



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2024 – 12:29 pm GMT

PDB ID : 8RV0
Title : Crystal structure of octaheme nitrite reductase from *Trichlorobacter ammonificans* 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

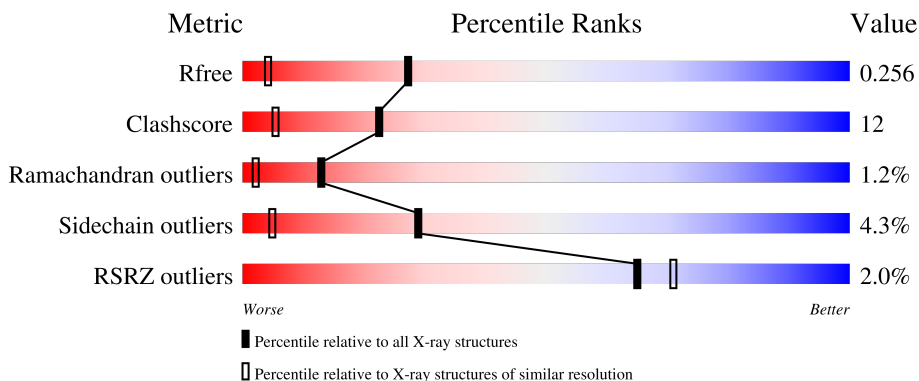
1 Overall quality at a glance

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}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (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	

2 Entry composition i

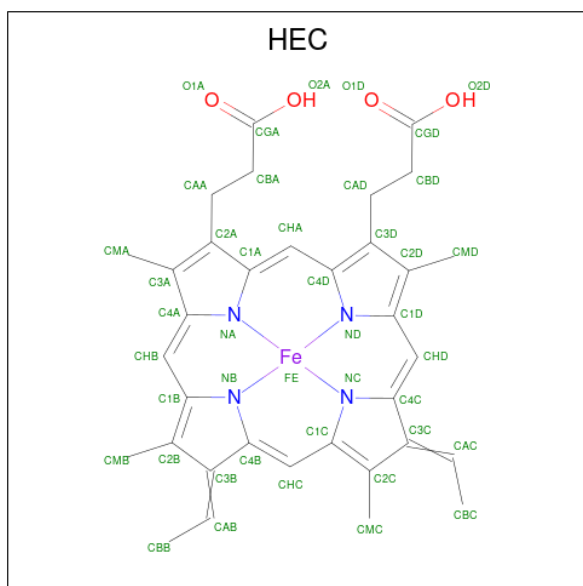
There are 6 unique types of molecules in this entry. The entry contains 4709 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	Y	495	3909	2445	714	721	29	0	6	0

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



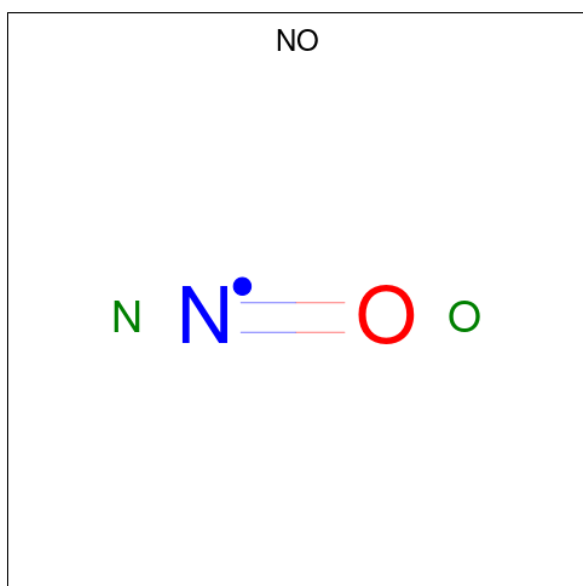
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	Y	1	43	34	1	4	4	0	0
2	Y	1	43	34	1	4	4	0	0
2	Y	1	43	34	1	4	4	0	0
2	Y	1	43	34	1	4	4	0	0
2	Y	1	43	34	1	4	4	0	0

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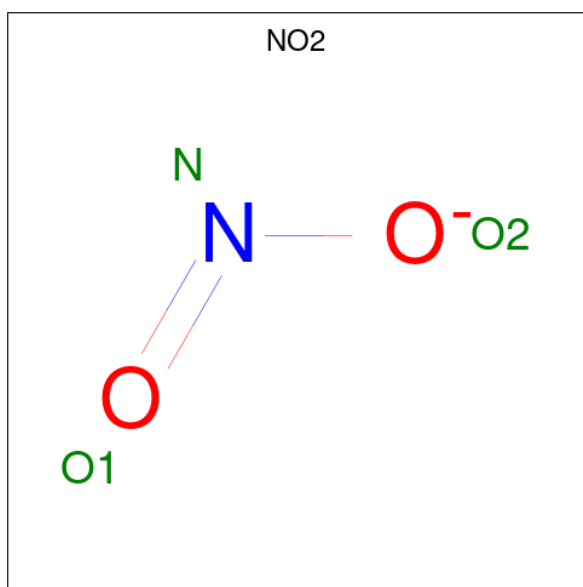
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	Y	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is NITRIC OXIDE (three-letter code: 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 (three-letter code: NO2) (formula: NO₂) (labeled as "Ligand of Interest" by depositor).



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

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

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

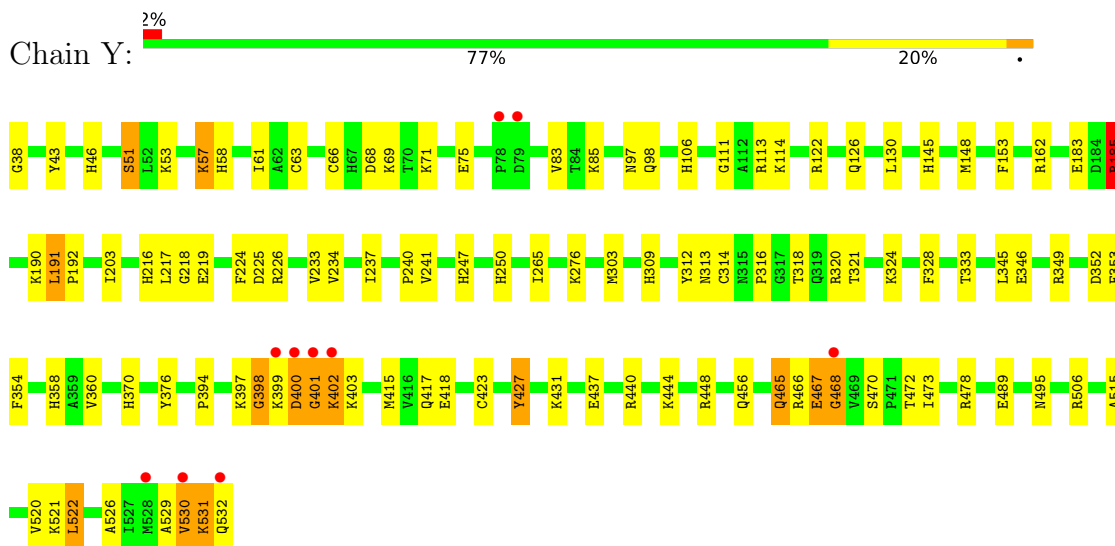
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	Y	450	Total O 450 450	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: 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 49.55 – 1.55	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.60-1.55) 98.8 (49.55-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.55Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.203 , 0.255 0.205 , 0.256	Depositor DCC
R_{free} test set	3361 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	16.6	Xtrriage
Anisotropy	0.505	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.037 for h,-h-k,-l	Xtrriage
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

Xtrriage'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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.82	5/4033 (0.1%)	1.22	15/5431 (0.3%)

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 (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Y	437	GLU	CD-OE2	-7.38	1.17	1.25
1	Y	423	CYS	CB-SG	-6.01	1.72	1.82
1	Y	346	GLU	CD-OE2	5.30	1.31	1.25
1	Y	489	GLU	CD-OE1	5.19	1.31	1.25
1	Y	38	GLY	N-CA	5.07	1.53	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	51	SER	N-CA-CB	7.28	121.43	110.50
1	Y	478	ARG	NE-CZ-NH2	-6.13	117.23	120.30
1	Y	185	ARG	CG-CD-NE	6.10	124.61	111.80
1	Y	515	ALA	N-CA-CB	5.84	118.28	110.10
1	Y	506	ARG	CG-CD-NE	-5.78	99.66	111.80
1	Y	427	TYR	CB-CG-CD2	-5.76	117.55	121.00
1	Y	506	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	Y	226	ARG	NE-CZ-NH1	5.35	122.97	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	448	ARG	NE-CZ-NH2	5.30	122.95	120.30
1	Y	162	ARG	CG-CD-NE	-5.29	100.69	111.80
1	Y	43	TYR	CB-CG-CD1	5.23	124.14	121.00
1	Y	185	ARG	NE-CZ-NH2	5.21	122.91	120.30
1	Y	113	ARG	CB-CA-C	5.20	120.79	110.40
1	Y	122	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	Y	219	GLU	CB-CG-CD	5.12	128.02	114.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Y	398	GLY	Peptide
1	Y	467	GLU	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	Y	3909	0	3816	89	0
2	Y	344	0	240	22	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	97	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 12.

All (97) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
2:Y:608:HEC:HBC3	2:Y:608:HEC:HMC1	1.74	0.68
1:Y:531:LYS:H	1:Y:531:LYS:CD	2.03	0.63
2:Y:606:HEC:HMA3	2:Y:607:HEC:HBA1	1.80	0.63
1:Y:265:ILE:CD1	1:Y:303[A]:MET:HE2	2.29	0.63
1:Y:495:ASN:HB3	2:Y:607:HEC:HAA1	1.80	0.63
1:Y:265:ILE:HD11	1:Y:303[A]:MET:HE2	1.84	0.60
1:Y:312:TYR:CE2	2:Y:604:HEC:HMC2	2.37	0.60
1:Y:465:GLN:O	1:Y:467:GLU:N	2.36	0.59
1:Y:376:TYR:CE1	2:Y:607:HEC:HMC2	2.38	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
2:Y:602:HEC:HMC1	2:Y:602:HEC:HBC3	1.86	0.57
1:Y:265:ILE:HD13	1:Y:303[A]:MET:HE1	1.87	0.57
2:Y:605:HEC:HMC1	2:Y:605:HEC:HBC3	1.85	0.57
2:Y:601:HEC:HMD1	2:Y:601:HEC:HBD2	1.87	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:376:TYR:CZ	2:Y:607:HEC:HMC2	2.42	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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:247:HIS:CG	2:Y:603:HEC:HMA1	2.49	0.47
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
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
1:Y:97:ASN:ND2	1:Y:399:LYS:HE3	2.32	0.45
2:Y:601:HEC:HMD1	2:Y:601:HEC:CB	2.46	0.45
1:Y:111:GLY:O	1:Y:114:LYS:HE3	2.17	0.45
1:Y:400:ASP:CG	1:Y:401:GLY:N	2.70	0.44
1:Y:309:HIS:CE1	2:Y:604:HEC:HMD1	2.52	0.44
1:Y:240:PRO:O	1:Y:241:VAL:C	2.56	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:61:ILE:HG21	2:Y:602:HEC:HMC1	2.00	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:398:GLY:C	1:Y:399:LYS:HG2	2.40	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:145:HIS:O	1:Y:148:MET:HG2	2.20	0.42
1:Y:398:GLY:C	1:Y:399:LYS:CG	2.88	0.42
1:Y:473:ILE:HG21	1:Y:526:ALA:CB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:522:LEU:C	1:Y:522:LEU:HD12	2.41	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
2:Y:607:HEC:HBB3	2:Y:607:HEC:HMB1	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	Y	499/495 (101%)	462 (93%)	31 (6%)	6 (1%)	13 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 [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	Y	420/414 (101%)	402 (96%)	18 (4%)	29 5

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Y	51	SER
1	Y	57	LYS
1	Y	71	LYS
1	Y	75	GLU
1	Y	85	LYS
1	Y	185	ARG
1	Y	190	LYS
1	Y	191	LEU
1	Y	276	LYS
1	Y	324	LYS
1	Y	397	LYS
1	Y	402	LYS
1	Y	403	LYS
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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	97	ASN
1	Y	106	HIS
1	Y	126	GLN
1	Y	524	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	608	1	32,50,50	1.84	9 (28%)	24,82,82	3.34	10 (41%)
3	NO	Y	609	4,2	0,1,1	-	-	-	-	-
2	HEC	Y	604	3,1,4	32,50,50	2.20	9 (28%)	24,82,82	1.32	4 (16%)
2	HEC	Y	607	1	32,50,50	1.62	9 (28%)	24,82,82	2.83	11 (45%)
2	HEC	Y	605	1	32,50,50	1.93	10 (31%)	24,82,82	2.59	11 (45%)
2	HEC	Y	606	1	32,50,50	1.91	5 (15%)	24,82,82	2.25	7 (29%)
2	HEC	Y	603	1	32,50,50	2.36	7 (21%)	24,82,82	2.64	11 (45%)
2	HEC	Y	602	1	32,50,50	3.09	11 (34%)	24,82,82	2.53	11 (45%)
2	HEC	Y	601	1	32,50,50	2.81	11 (34%)	24,82,82	4.36	9 (37%)
4	NO2	Y	610	3,2	1,2,2	0.49	0	0,1,1	-	-

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

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	602	HEC	C3C-C2C	9.75	1.50	1.40
2	Y	601	HEC	C2B-C3B	9.40	1.50	1.40
2	Y	602	HEC	C4B-C3B	9.02	1.59	1.43
2	Y	603	HEC	C2B-C3B	8.21	1.49	1.40
2	Y	606	HEC	C3C-C2C	7.08	1.48	1.40
2	Y	601	HEC	C4D-ND	-6.54	1.22	1.36
2	Y	604	HEC	C2B-C3B	6.50	1.47	1.40
2	Y	604	HEC	C3C-C2C	6.35	1.47	1.40
2	Y	601	HEC	C3C-C2C	5.61	1.46	1.40
2	Y	603	HEC	C3C-C2C	5.59	1.46	1.40
2	Y	605	HEC	C3C-C2C	5.20	1.46	1.40
2	Y	602	HEC	C3A-C4A	5.17	1.54	1.42
2	Y	602	HEC	C1C-CHC	4.28	1.52	1.41
2	Y	605	HEC	C2B-C3B	3.87	1.44	1.40
2	Y	603	HEC	C3D-C2D	3.79	1.48	1.37
2	Y	601	HEC	C3A-C4A	3.71	1.51	1.42
2	Y	608	HEC	C4D-CHA	3.70	1.51	1.41
2	Y	605	HEC	C4D-ND	-3.55	1.28	1.36
2	Y	602	HEC	C2B-C3B	3.54	1.44	1.40
2	Y	608	HEC	CBA-CGA	3.54	1.58	1.50
2	Y	606	HEC	C2B-C3B	3.50	1.44	1.40
2	Y	606	HEC	C4B-C3B	3.43	1.49	1.43
2	Y	605	HEC	C1B-CHB	3.38	1.50	1.41
2	Y	601	HEC	C1B-NB	3.35	1.43	1.36
2	Y	607	HEC	C2B-C3B	3.35	1.44	1.40
2	Y	602	HEC	CMC-C2C	-3.33	1.43	1.51
2	Y	602	HEC	O1A-CGA	3.19	1.32	1.22
2	Y	601	HEC	C2A-C3A	3.13	1.47	1.37
2	Y	608	HEC	C3C-C2C	3.10	1.44	1.40
2	Y	602	HEC	O1D-CGD	3.09	1.32	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	602	HEC	C3D-C2D	3.09	1.46	1.37
2	Y	607	HEC	CBD-CGD	2.96	1.57	1.50
2	Y	604	HEC	C1C-CHC	2.94	1.49	1.41
2	Y	607	HEC	C4D-CHA	2.93	1.49	1.41
2	Y	606	HEC	C1B-CHB	2.92	1.49	1.41
2	Y	601	HEC	C1B-CHB	2.90	1.49	1.41
2	Y	608	HEC	C4D-ND	-2.89	1.30	1.36
2	Y	604	HEC	C1C-NC	-2.89	1.30	1.36
2	Y	602	HEC	CBD-CGD	2.86	1.57	1.50
2	Y	601	HEC	C4D-CHA	2.83	1.48	1.41
2	Y	605	HEC	C1B-NB	-2.83	1.30	1.36
2	Y	601	HEC	C2A-C1A	2.79	1.48	1.42
2	Y	603	HEC	C1D-CHD	2.77	1.48	1.41
2	Y	603	HEC	C4D-CHA	2.72	1.48	1.41
2	Y	601	HEC	C3C-C4C	2.67	1.47	1.43
2	Y	608	HEC	C3D-C2D	2.66	1.45	1.37
2	Y	604	HEC	CAD-C3D	-2.62	1.48	1.52
2	Y	607	HEC	C2A-C3A	2.51	1.45	1.37
2	Y	605	HEC	C2A-C1A	2.46	1.48	1.42
2	Y	607	HEC	O2D-CGD	-2.46	1.22	1.30
2	Y	601	HEC	C1D-CHD	2.40	1.47	1.41
2	Y	607	HEC	C3D-C2D	2.31	1.44	1.37
2	Y	604	HEC	C2A-C3A	2.31	1.44	1.37
2	Y	608	HEC	C1D-ND	2.30	1.40	1.36
2	Y	608	HEC	C1C-CHC	2.29	1.47	1.41
2	Y	604	HEC	C2A-C1A	2.26	1.47	1.42
2	Y	607	HEC	O1A-CGA	2.23	1.29	1.22
2	Y	604	HEC	CBD-CGD	2.21	1.55	1.50
2	Y	607	HEC	CBA-CGA	-2.19	1.45	1.50
2	Y	605	HEC	C2A-C3A	2.14	1.44	1.37
2	Y	603	HEC	C1C-CHC	2.13	1.46	1.41
2	Y	605	HEC	CBA-CGA	2.13	1.55	1.50
2	Y	603	HEC	CBD-CGD	2.13	1.55	1.50
2	Y	605	HEC	C1D-ND	-2.09	1.31	1.36
2	Y	605	HEC	C3D-C2D	2.09	1.43	1.37
2	Y	608	HEC	O2D-CGD	-2.08	1.23	1.30
2	Y	602	HEC	C1D-ND	-2.07	1.31	1.36
2	Y	604	HEC	C3D-C2D	2.05	1.43	1.37
2	Y	607	HEC	C4D-ND	-2.05	1.31	1.36
2	Y	608	HEC	C1B-CHB	2.04	1.46	1.41
2	Y	606	HEC	CAA-C2A	-2.03	1.48	1.52

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	601	HEC	C1D-C2D-C3D	-14.68	96.78	107.00
2	Y	608	HEC	CBA-CAA-C2A	-9.97	95.81	112.60
2	Y	608	HEC	C1D-C2D-C3D	-8.52	101.07	107.00
2	Y	601	HEC	CBA-CAA-C2A	8.15	126.34	112.60
2	Y	603	HEC	CBD-CAD-C3D	-7.04	100.61	112.62
2	Y	605	HEC	C1D-C2D-C3D	-6.57	102.42	107.00
2	Y	602	HEC	CMC-C2C-C3C	6.55	133.53	125.82
2	Y	601	HEC	CMC-C2C-C3C	6.47	133.43	125.82
2	Y	607	HEC	C1D-C2D-C3D	-6.07	102.78	107.00
2	Y	607	HEC	CMB-C2B-C3B	5.67	132.48	125.82
2	Y	601	HEC	CMD-C2D-C1D	5.58	137.04	128.46
2	Y	606	HEC	CBA-CAA-C2A	-5.49	103.36	112.60
2	Y	607	HEC	CMC-C2C-C3C	5.49	132.27	125.82
2	Y	603	HEC	C1D-C2D-C3D	-4.95	103.55	107.00
2	Y	607	HEC	CMC-C2C-C1C	-4.95	120.86	128.46
2	Y	601	HEC	CBD-CAD-C3D	4.92	121.02	112.62
2	Y	605	HEC	C2B-C3B-C4B	-4.51	101.48	106.35
2	Y	608	HEC	CBD-CAD-C3D	4.49	120.28	112.62
2	Y	601	HEC	CAD-CBD-CGD	-4.45	101.28	113.76
2	Y	603	HEC	CMC-C2C-C3C	4.24	130.80	125.82
2	Y	605	HEC	CBD-CAD-C3D	-4.15	105.54	112.62
2	Y	606	HEC	O2A-CGA-O1A	-4.03	113.26	123.30
2	Y	602	HEC	CBD-CAD-C3D	4.00	119.44	112.62
2	Y	602	HEC	CMB-C2B-C3B	3.98	130.50	125.82
2	Y	603	HEC	CAD-CBD-CGD	-3.86	102.92	113.76
2	Y	601	HEC	CMB-C2B-C3B	3.82	130.31	125.82
2	Y	603	HEC	CAA-CBA-CGA	-3.80	103.10	113.76
2	Y	606	HEC	CMD-C2D-C1D	-3.76	122.68	128.46
2	Y	606	HEC	C2B-C3B-C4B	-3.69	102.36	106.35
2	Y	608	HEC	CMC-C2C-C3C	3.66	130.12	125.82
2	Y	605	HEC	CMB-C2B-C3B	3.61	130.07	125.82
2	Y	607	HEC	C4C-C3C-C2C	-3.60	102.46	106.35
2	Y	602	HEC	C1D-C2D-C3D	-3.46	104.59	107.00
2	Y	606	HEC	CMC-C2C-C3C	3.41	129.82	125.82
2	Y	608	HEC	CAD-CBD-CGD	-3.33	104.42	113.76
2	Y	608	HEC	CMB-C2B-C3B	3.32	129.73	125.82
2	Y	602	HEC	CMC-C2C-C1C	-3.31	123.38	128.46
2	Y	602	HEC	C4C-C3C-C2C	-3.22	102.88	106.35
2	Y	605	HEC	CAD-CBD-CGD	-3.20	104.79	113.76
2	Y	606	HEC	O2A-CGA-CBA	3.15	124.15	114.03
2	Y	608	HEC	O2A-CGA-CBA	3.12	124.06	114.03
2	Y	607	HEC	O1D-CGD-CBD	-3.10	113.14	123.08
2	Y	601	HEC	CAA-CBA-CGA	-3.02	105.30	113.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	606	HEC	CMD-C2D-C3D	2.98	130.57	124.94
2	Y	604	HEC	C4C-C3C-C2C	-2.93	103.19	106.35
2	Y	608	HEC	O1A-CGA-CBA	-2.91	113.74	123.08
2	Y	607	HEC	O1A-CGA-CBA	-2.90	113.77	123.08
2	Y	607	HEC	CBD-CAD-C3D	2.87	117.52	112.62
2	Y	603	HEC	CMB-C2B-C3B	2.76	129.07	125.82
2	Y	603	HEC	CMA-C3A-C2A	2.75	130.12	124.94
2	Y	605	HEC	CMC-C2C-C1C	2.73	132.66	128.46
2	Y	601	HEC	O2D-CGD-CBD	2.70	122.69	114.03
2	Y	605	HEC	CMB-C2B-C1B	-2.70	124.32	128.46
2	Y	603	HEC	CBA-CAA-C2A	-2.68	108.08	112.60
2	Y	602	HEC	O1A-CGA-CBA	2.62	131.49	123.08
2	Y	607	HEC	O2A-CGA-CBA	2.60	122.39	114.03
2	Y	605	HEC	O2D-CGD-CBD	2.56	122.26	114.03
2	Y	602	HEC	O2A-CGA-O1A	-2.55	116.94	123.30
2	Y	604	HEC	CMC-C2C-C3C	2.46	128.72	125.82
2	Y	605	HEC	CMD-C2D-C1D	2.46	132.24	128.46
2	Y	604	HEC	CMA-C3A-C2A	2.43	129.52	124.94
2	Y	605	HEC	O2D-CGD-O1D	-2.37	117.38	123.30
2	Y	603	HEC	C3B-C4B-NB	2.30	115.29	110.94
2	Y	605	HEC	CAD-C3D-C2D	2.24	133.68	127.25
2	Y	602	HEC	CAD-C3D-C2D	2.23	133.64	127.25
2	Y	603	HEC	CMB-C2B-C1B	2.21	131.86	128.46
2	Y	604	HEC	CBA-CAA-C2A	-2.19	108.92	112.60
2	Y	603	HEC	CMD-C2D-C3D	2.18	129.05	124.94
2	Y	607	HEC	CBA-CAA-C2A	-2.18	108.94	112.60
2	Y	608	HEC	CAA-CBA-CGA	2.17	119.84	113.76
2	Y	602	HEC	O1D-CGD-CBD	-2.10	116.35	123.08
2	Y	602	HEC	CAD-CBD-CGD	2.09	119.61	113.76
2	Y	608	HEC	CMD-C2D-C1D	2.06	131.63	128.46
2	Y	607	HEC	O2D-CGD-CBD	2.05	120.61	114.03

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Y	601	HEC	C2D-C3D-CAD-CBD
2	Y	601	HEC	C4D-C3D-CAD-CBD
2	Y	602	HEC	C3D-CAD-CBD-CGD
2	Y	601	HEC	C3A-C2A-CAA-CBA
2	Y	608	HEC	CAD-CBD-CGD-O1D
2	Y	607	HEC	CAA-CBA-CGA-O2A

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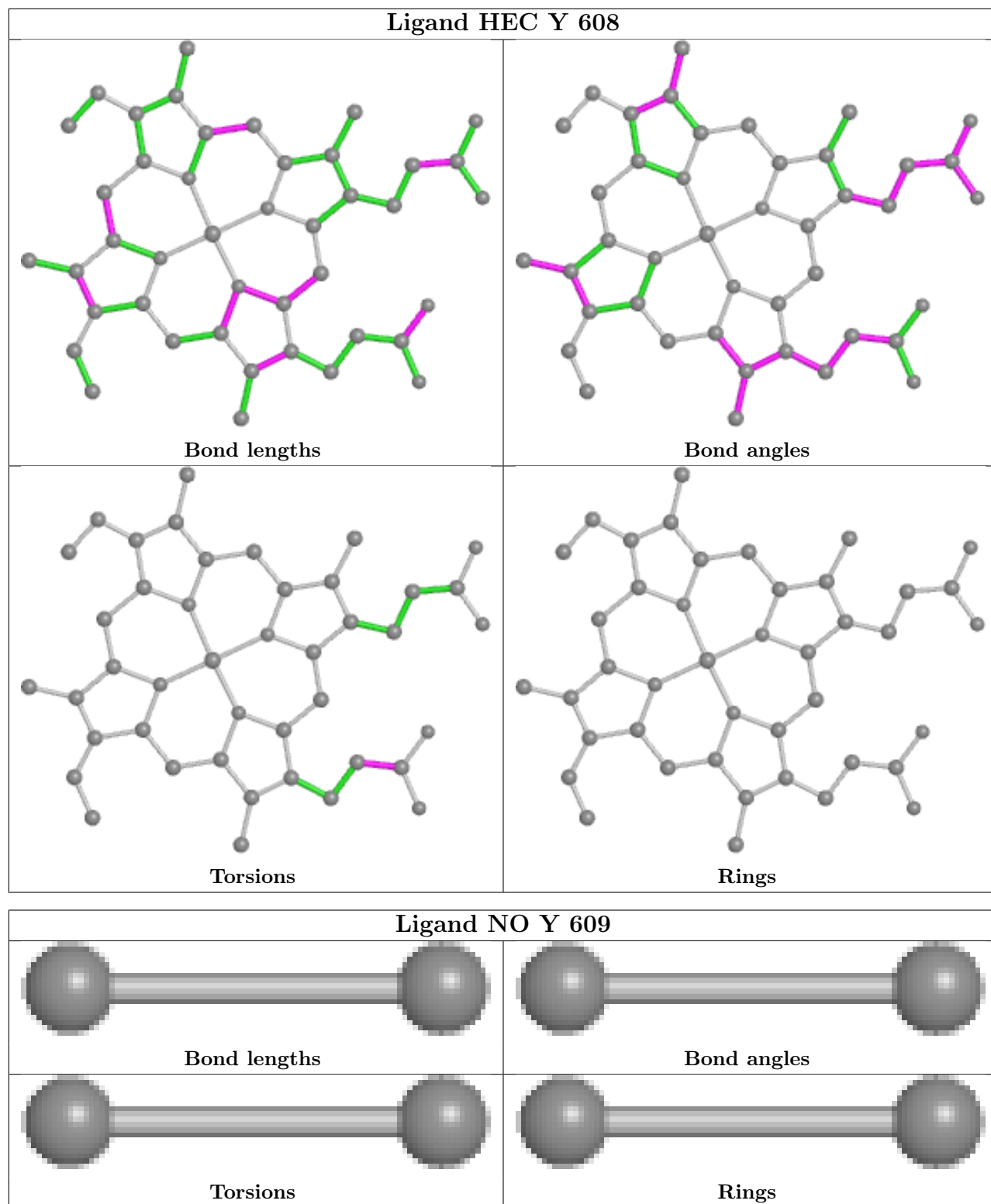
Mol	Chain	Res	Type	Atoms
2	Y	604	HEC	CAA-CBA-CGA-O1A
2	Y	601	HEC	CAD-CBD-CGD-O2D
2	Y	608	HEC	CAD-CBD-CGD-O2D
2	Y	604	HEC	CAA-CBA-CGA-O2A
2	Y	602	HEC	CAA-CBA-CGA-O1A
2	Y	602	HEC	CAA-CBA-CGA-O2A
2	Y	601	HEC	CAD-CBD-CGD-O1D
2	Y	607	HEC	CAA-CBA-CGA-O1A
2	Y	603	HEC	CAD-CBD-CGD-O1D
2	Y	605	HEC	CAA-CBA-CGA-O2A
2	Y	602	HEC	CAD-CBD-CGD-O1D
2	Y	605	HEC	CAA-CBA-CGA-O1A
2	Y	601	HEC	CAA-CBA-CGA-O1A
2	Y	603	HEC	CAD-CBD-CGD-O2D
2	Y	606	HEC	CAA-CBA-CGA-O1A

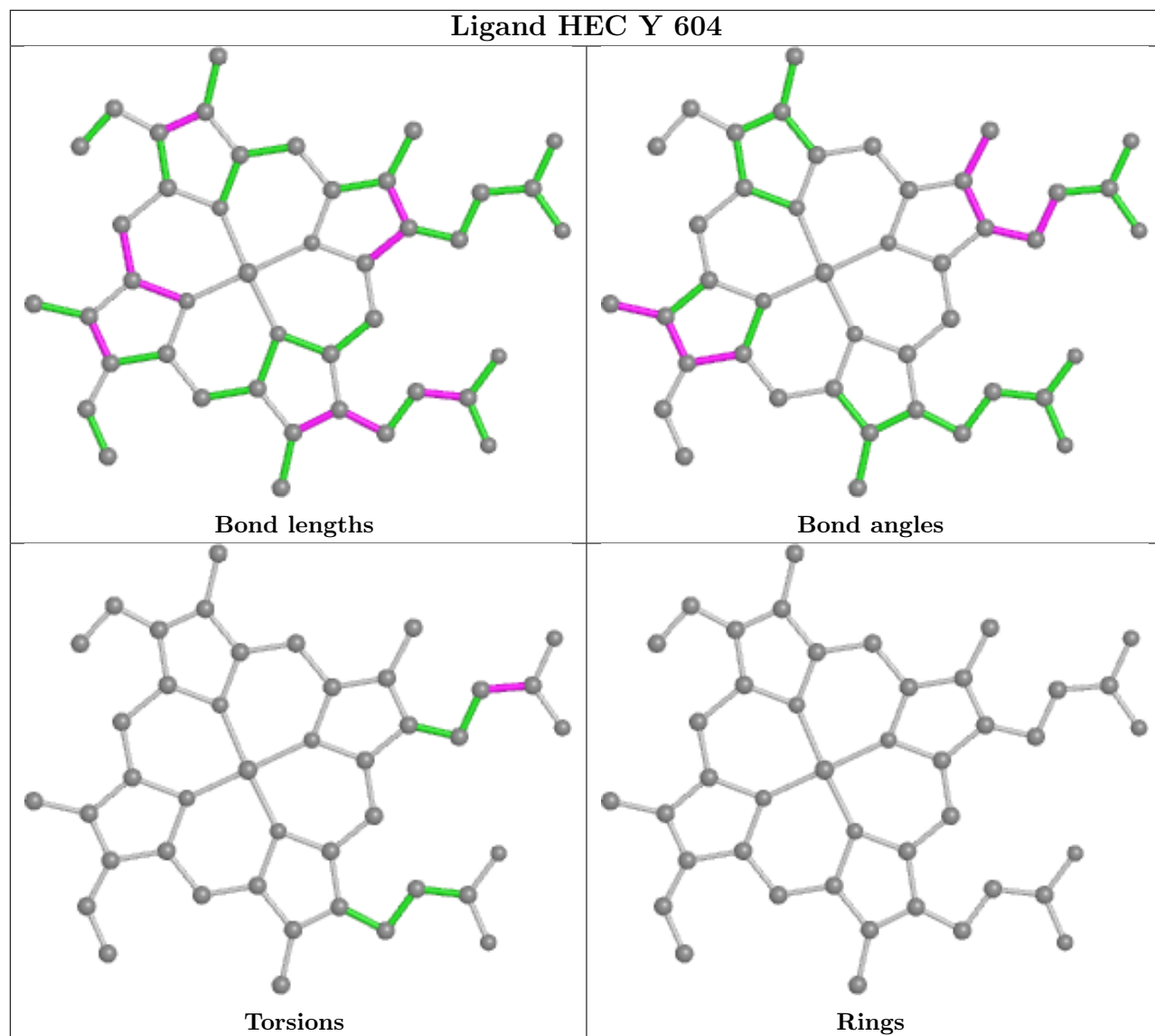
There are no ring outliers.

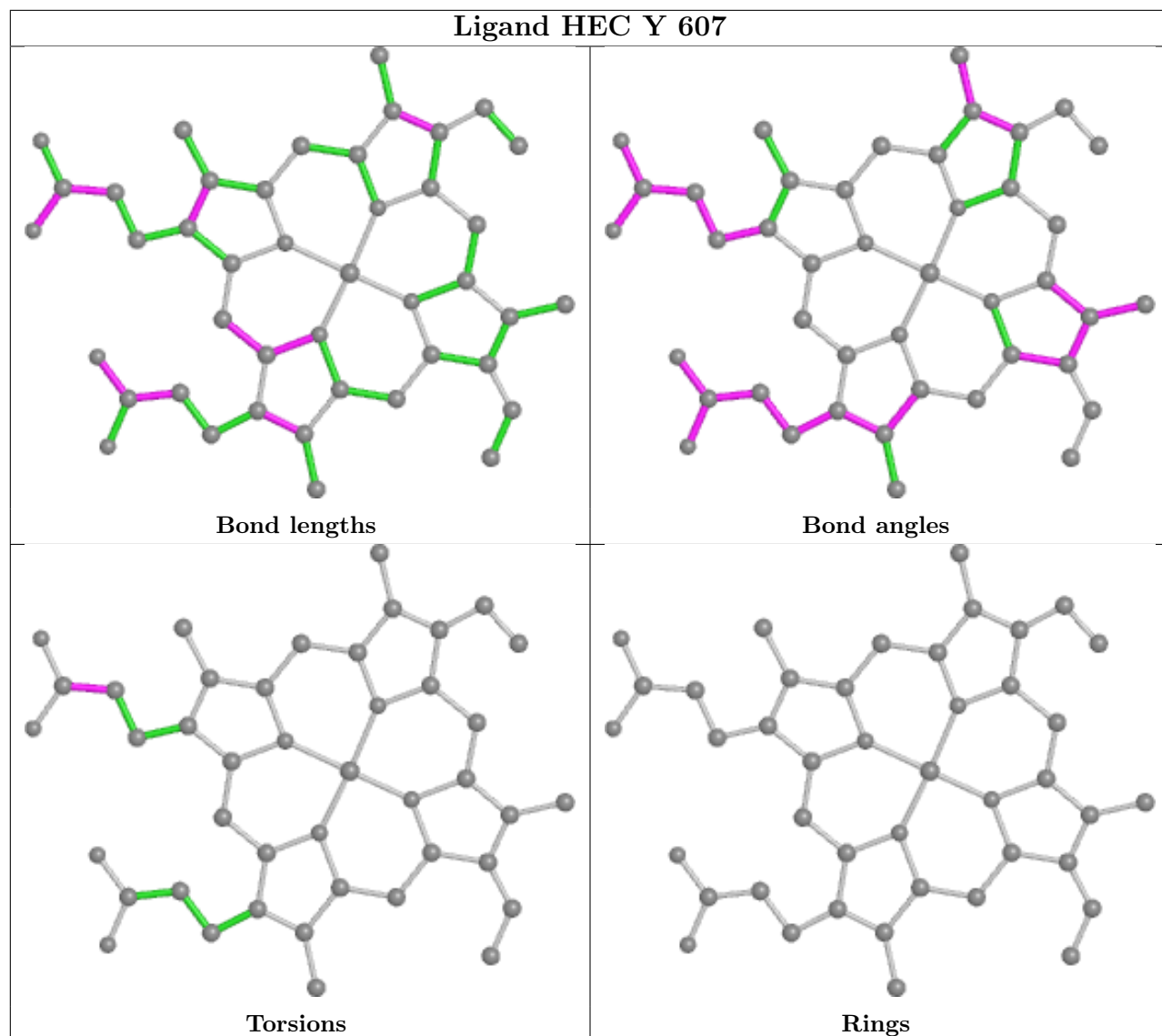
9 monomers are involved in 23 short contacts:

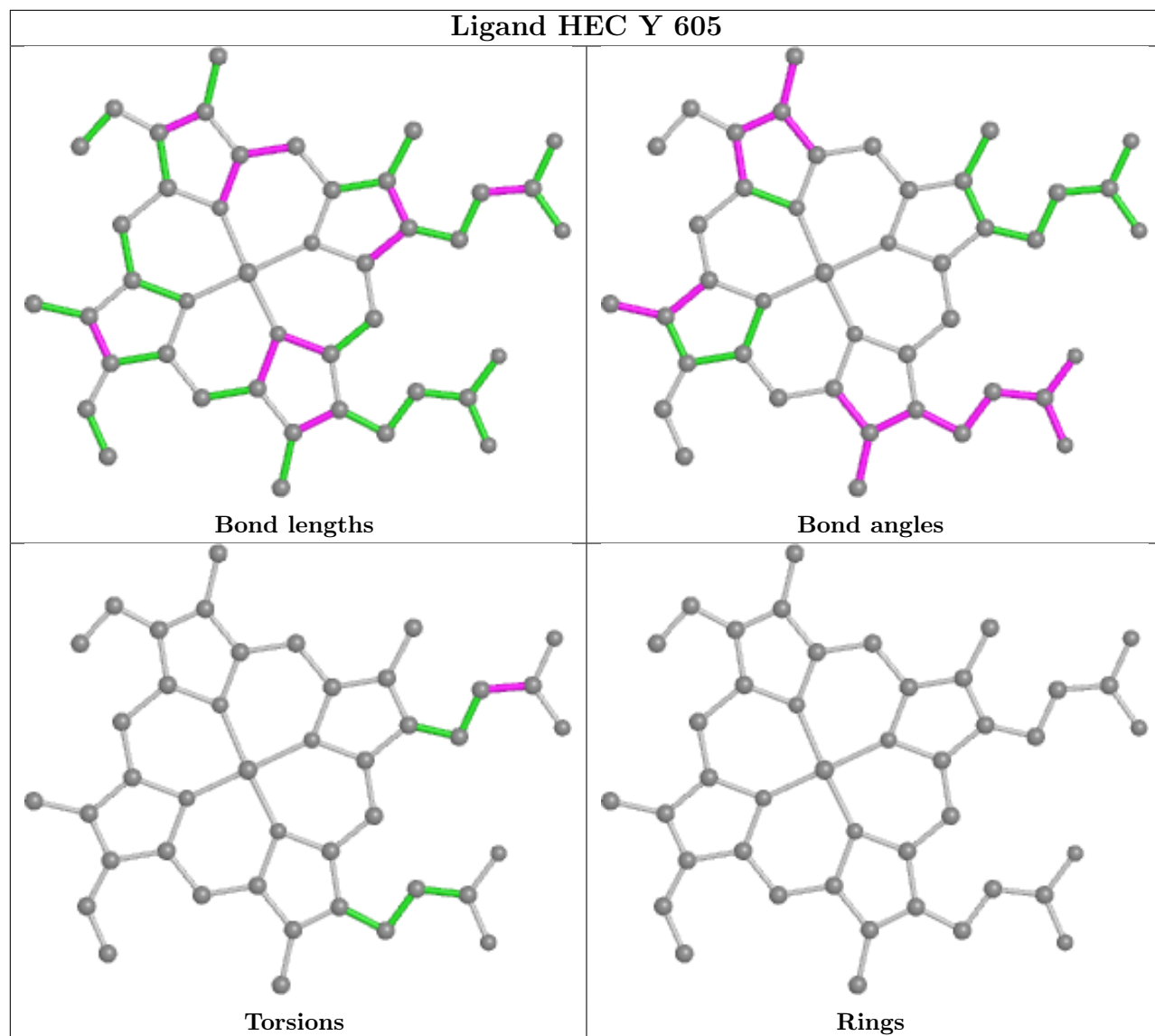
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Y	608	HEC	1	0
2	Y	604	HEC	2	0
2	Y	607	HEC	5	0
2	Y	605	HEC	2	0
2	Y	606	HEC	2	0
2	Y	603	HEC	2	0
2	Y	602	HEC	5	0
2	Y	601	HEC	4	0
4	Y	610	NO2	1	0

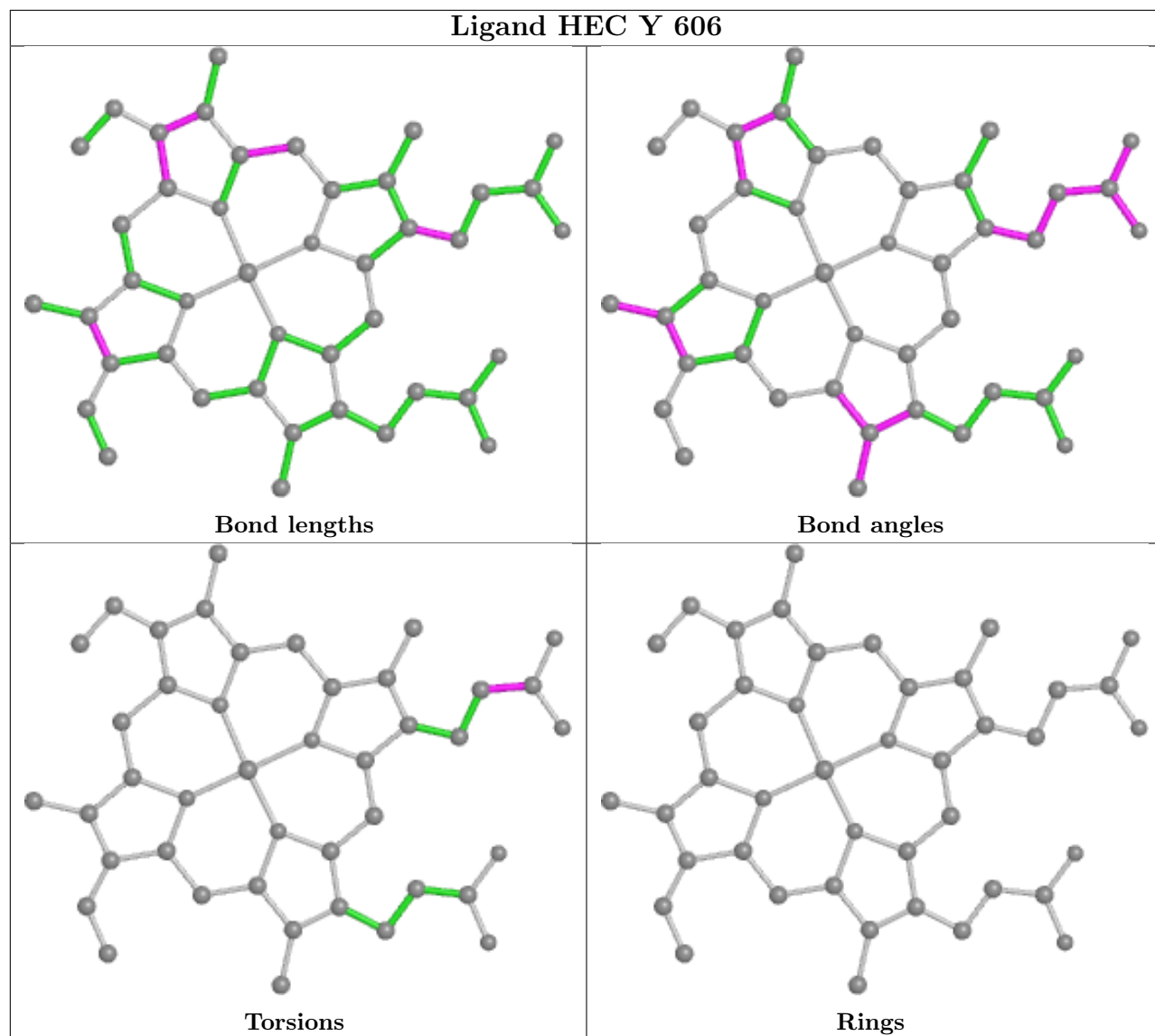
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

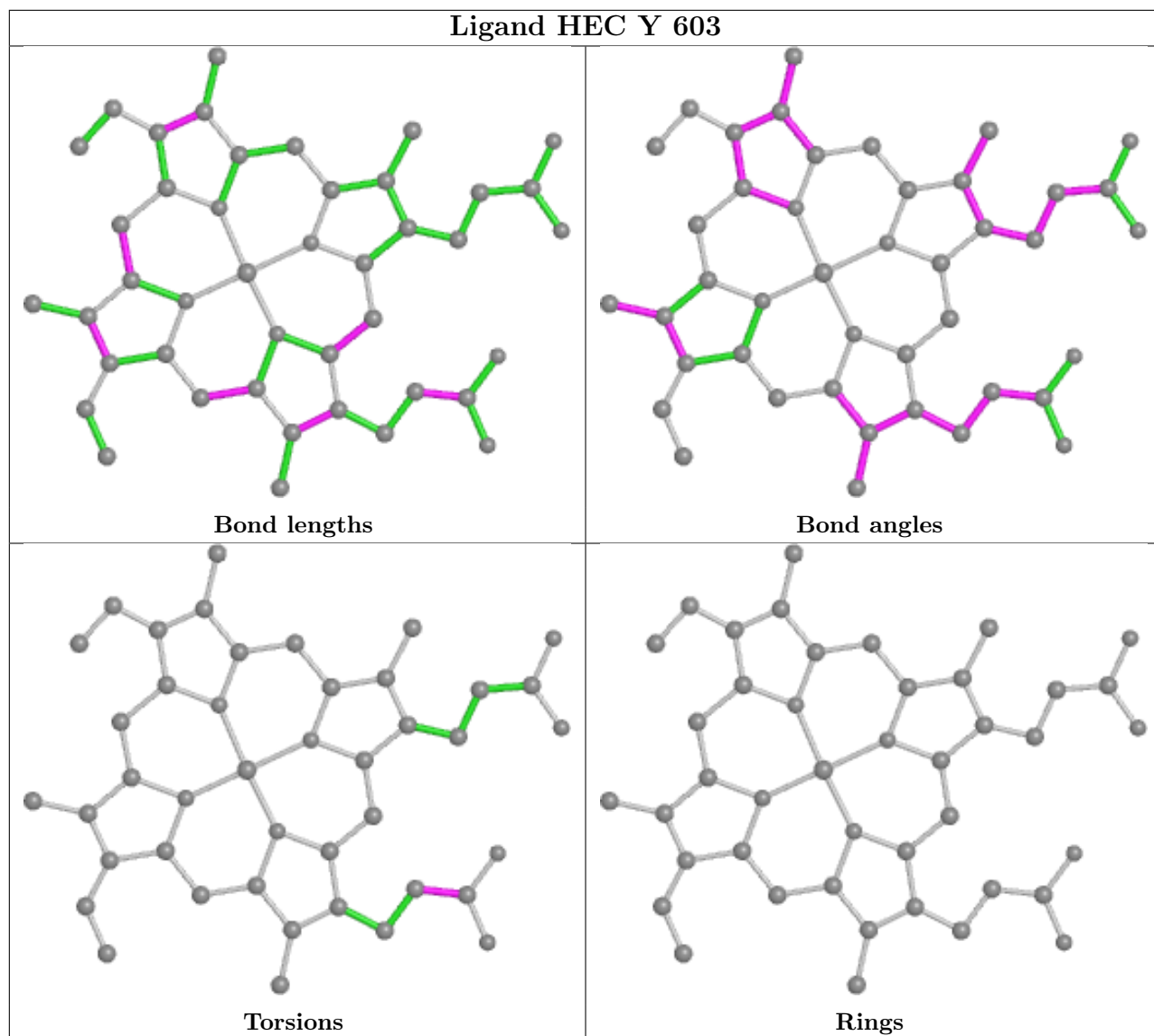


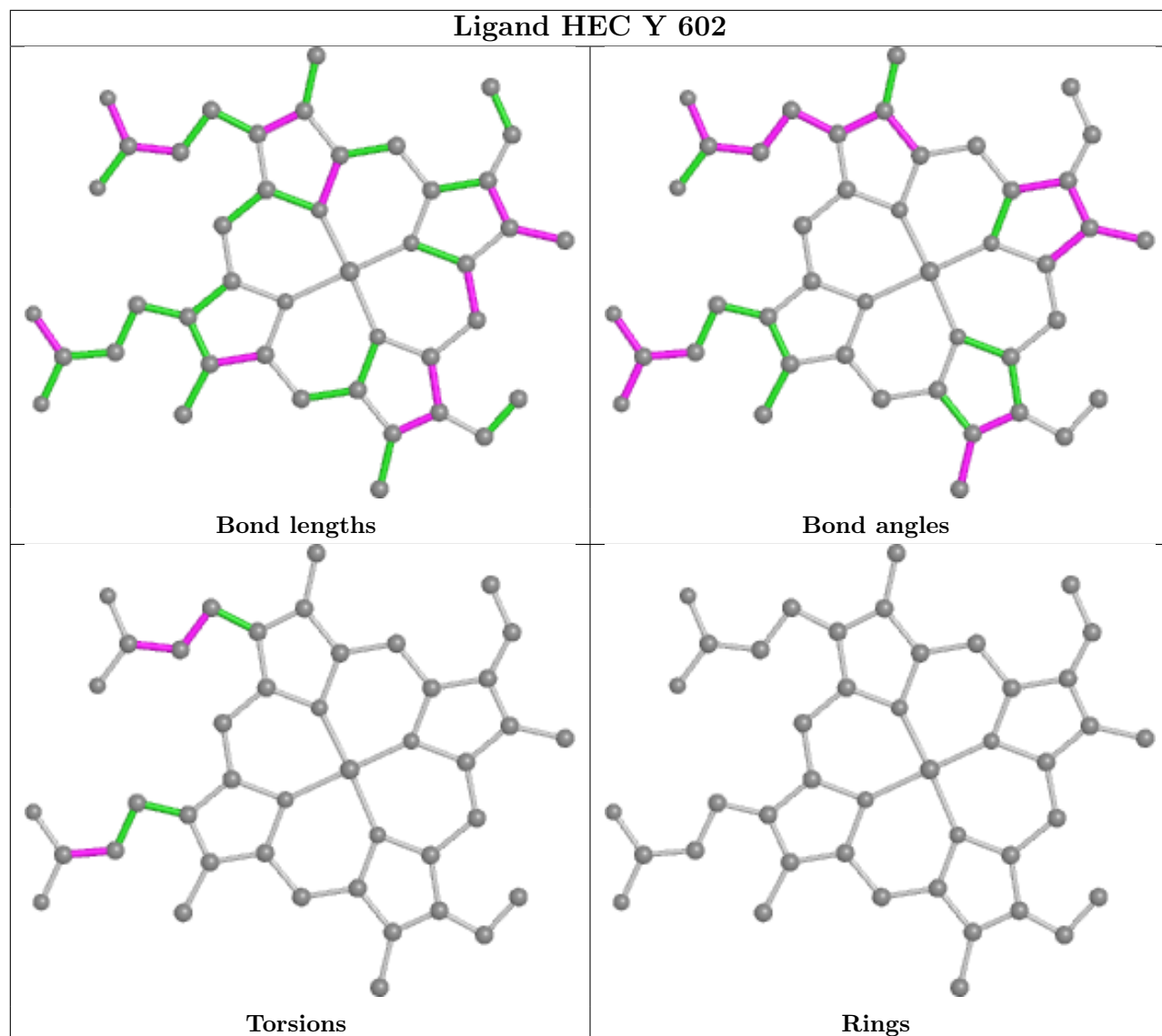


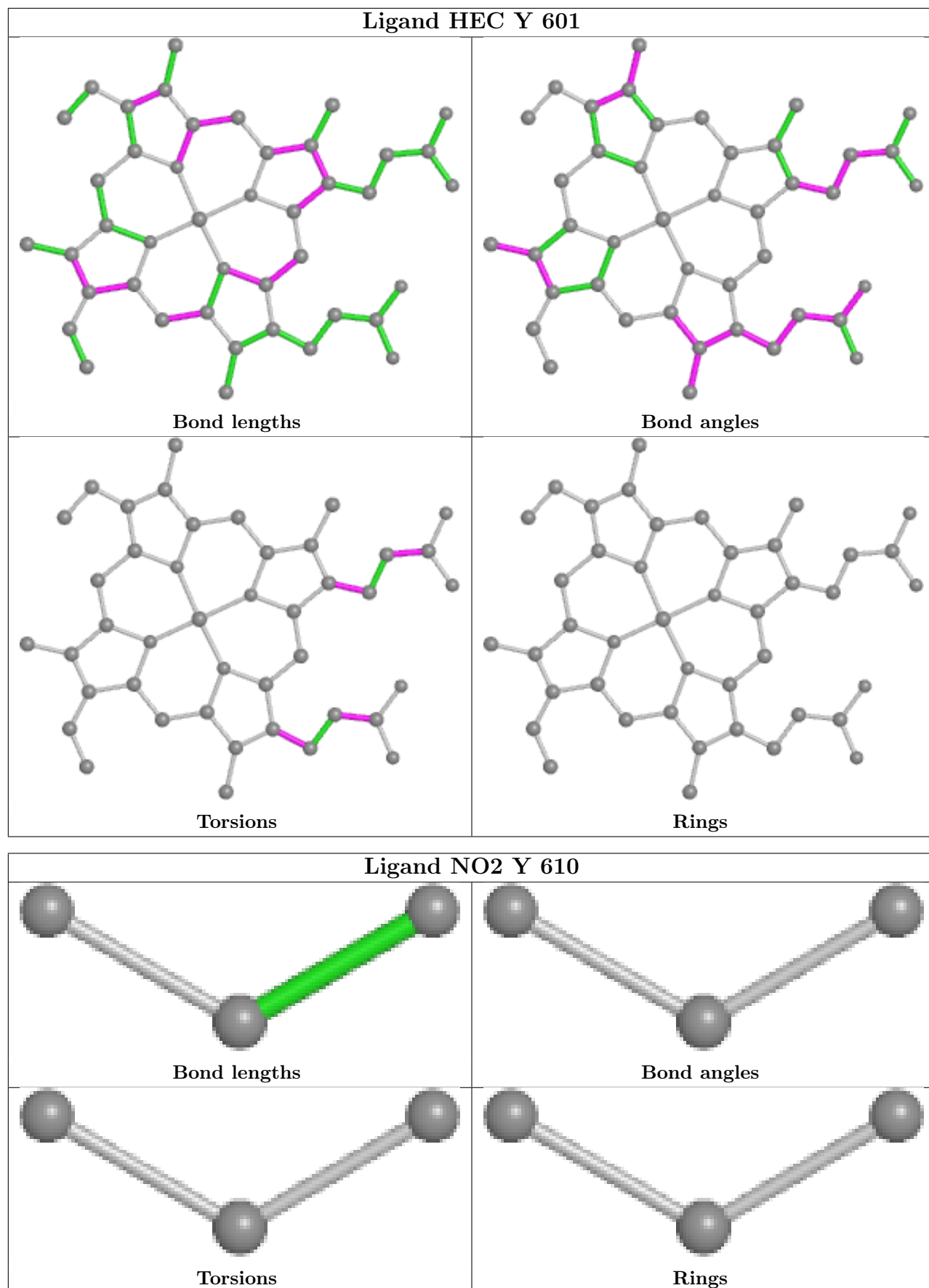












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Y	495/495 (100%)	-0.12	10 (2%) 65 71	11, 22, 50, 94	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	530	VAL	5.6
1	Y	528	MET	5.2
1	Y	400	ASP	3.9
1	Y	468	GLY	2.6
1	Y	532	GLN	2.6
1	Y	399	LYS	2.5
1	Y	79	ASP	2.5
1	Y	78	PRO	2.3
1	Y	401	GLY	2.3
1	Y	402	LYS	2.1

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](#)

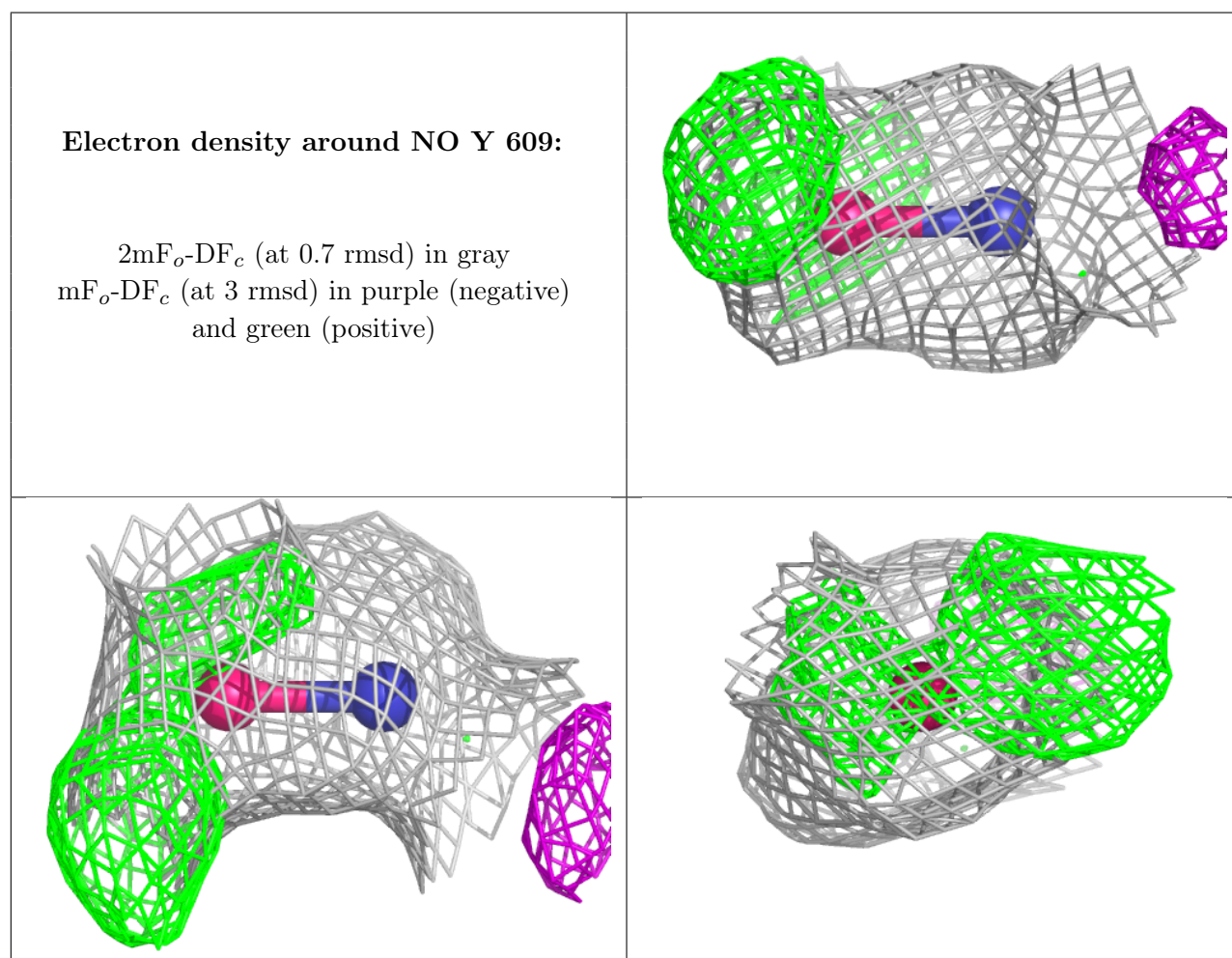
There are no monosaccharides in this entry.

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.

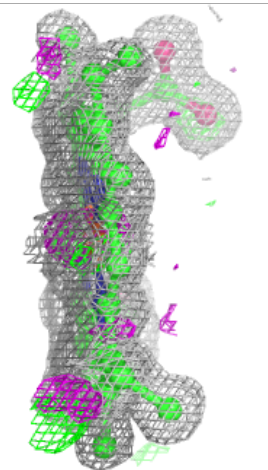
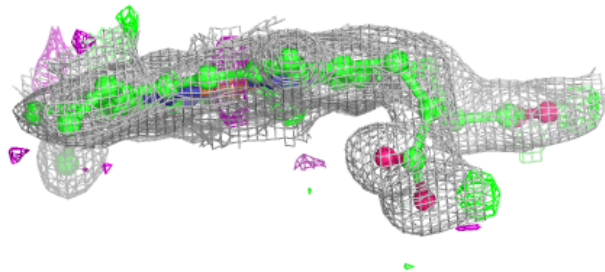
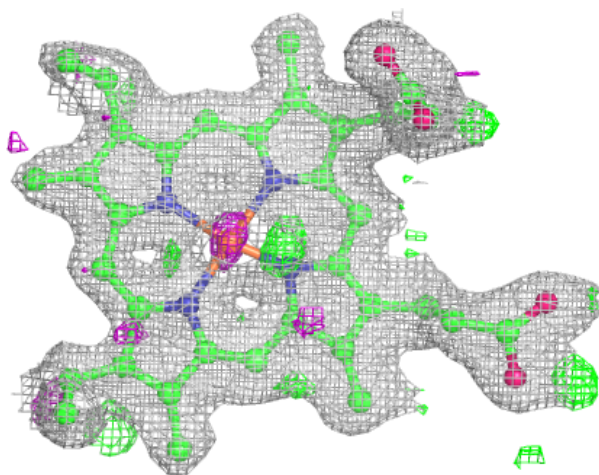
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NO	Y	609	2/2	0.93	0.15	14,14,14,15	2
2	HEC	Y	602	43/43	0.95	0.09	10,20,28,33	0
2	HEC	Y	603	43/43	0.96	0.10	20,28,39,46	0
2	HEC	Y	601	43/43	0.96	0.10	12,25,40,57	0
2	HEC	Y	605	43/43	0.97	0.07	15,21,28,35	0
4	NO2	Y	610	3/3	0.97	0.15	7,7,10,10	3
2	HEC	Y	606	43/43	0.98	0.07	11,14,16,18	0
2	HEC	Y	608	43/43	0.98	0.07	13,17,32,47	0
2	HEC	Y	607	43/43	0.99	0.07	12,13,17,21	0
2	HEC	Y	604	43/43	0.99	0.07	10,14,17,18	0
5	CA	Y	611	1/1	0.99	0.03	19,19,19,19	0

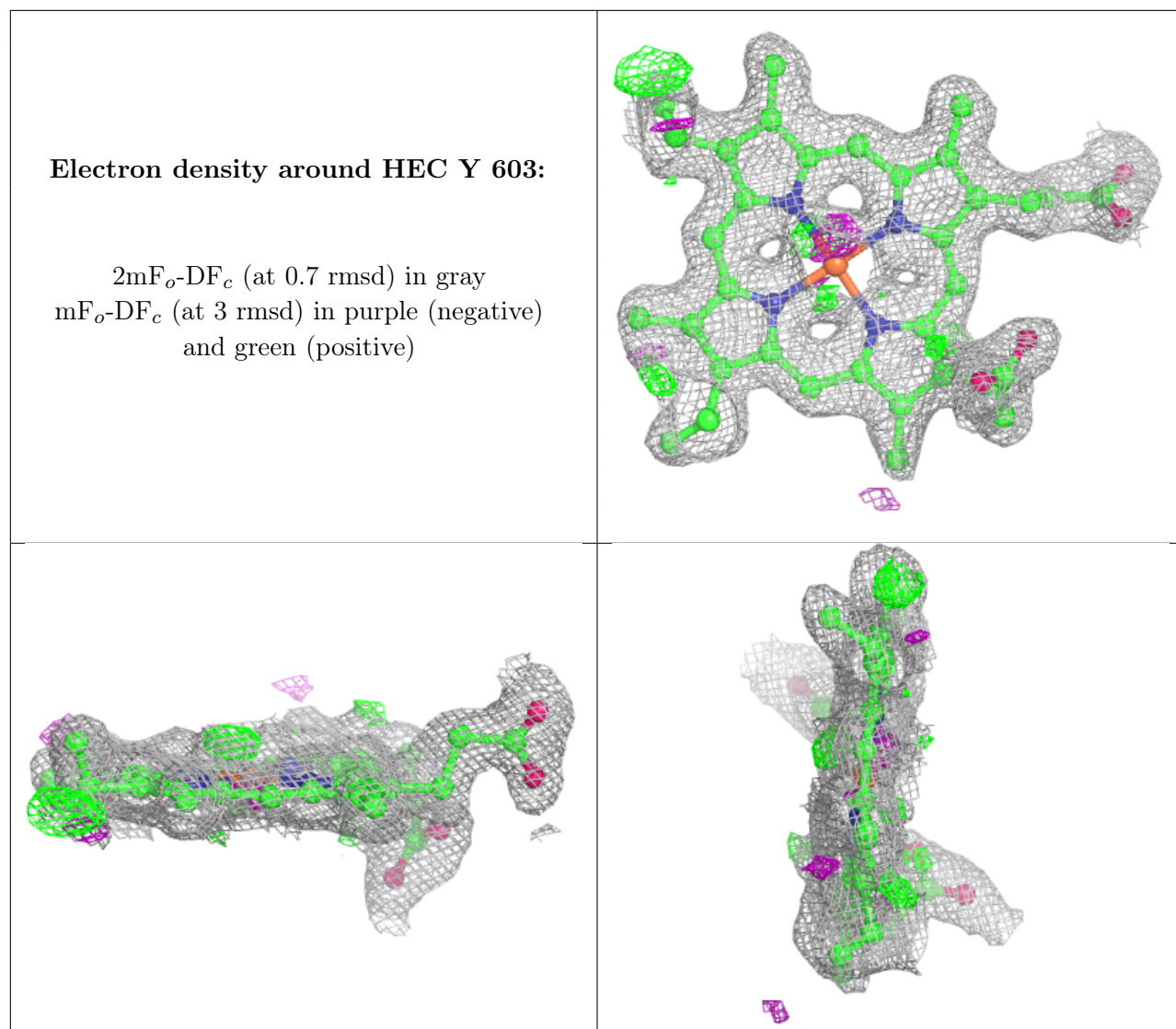
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around HEC Y 602:

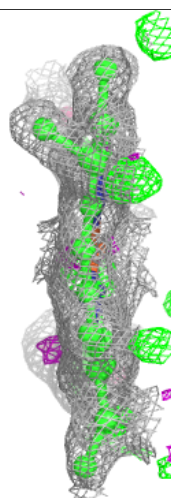
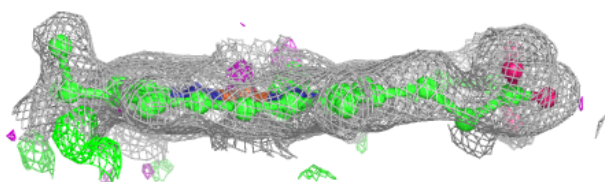
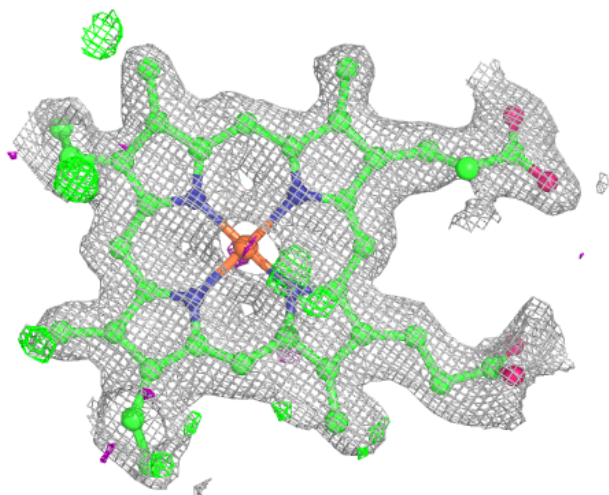
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





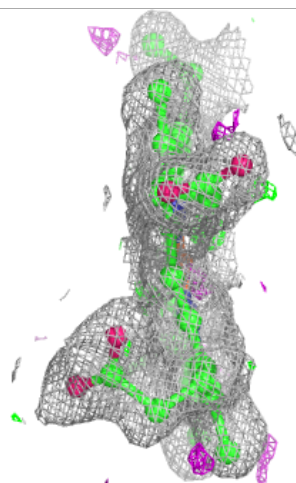
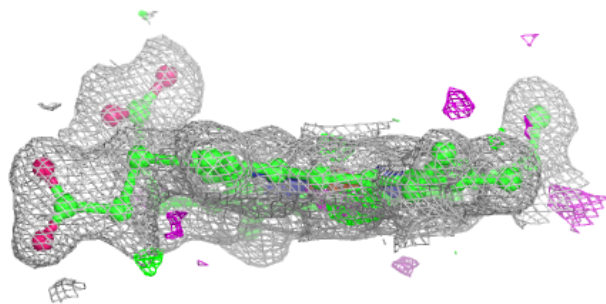
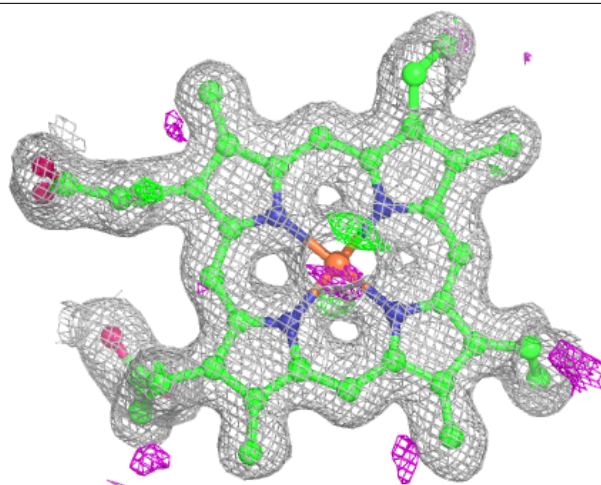
Electron density around HEC Y 601:

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



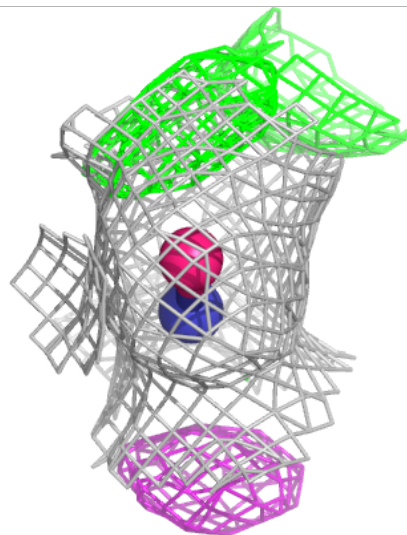
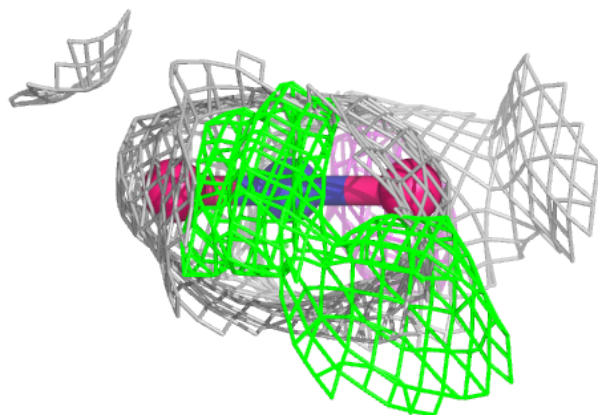
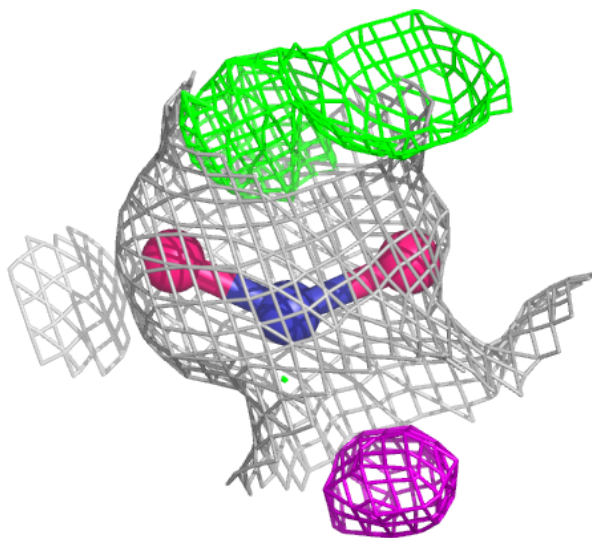
Electron density around HEC Y 605:

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



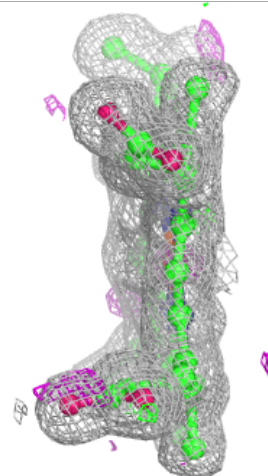
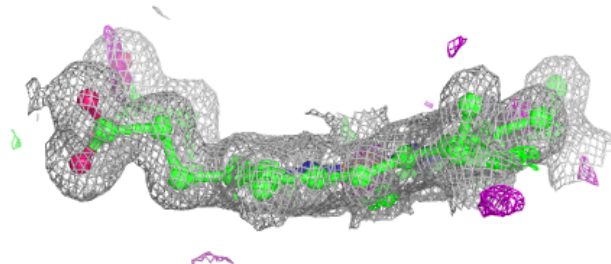
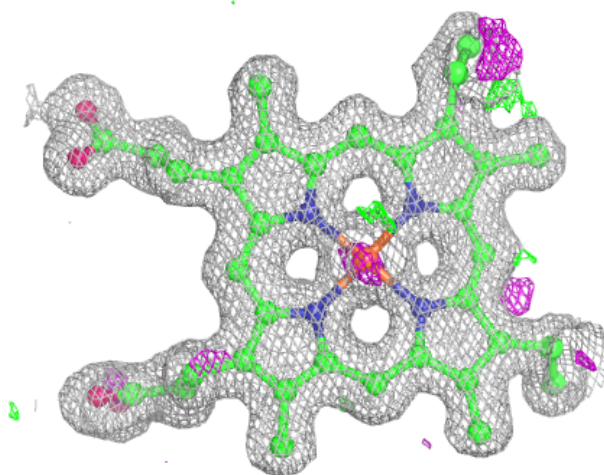
Electron density around NO2 Y 610:

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



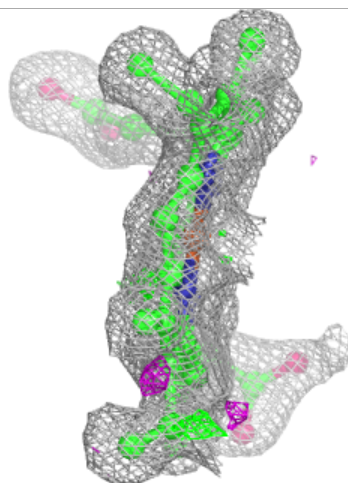
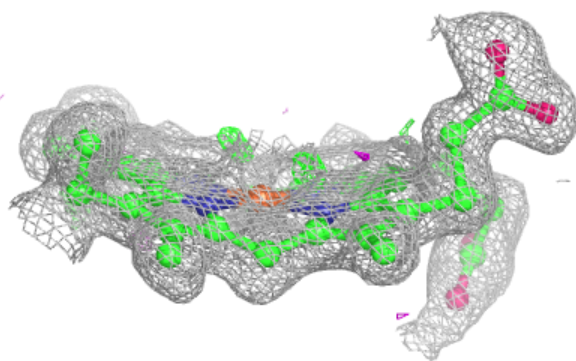
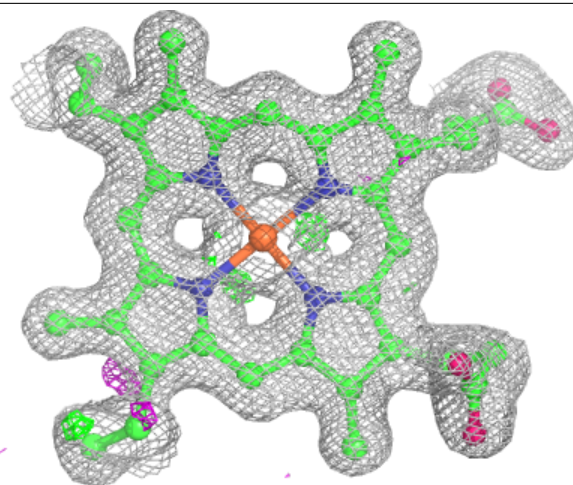
Electron density around HEC Y 606:

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



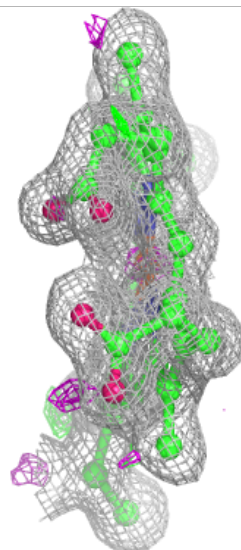
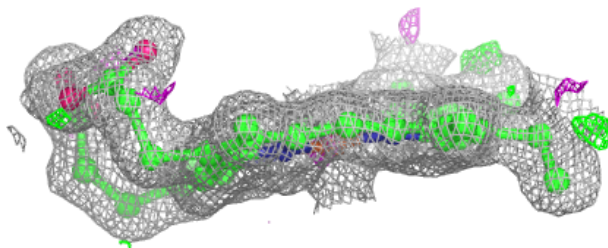
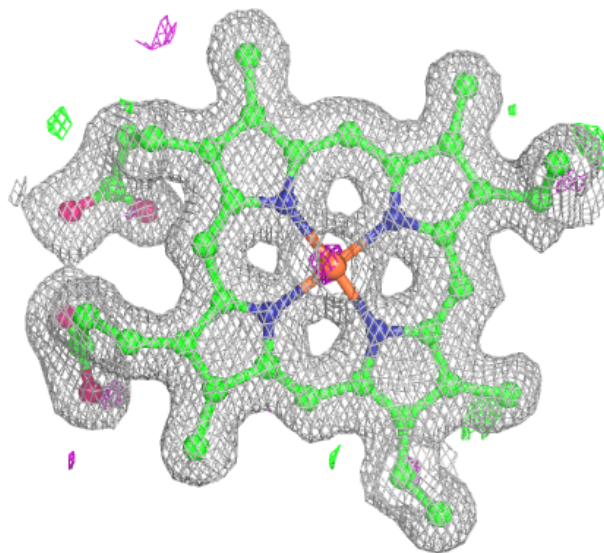
Electron density around HEC Y 608:

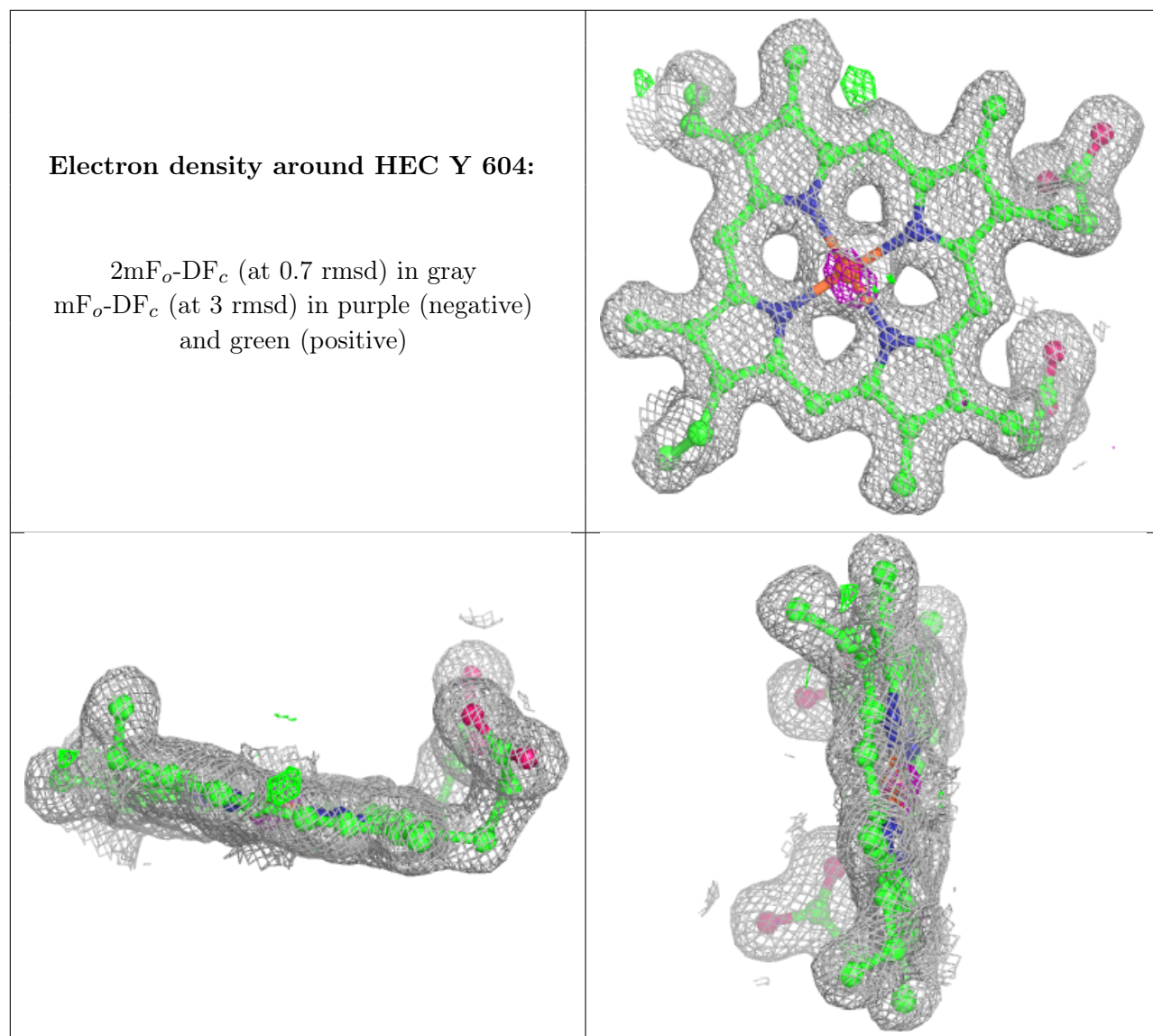
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

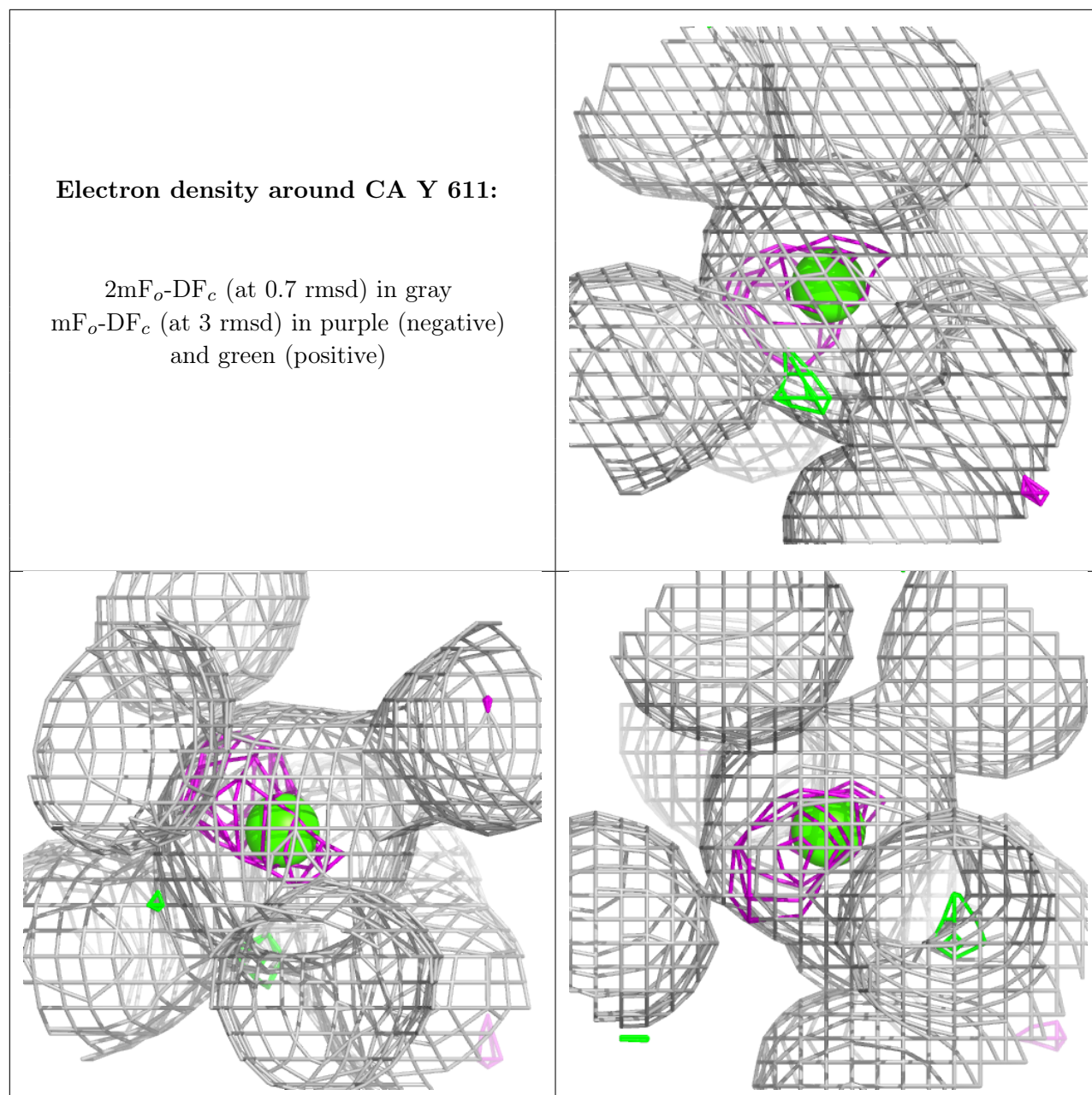


Electron density around HEC Y 607:

$2mF_o-DF_c$ (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.