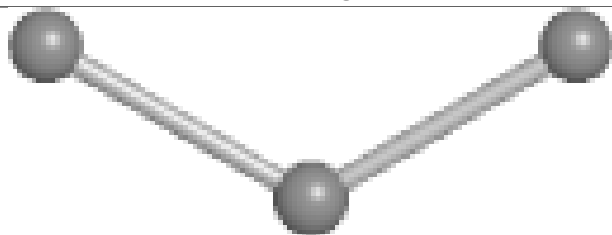
Ligand NO2 Y 610



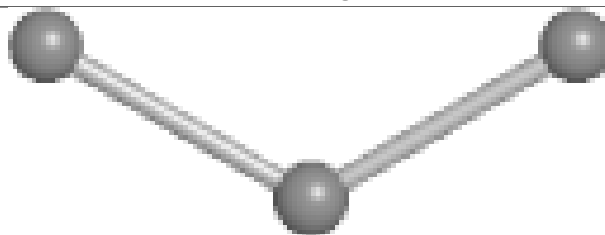
Bond lengths



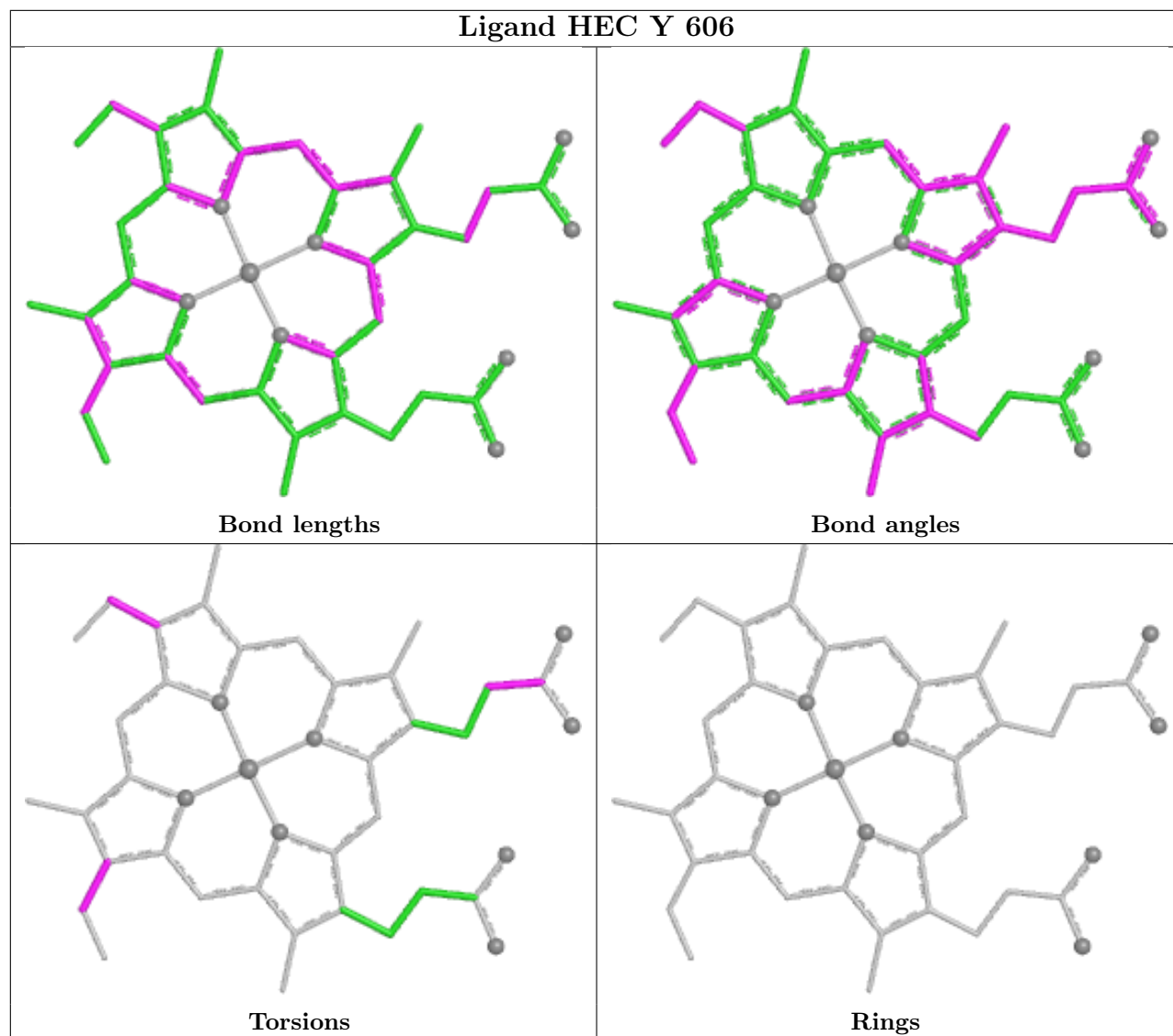
Bond angles

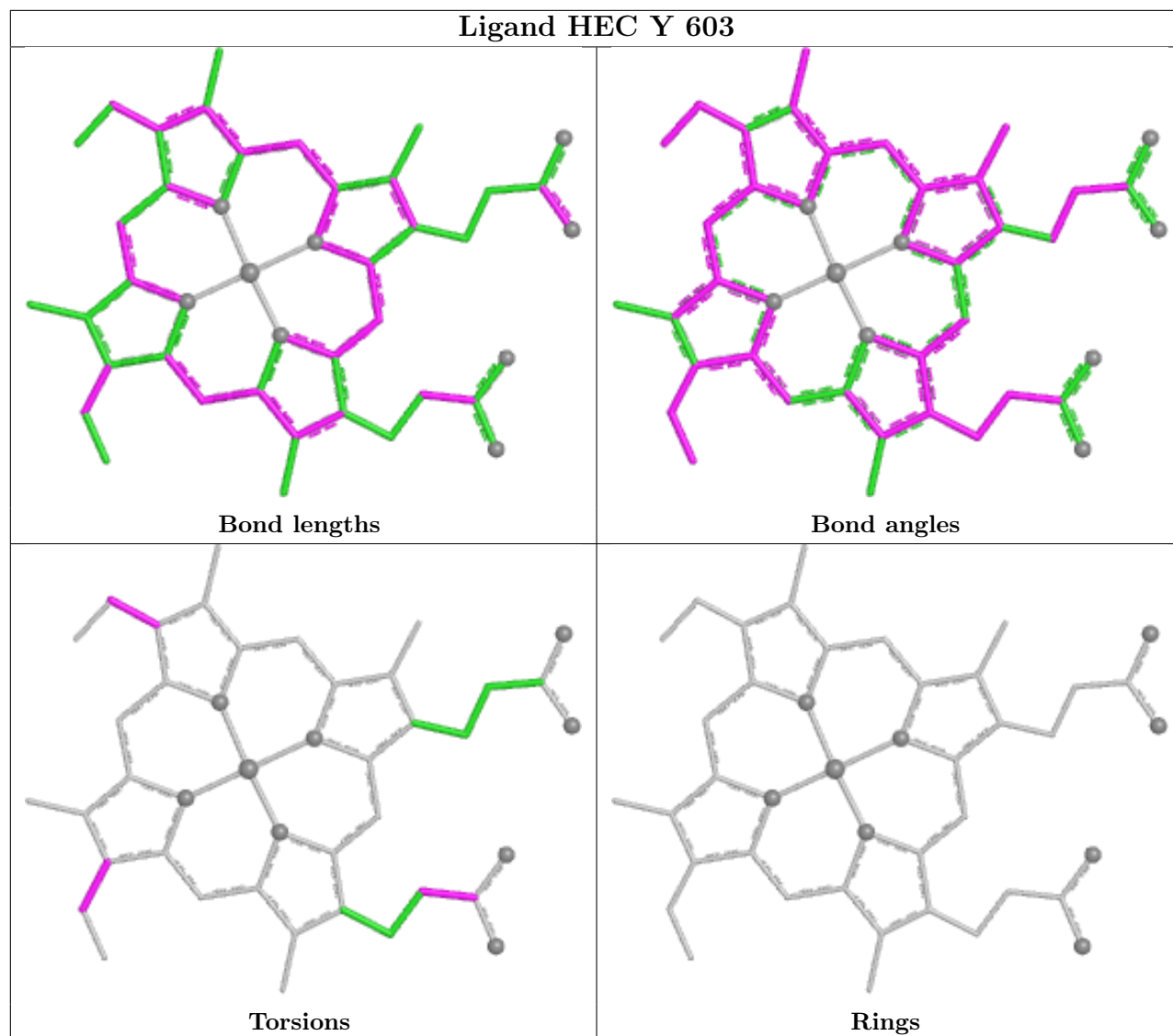


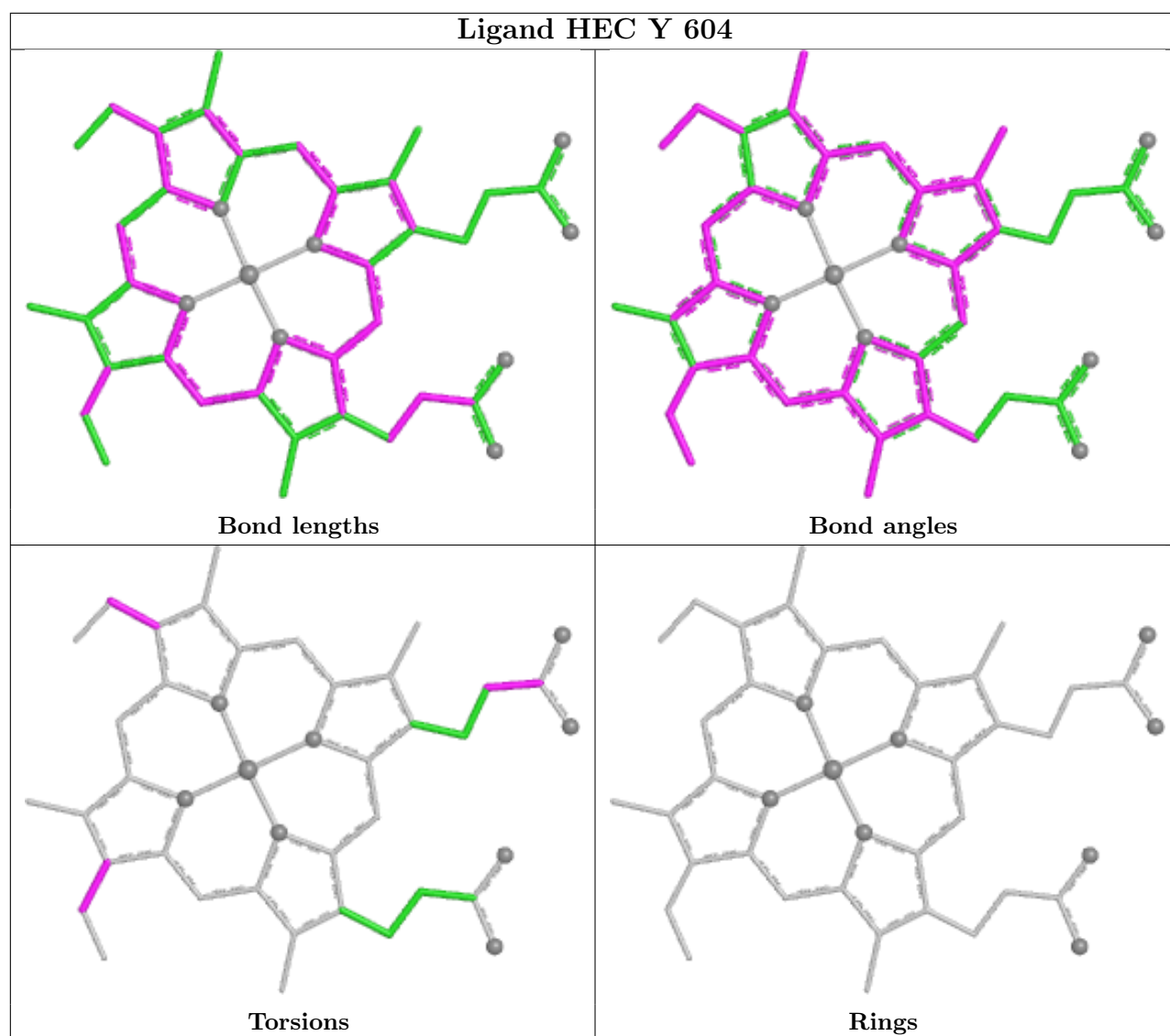
Torsions



Rings







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	Y	495/495 (100%)	0.49	47 (9%)	14 15	11, 22, 50, 94	6 (1%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	530	VAL	4.8
1	Y	529	ALA	3.9
1	Y	528	MET	3.6
1	Y	78	PRO	3.5
1	Y	38	GLY	3.4
1	Y	80	VAL	3.4
1	Y	74	LEU	3.0
1	Y	469	VAL	2.8
1	Y	527	ILE	2.7
1	Y	462	ALA	2.6
1	Y	471	PRO	2.6
1	Y	468	GLY	2.6
1	Y	83	VAL	2.6
1	Y	45	CYS	2.6
1	Y	464	ALA	2.5
1	Y	526	ALA	2.5
1	Y	43	TYR	2.5
1	Y	283	LYS	2.5
1	Y	79	ASP	2.5
1	Y	61	ILE	2.5
1	Y	190	LYS	2.4
1	Y	77	GLY	2.4
1	Y	346	GLU	2.4
1	Y	44	ALA	2.3
1	Y	59	ALA	2.3
1	Y	285	ILE	2.3
1	Y	523	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	Y	467	GLU	2.3
1	Y	470	SER	2.2
1	Y	531	LYS	2.2
1	Y	290	PHE	2.2
1	Y	463	VAL	2.2
1	Y	76	LYS	2.2
1	Y	75	GLU	2.2
1	Y	401	GLY	2.1
1	Y	42	CYS	2.1
1	Y	532	GLN	2.1
1	Y	473	ILE	2.1
1	Y	522	LEU	2.1
1	Y	86	ILE	2.1
1	Y	251	GLY	2.1
1	Y	321	THR	2.0
1	Y	466	ARG	2.0
1	Y	322	ASP	2.0
1	Y	41	THR	2.0
1	Y	189	ALA	2.0
1	Y	270	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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.

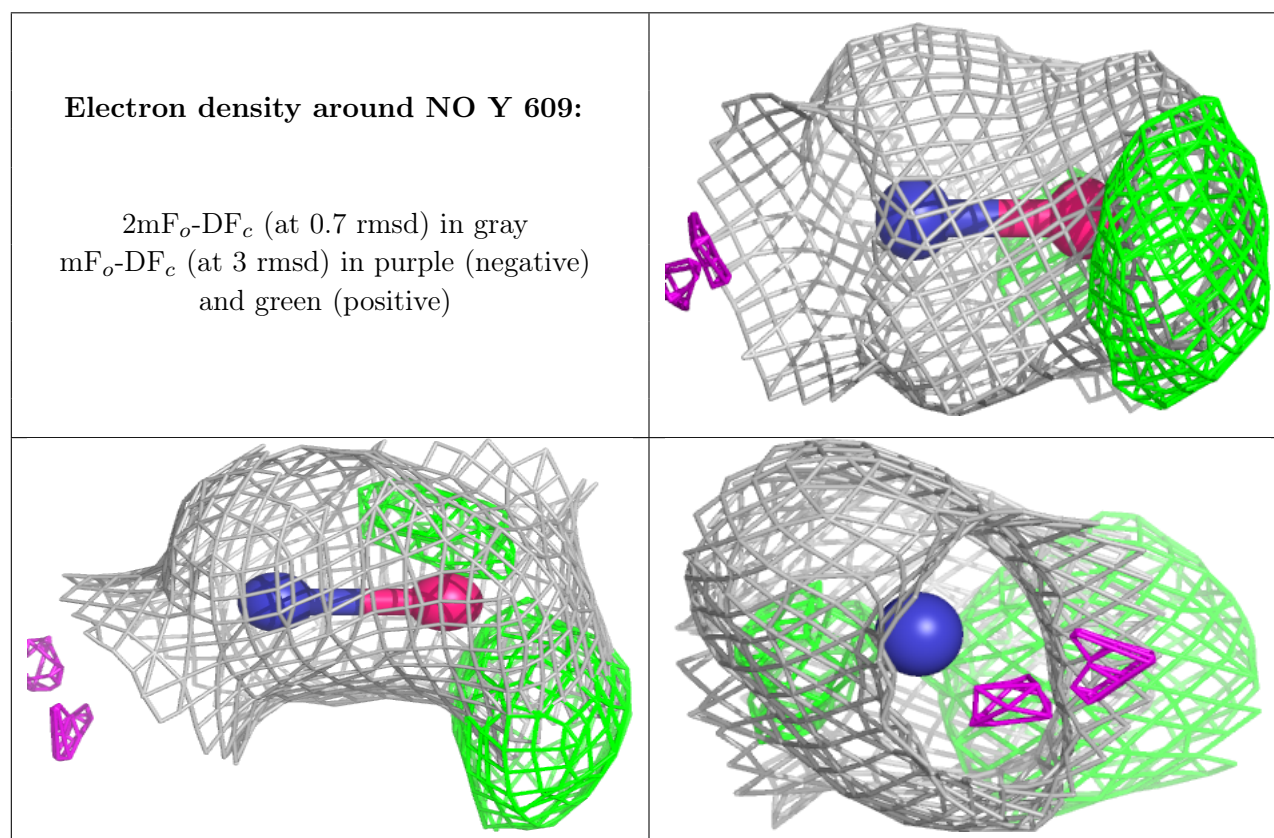
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NO	Y	609	2/2	0.88	0.11	14,14,14,15	2
2	HEC	Y	602	43/43	0.95	0.09	10,20,28,33	0
2	HEC	Y	603	43/43	0.95	0.10	20,28,39,46	0

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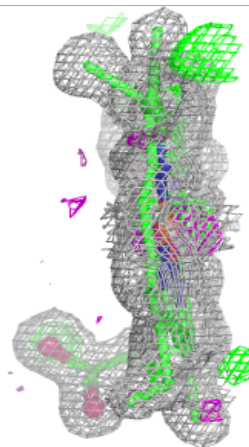
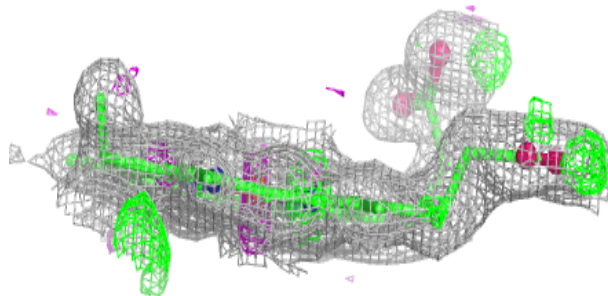
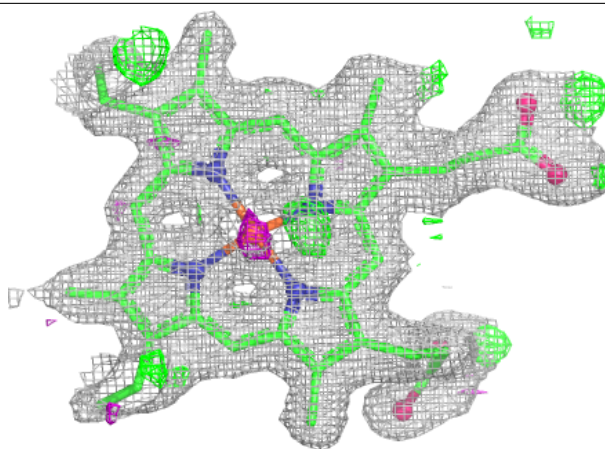
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	HEC	Y	601	43/43	0.95	0.10	12,25,40,57	0
4	NO2	Y	610	3/3	0.96	0.07	7,7,10,10	3
2	HEC	Y	605	43/43	0.97	0.07	15,21,28,35	0
2	HEC	Y	608	43/43	0.98	0.07	13,17,32,47	0
2	HEC	Y	606	43/43	0.98	0.06	11,14,16,18	0
2	HEC	Y	607	43/43	0.98	0.05	12,13,17,21	0
2	HEC	Y	604	43/43	0.99	0.05	10,14,17,18	0
5	CA	Y	611	1/1	0.99	0.05	19,19,19,19	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.



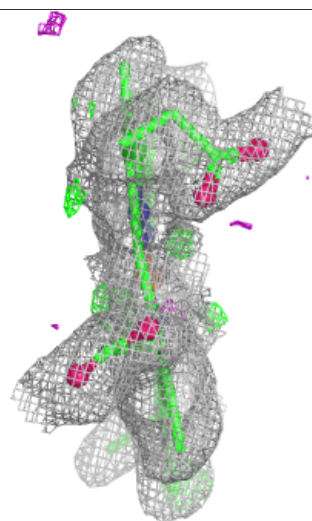
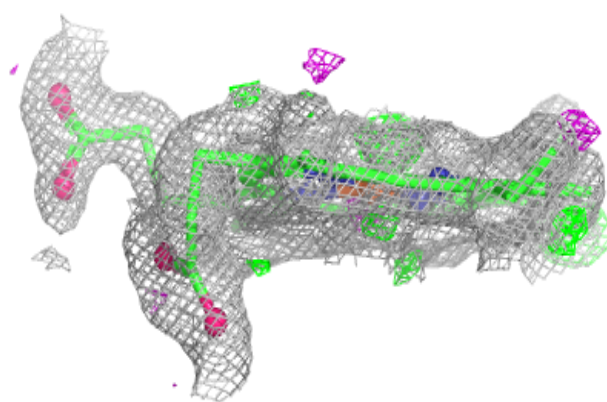
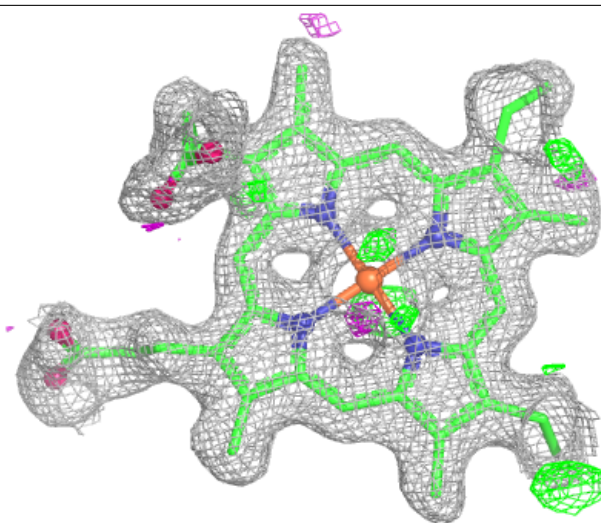
Electron density around HEC Y 602:

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



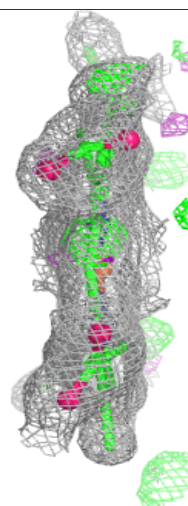
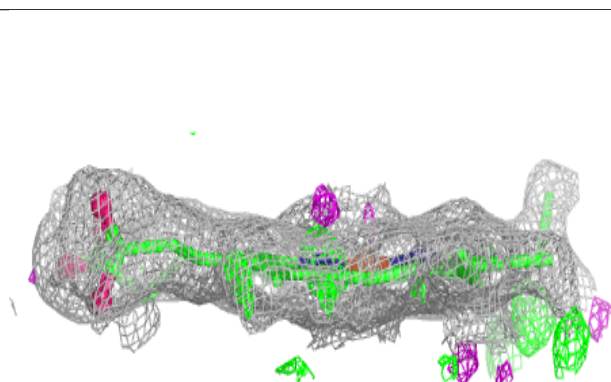
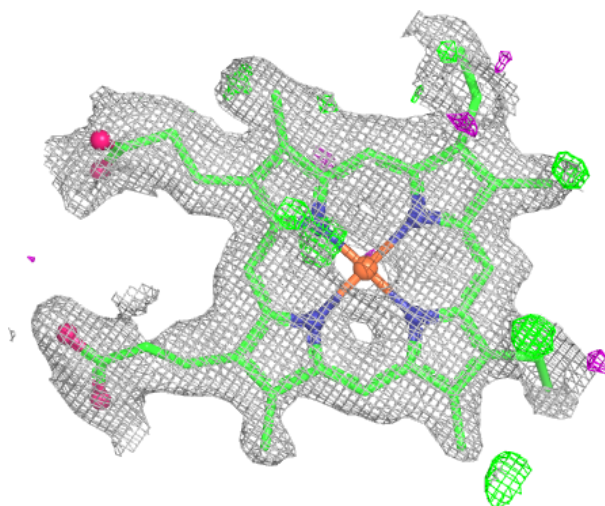
Electron density around HEC Y 603:

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



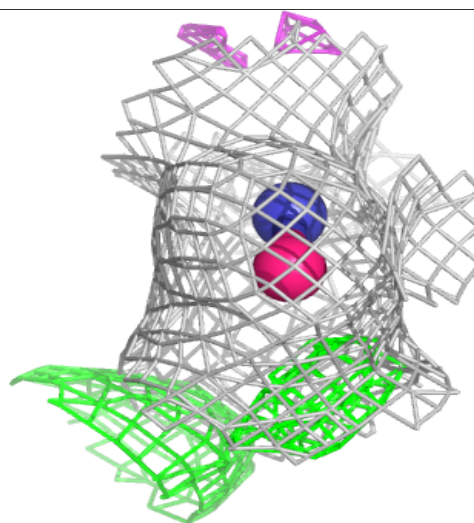
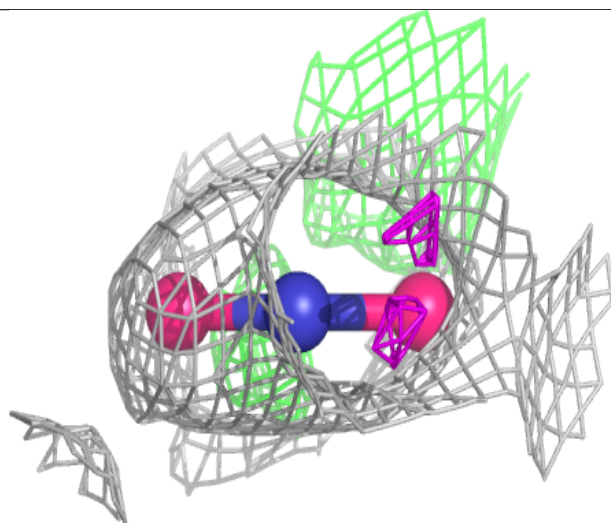
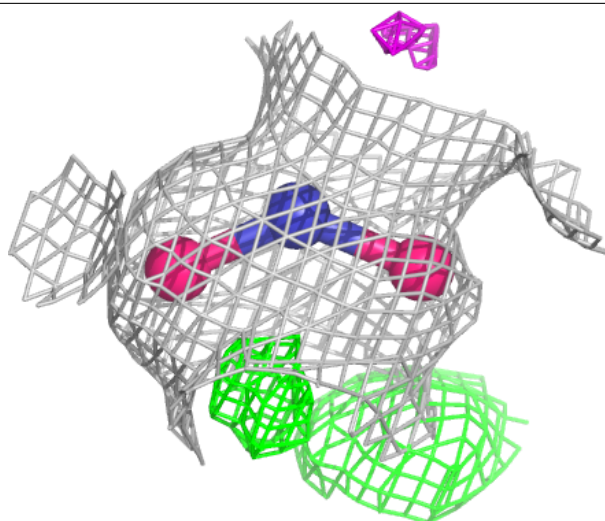
Electron density around HEC Y 601:

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



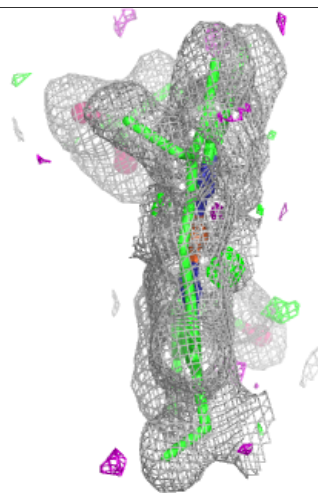
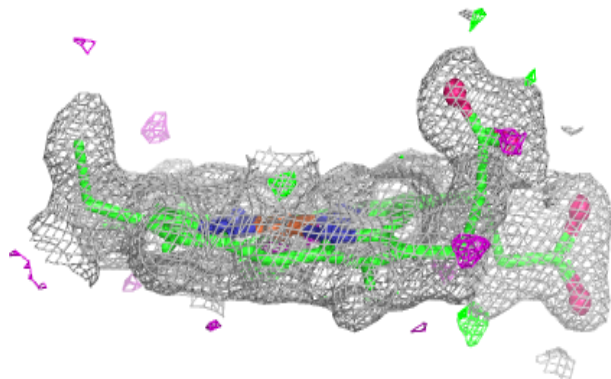
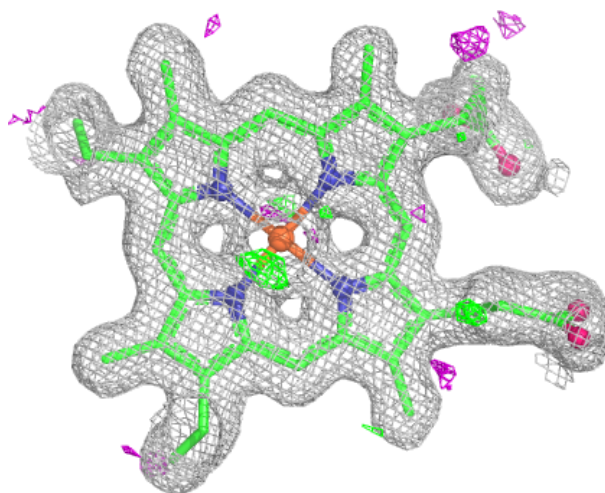
Electron density around NO2 Y 610:

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



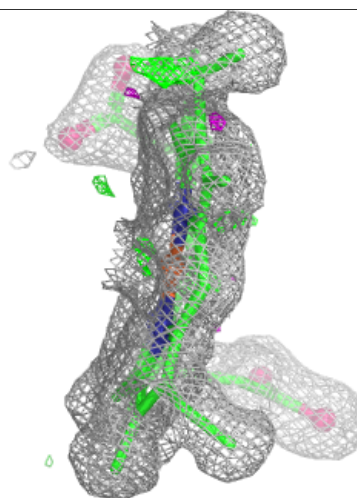
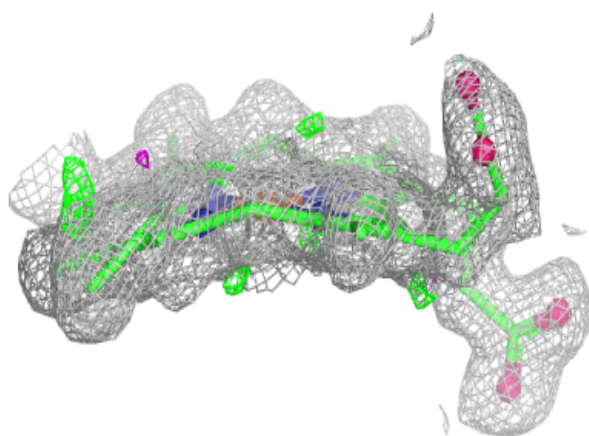
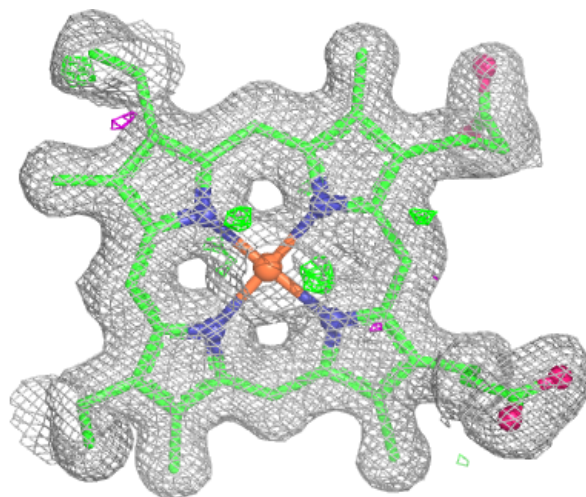
Electron density around HEC Y 605:

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



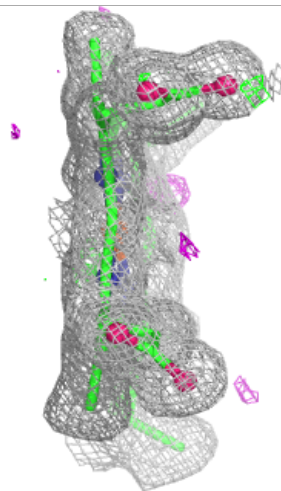
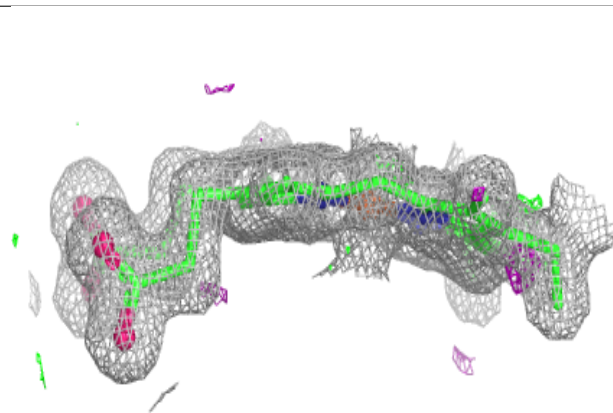
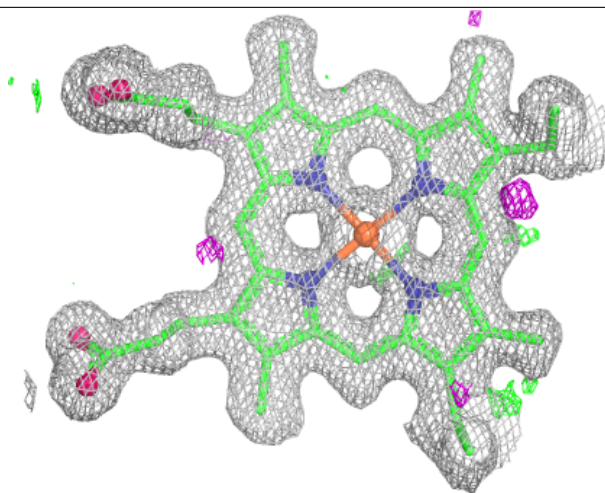
Electron density around HEC Y 608:

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



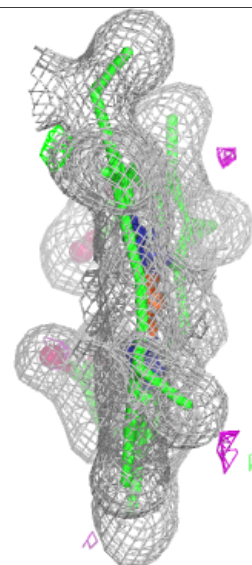
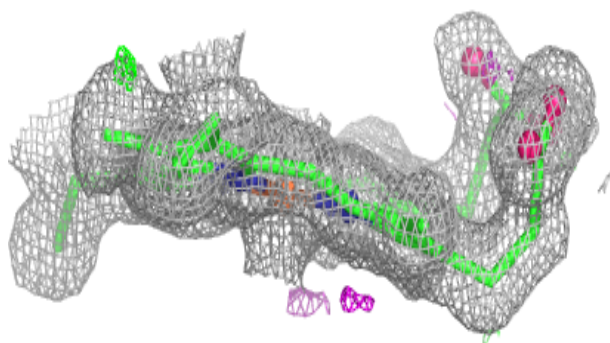
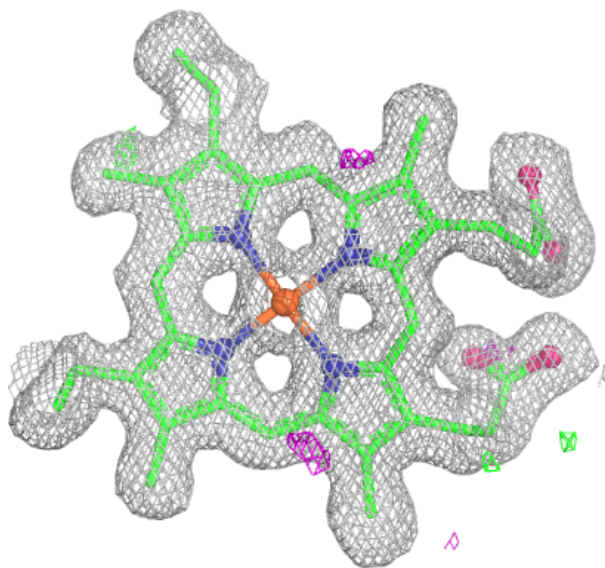
Electron density around HEC Y 606:

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



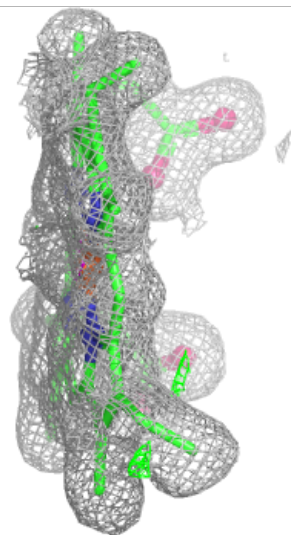
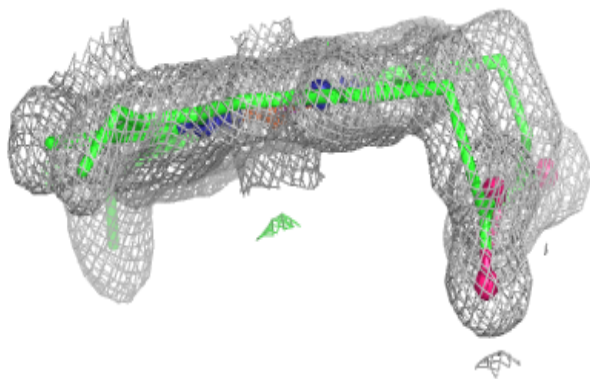
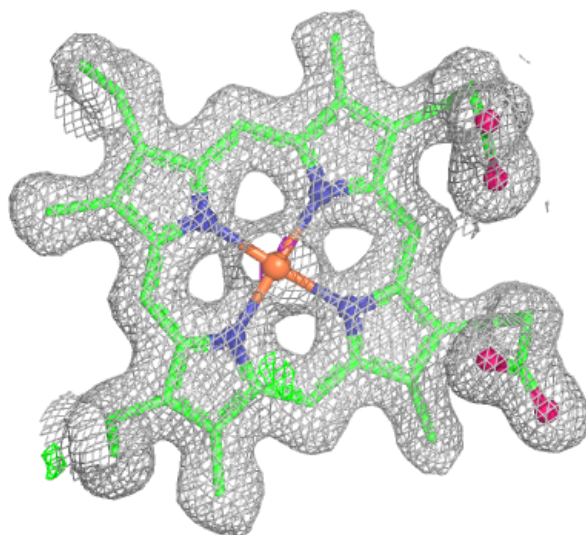
Electron density around HEC Y 607:

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



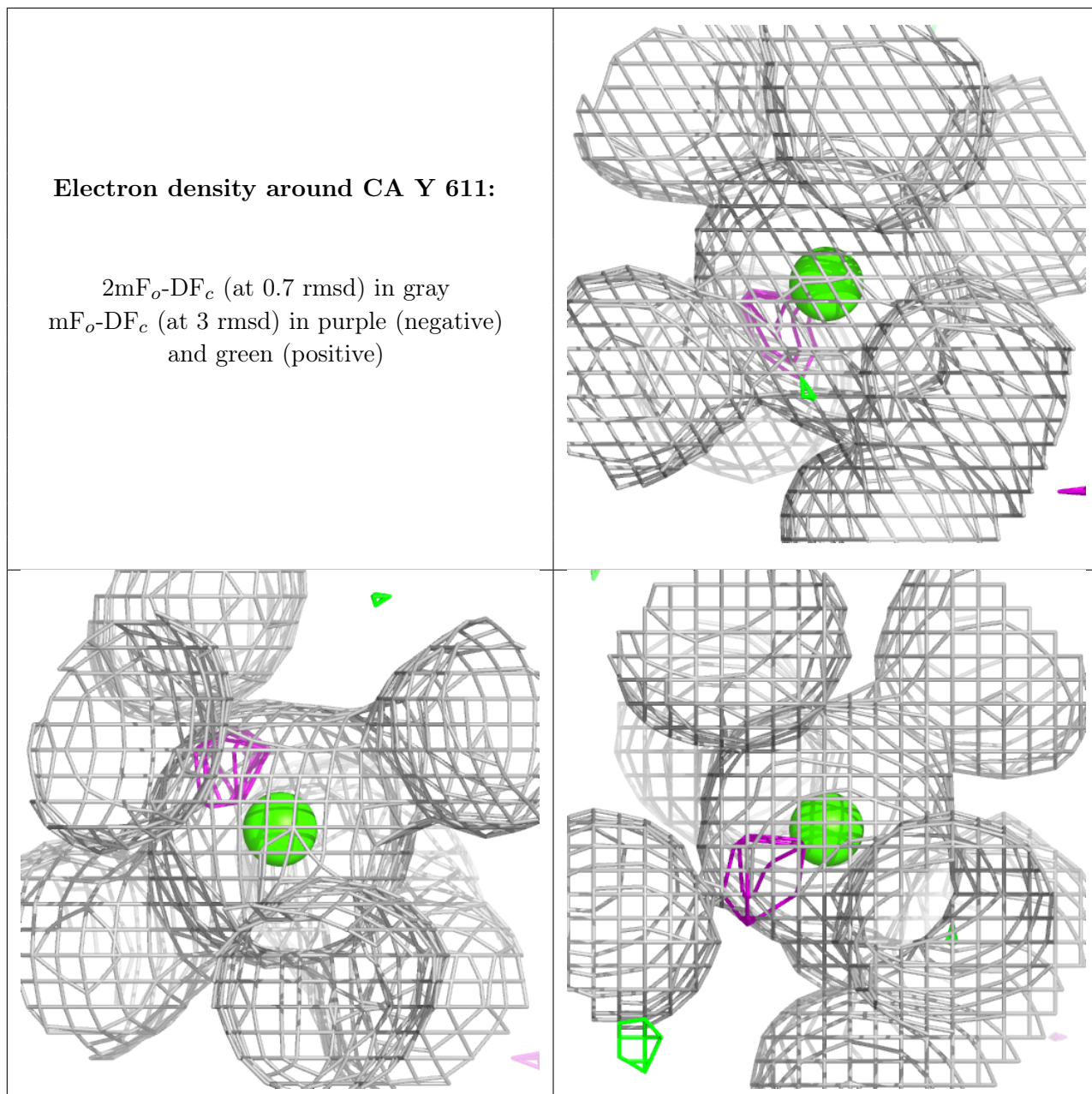
Electron density around HEC Y 604:

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



Electron density around CA Y 611:

$2mF_o-DF_c$ (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.