



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2026 – 09:31 AM JST

PDB ID : 9ILT / pdb_00009ilt
Title : Crystal structure of alternative complex III from *Chloroflexus aurantiacus*
Authors : Xu, X.; Wu, W.
Deposited on : 2024-07-01
Resolution : 3.25 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:

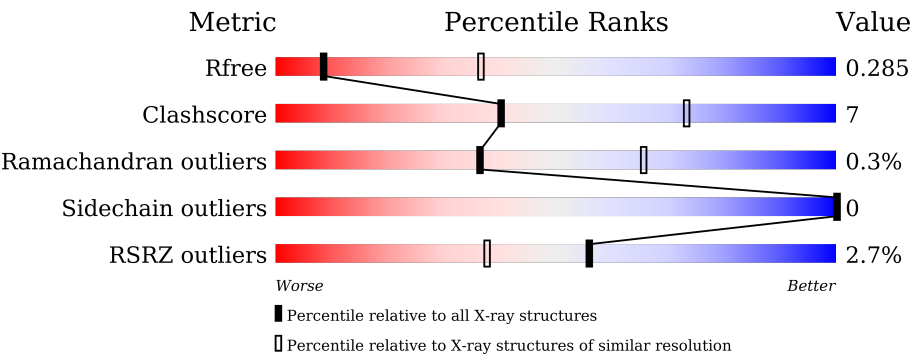
MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.25 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	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	A	219	
2	B	1029	
3	C	486	
4	D	179	
5	E	205	
6	F	411	

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Mol	Chain	Length	Quality of chain
7	G	112	4% 62% 10% 29%
8	I	37	3% 49% 24% 27%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	F3S	B	1104	-	-	X	-
9	HEC	A	302	X	-	-	-
9	HEC	A	305	X	-	-	-
9	HEC	E	301	X	-	-	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 19668 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 Cytochrome c7-like domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1763	1129	306	313	15			

- Molecule 2 is a protein called Fe-S-cluster-containing hydrogenase components 1-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	952	Total	C	N	O	S	0	0	0
			7356	4625	1304	1397	30			

- Molecule 3 is a protein called Polysulphide reductase NrfD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	449	Total	C	N	O	S	0	0	0
			3655	2476	576	586	17			

- Molecule 4 is a protein called Quinol:cytochrome c oxidoreductase membrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	175	Total	C	N	O	S	0	0	0
			1350	884	215	245	6			

- Molecule 5 is a protein called Cytochrome c domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	164	Total	C	N	O	S	0	0	0
			1292	819	220	246	7			

- Molecule 6 is a protein called Quinol:cytochrome c oxidoreductase quinone-binding subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	396	Total	C	N	O	S	0	0	0
			3120	2087	504	512	17			

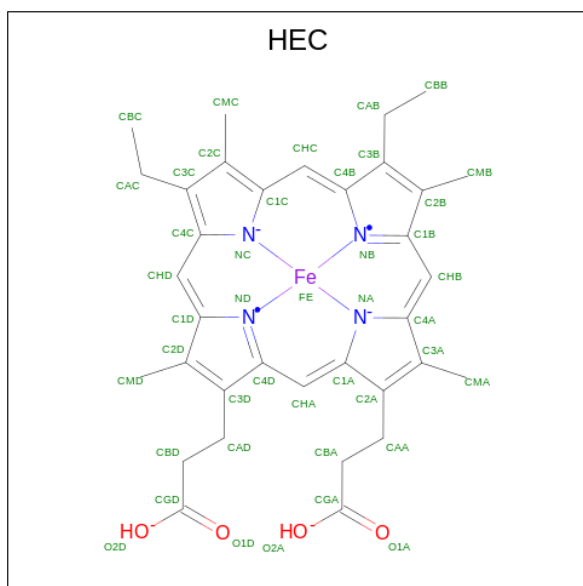
- Molecule 7 is a protein called ActG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	80	Total	C	N	O	S	0	0	0
			619	401	107	107	4			

- Molecule 8 is a protein called subunit I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	27	Total	C	N	O	S	0	0	0
			224	162	30	30	2			

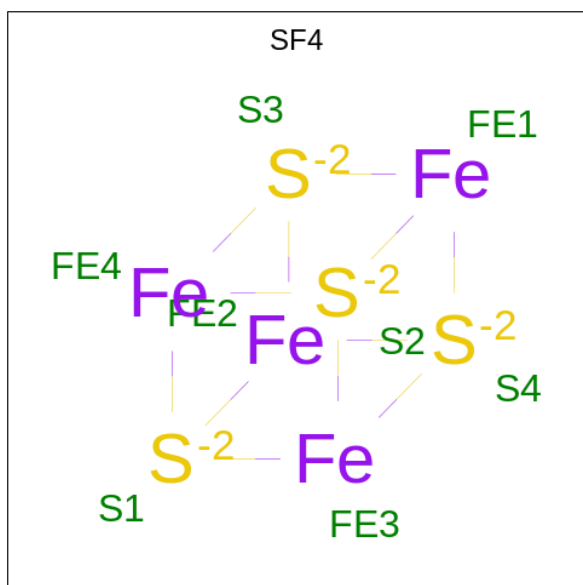
- Molecule 9 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



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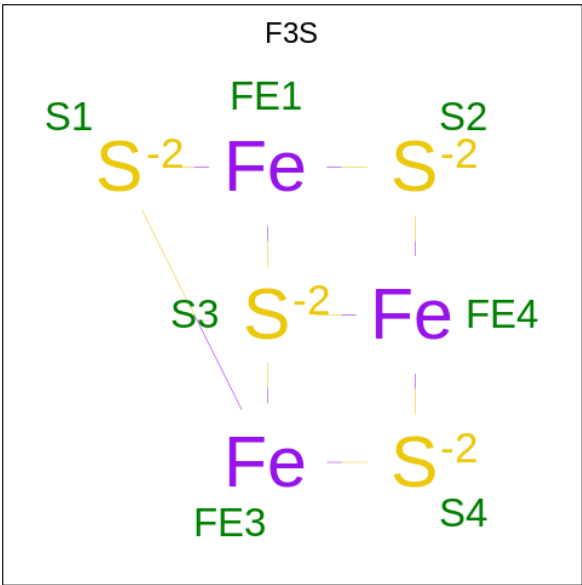
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
9	E	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 10 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	Fe	S	0	0
			8	4	4		
10	B	1	Total	Fe	S	0	0
			8	4	4		
10	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 11 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4).

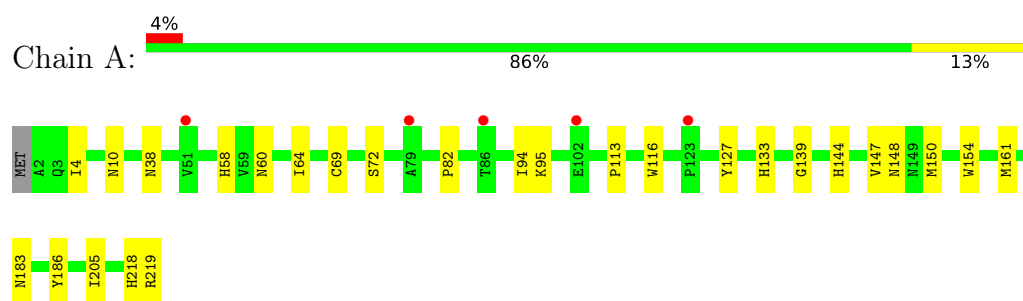


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	Fe	S	0	0
			7	3	4		

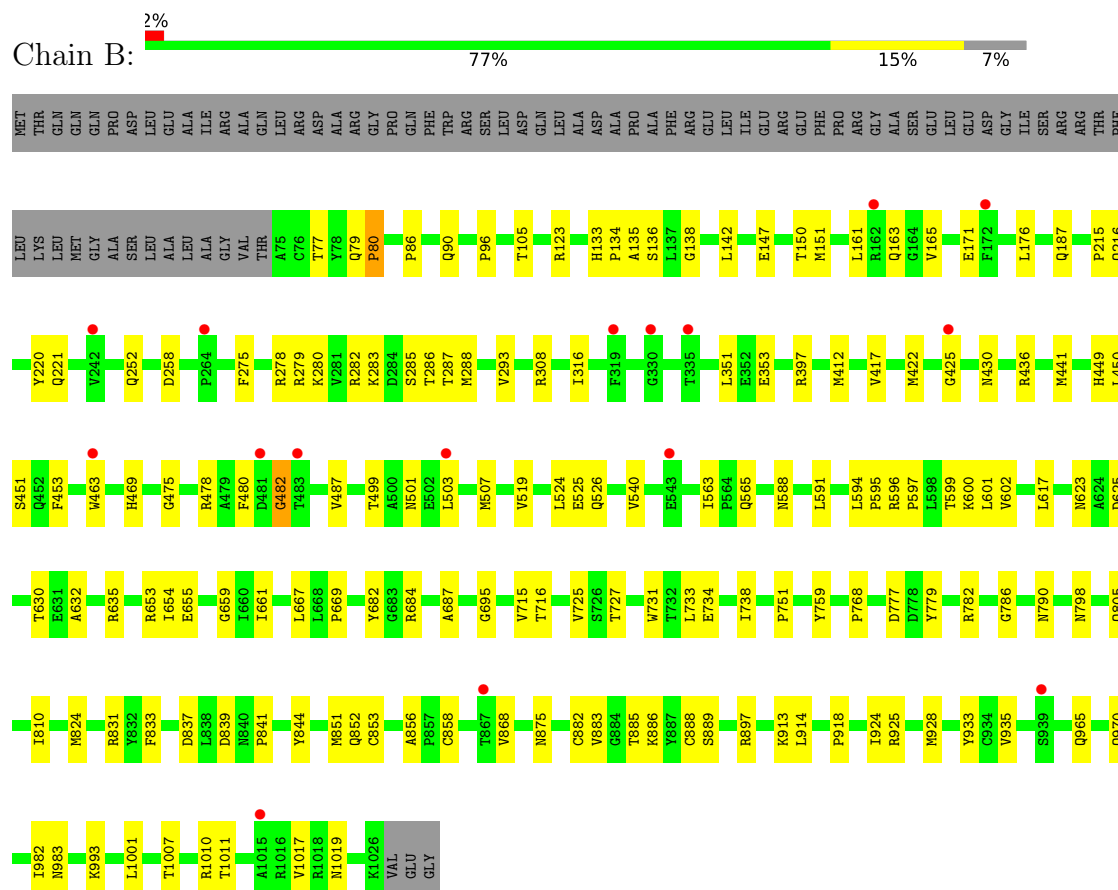
3 Residue-property plots [i](#)

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.

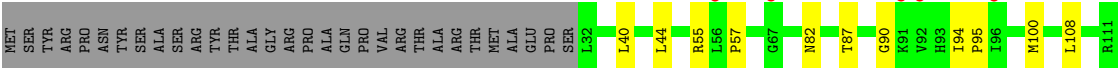
- Molecule 1: Cytochrome c7-like domain-containing protein



- Molecule 2: Fe-S-cluster-containing hydrogenase components 1-like protein



- Molecule 3: Polysulphide reductase NrfD



GLU

● Molecule 8: subunit I



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	142.02Å 153.06Å 173.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.30 – 3.25 40.30 – 3.25	Depositor EDS
% Data completeness (in resolution range)	89.8 (40.30-3.25) 89.8 (40.30-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 3.25Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158)	Depositor
R, R_{free}	0.249 , 0.286 0.251 , 0.285	Depositor DCC
R_{free} test set	2653 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å ²)	88.6	Xtriage
Anisotropy	0.380	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	19668	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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, F3S, SF4

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	0.09	0/1812	0.26	0/2472
2	B	0.12	0/7524	0.29	1/10257 (0.0%)
3	C	0.10	0/3787	0.25	0/5179
4	D	0.14	0/1388	0.33	0/1895
5	E	0.11	0/1327	0.32	0/1803
6	F	0.10	0/3218	0.27	0/4397
7	G	0.10	0/631	0.26	0/861
8	I	0.15	0/233	0.37	0/319
All	All	0.11	0/19920	0.28	1/27183 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	883	VAL	N-CA-C	-5.65	104.74	113.16

There are no chirality outliers.

There are no planarity outliers.

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	1763	0	1713	29	0
2	B	7356	0	7186	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	3655	0	3688	50	0
4	D	1350	0	1341	29	0
5	E	1292	0	1217	29	0
6	F	3120	0	3169	28	0
7	G	619	0	649	11	0
8	I	224	0	234	8	0
9	A	215	0	149	12	0
9	E	43	0	30	6	0
10	B	24	0	0	1	0
11	B	7	0	0	5	0
All	All	19668	0	19376	255	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 7.

All (255) 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)
3:C:200:ARG:HG2	4:D:143:GLN:NE2	1.78	0.99
4:D:158:ASP:HB3	4:D:161:ARG:HB2	1.57	0.86
6:F:56:THR:HG21	6:F:351:MET:HE1	1.60	0.81
3:C:200:ARG:CG	4:D:143:GLN:NE2	2.45	0.80
2:B:80:PRO:HD3	5:E:28:GLN:HE22	1.49	0.77
2:B:422:MET:HE1	2:B:441:MET:HE3	1.69	0.74
4:D:9:MET:HG3	4:D:135:VAL:HG21	1.70	0.73
3:C:200:ARG:HG2	4:D:143:GLN:HE21	1.54	0.72
3:C:222:ARG:HG2	4:D:49:ALA:HB2	1.72	0.71
3:C:277:ALA:HB2	3:C:390:MET:HG3	1.72	0.71
7:G:44:LEU:HD13	8:I:24:VAL:HG13	1.74	0.69
5:E:162:MET:HE1	9:E:301:HEC:C4B	2.23	0.69
2:B:425:GLY:O	2:B:430:ASN:ND2	2.28	0.66
2:B:450:LEU:HD11	2:B:503:LEU:HD22	1.77	0.66
2:B:868:VAL:HG11	4:D:84:LEU:HD13	1.77	0.66
2:B:617:LEU:HB3	2:B:715:VAL:HG21	1.78	0.65
2:B:563:ILE:O	2:B:565:GLN:NE2	2.30	0.64
1:A:4:ILE:HG21	3:C:207:LYS:HD3	1.80	0.64
1:A:94:ILE:HG13	5:E:123:ILE:HD11	1.80	0.64
5:E:136:ALA:O	5:E:182:ARG:NH2	2.32	0.63
2:B:499:THR:OG1	2:B:501:ASN:OD1	2.16	0.62
1:A:144:HIS:CE1	9:A:303:HEC:ND	2.67	0.61
2:B:782:ARG:O	2:B:983:ASN:ND2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:412:MET:HG2	2:B:417:VAL:HG21	1.82	0.61
3:C:196:THR:HG22	4:D:142:SER:HB3	1.84	0.60
2:B:258:ASP:HB2	2:B:316:ILE:HD13	1.82	0.60
2:B:805:GLN:HG3	2:B:810:ILE:HB	1.83	0.59
4:D:59:VAL:HG13	4:D:111:ALA:HB1	1.84	0.59
5:E:187:SER:HA	7:G:94:ILE:HB	1.84	0.59
1:A:127:TYR:OH	5:E:35:LYS:NZ	2.36	0.58
1:A:69:CYS:HB3	1:A:82:PRO:HG3	1.85	0.58
4:D:169:LEU:O	4:D:171:PRO:HD3	2.03	0.58
3:C:35:VAL:HG11	3:C:444:MET:HE3	1.86	0.57
4:D:120:ILE:HG23	4:D:125:LEU:HB3	1.86	0.57
2:B:283:LYS:HD3	2:B:751:PRO:HG3	1.86	0.57
3:C:258:VAL:HB	3:C:261:TRP:HB2	1.85	0.57
7:G:82:ASN:HA	7:G:95:PRO:HB3	1.87	0.57
3:C:284:LEU:HD13	3:C:383:SER:HB2	1.86	0.57
6:F:53:VAL:HG11	6:F:374:PRO:HB3	1.87	0.57
4:D:125:LEU:O	4:D:127:SER:N	2.37	0.56
2:B:684:ARG:HE	2:B:687:ALA:HB2	1.71	0.56
3:C:197:LEU:HD11	3:C:443:PRO:HD3	1.85	0.56
2:B:630:THR:HG23	2:B:632:ALA:H	1.71	0.56
2:B:882:CYS:SG	11:B:1104:F3S:S4	3.03	0.56
2:B:888:CYS:HG	11:B:1104:F3S:FE3	1.20	0.56
2:B:176:LEU:HD21	2:B:507:MET:HG2	1.87	0.56
3:C:126:MET:HE3	3:C:285:LEU:HD12	1.88	0.56
3:C:356:LEU:HD12	3:C:393:GLU:HA	1.88	0.56
6:F:137:ILE:HG12	6:F:215:PRO:HB2	1.89	0.55
9:A:303:HEC:HBC3	9:A:303:HEC:HHD	1.89	0.55
2:B:288:MET:HE2	2:B:1019:ASN:HB2	1.89	0.55
2:B:882:CYS:HG	11:B:1104:F3S:FE4	1.22	0.55
1:A:133:HIS:HE1	9:A:302:HEC:NA	2.03	0.55
2:B:993:LYS:NZ	2:B:1010:ARG:O	2.39	0.54
2:B:286:THR:HG23	2:B:287:THR:HG23	1.89	0.54
2:B:422:MET:HB2	2:B:449:HIS:HD2	1.73	0.54
2:B:596:ARG:NH2	2:B:682:TYR:OH	2.39	0.54
4:D:96:TRP:CD1	4:D:97:PRO:HD3	2.43	0.54
7:G:40:LEU:HD13	8:I:21:THR:HA	1.88	0.54
2:B:123:ARG:NH1	2:B:914:LEU:O	2.40	0.54
1:A:60:ASN:ND2	1:A:148:ASN:O	2.41	0.54
2:B:451:SER:C	2:B:453:PHE:H	2.16	0.54
5:E:116:MET:HE3	5:E:120:ARG:HD2	1.90	0.54
6:F:90:LEU:HD13	6:F:160:TRP:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:116:PRO:HG2	6:F:122:ASN:HA	1.90	0.53
7:G:55:ARG:NH1	8:I:37:TRP:O	2.41	0.53
4:D:18:LEU:HD11	4:D:148:LEU:HB2	1.91	0.53
4:D:96:TRP:CG	4:D:97:PRO:HD3	2.43	0.53
2:B:853:CYS:HB3	2:B:1007:THR:HB	1.91	0.52
1:A:116:TRP:CD1	9:A:304:HEC:HBD2	2.45	0.52
9:A:304:HEC:HBC3	9:A:304:HEC:HHD	1.91	0.52
5:E:107:HIS:HE1	9:E:301:HEC:C4D	2.13	0.52
5:E:149:VAL:HG11	5:E:161:SER:HB2	1.91	0.52
1:A:139:GLY:HA2	1:A:180:GLU:HB2	1.91	0.52
2:B:133:HIS:HD2	2:B:540:VAL:HG12	1.75	0.52
2:B:886:LYS:NZ	3:C:141:HIS:O	2.39	0.52
6:F:48:ILE:HD11	6:F:117:LEU:HD21	1.92	0.52
3:C:201:ALA:O	3:C:203:ASN:N	2.43	0.52
3:C:221:ALA:C	3:C:223:HIS:H	2.17	0.52
3:C:226:ARG:HG2	4:D:53:THR:HB	1.91	0.52
1:A:113:PRO:HB3	5:E:49:ARG:HH11	1.74	0.52
6:F:245:VAL:HG22	6:F:248:ALA:HB2	1.92	0.51
2:B:852:GLN:HG3	2:B:933:TYR:CZ	2.45	0.51
1:A:205:ILE:HG23	9:A:302:HEC:HBD1	1.92	0.51
1:A:168:HIS:HE1	9:A:302:HEC:NA	2.08	0.51
2:B:163:GLN:H	2:B:165:VAL:HG12	1.76	0.51
1:A:133:HIS:HE1	9:A:302:HEC:C4A	2.23	0.51
2:B:654:ILE:HB	2:B:661:ILE:HG22	1.91	0.51
3:C:207:LYS:C	3:C:209:LEU:H	2.19	0.51
5:E:106:CYS:HA	5:E:117:VAL:HB	1.93	0.51
2:B:171:GLU:HG2	2:B:463:TRP:HH2	1.75	0.50
6:F:141:VAL:O	6:F:145:SER:OG	2.29	0.50
3:C:252:ASP:OD1	3:C:253:PHE:N	2.44	0.50
3:C:200:ARG:HH11	4:D:143:GLN:HE21	1.57	0.50
8:I:24:VAL:O	8:I:28:LEU:HG	2.11	0.50
2:B:187:GLN:HB2	2:B:216:GLN:HG2	1.93	0.50
4:D:82:TYR:HD2	4:D:84:LEU:HG	1.77	0.50
2:B:599:THR:HG22	2:B:601:LEU:HG	1.93	0.50
5:E:149:VAL:HG12	5:E:162:MET:H	1.76	0.50
2:B:885:THR:OG1	11:B:1104:F3S:S1	2.69	0.49
3:C:147:LEU:HD11	5:E:27:HIS:CE1	2.47	0.49
3:C:57:MET:HB2	3:C:429:GLY:HA3	1.93	0.49
2:B:161:LEU:HA	2:B:165:VAL:O	2.11	0.49
6:F:108:TYR:O	6:F:109:LYS:HB2	2.12	0.49
2:B:731:TRP:CD1	2:B:831:ARG:HH12	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:786:GLY:HA3	2:B:982:ILE:HD11	1.94	0.49
1:A:4:ILE:HD12	3:C:207:LYS:HB3	1.95	0.49
4:D:13:PRO:HB3	4:D:172:MET:SD	2.52	0.49
2:B:150:THR:OG1	2:B:588:ASN:ND2	2.43	0.48
4:D:11:GLU:HG2	4:D:147:PHE:CZ	2.49	0.48
5:E:181:ILE:HD11	9:E:301:HEC:HMB2	1.96	0.48
7:G:87:THR:HG23	7:G:90:GLY:H	1.78	0.48
2:B:351:LEU:C	2:B:353:GLU:H	2.22	0.48
1:A:218:HIS:CE1	9:A:301:HEC:ND	2.82	0.48
2:B:77:THR:O	2:B:79:GLN:N	2.40	0.47
2:B:524:LEU:O	2:B:525:GLU:HG2	2.13	0.47
1:A:168:HIS:HE1	9:A:302:HEC:C1A	2.28	0.47
3:C:288:PRO:HA	3:C:291:THR:HG22	1.96	0.47
2:B:594:LEU:HD21	2:B:798:ASN:HB3	1.96	0.47
2:B:918:PRO:HA	5:E:35:LYS:HD2	1.95	0.47
1:A:219:ARG:HD2	2:B:935:VAL:HG13	1.97	0.47
2:B:623:ASN:C	2:B:625:ASP:H	2.23	0.47
2:B:733:LEU:HA	3:C:408:PRO:HG2	1.96	0.47
2:B:777:ASP:HB3	2:B:779:TYR:CZ	2.49	0.47
3:C:110:LEU:HD11	3:C:236:GLY:HA2	1.97	0.47
5:E:182:ARG:NH1	5:E:185:GLN:OE1	2.47	0.47
6:F:251:PHE:HE1	6:F:394:LEU:HD22	1.79	0.47
6:F:70:LEU:HD11	6:F:192:GLY:HA2	1.97	0.46
2:B:151:MET:HB2	2:B:469:HIS:CE1	2.50	0.46
2:B:653:ARG:HB3	2:B:716:THR:HB	1.97	0.46
4:D:79:LEU:HD22	4:D:91:LEU:HA	1.98	0.46
7:G:55:ARG:HG3	8:I:36:TYR:CE1	2.50	0.46
3:C:99:HIS:CE1	3:C:271:VAL:HG13	2.50	0.46
3:C:123:ALA:O	3:C:127:THR:HG23	2.15	0.46
2:B:135:ALA:HB2	2:B:480:PHE:CE1	2.51	0.46
2:B:600:LYS:HA	2:B:600:LYS:HD3	1.78	0.46
6:F:152:ARG:NH1	6:F:208:ASP:OD1	2.49	0.46
3:C:21:PRO:HG2	3:C:23:GLU:HG2	1.97	0.46
4:D:18:LEU:HD22	4:D:146:PHE:HB3	1.97	0.46
4:D:119:MET:HE3	4:D:119:MET:HB3	1.85	0.46
2:B:451:SER:HB3	2:B:453:PHE:O	2.17	0.45
3:C:240:PRO:HB2	4:D:104:PHE:HZ	1.81	0.45
3:C:408:PRO:HA	3:C:411:TRP:CE2	2.51	0.45
3:C:255:ILE:HD12	6:F:287:SER:HB2	1.97	0.45
5:E:68:GLU:O	5:E:72:THR:N	2.41	0.45
5:E:69:PHE:HE1	5:E:80:VAL:HG21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:831:ARG:HA	2:B:844:TYR:O	2.16	0.45
2:B:837:ASP:C	2:B:839:ASP:H	2.25	0.45
5:E:87:VAL:HG21	7:G:108:LEU:HD13	1.99	0.45
1:A:150:MET:HE2	1:A:154:TRP:CE2	2.52	0.45
2:B:133:HIS:CD2	2:B:540:VAL:HG12	2.51	0.45
3:C:267:PRO:HB2	3:C:268:PRO:HD3	1.98	0.45
6:F:221:ILE:HG21	6:F:281:GLN:HB2	1.99	0.44
6:F:319:LEU:HB3	6:F:320:PRO:HD3	1.99	0.44
2:B:105:THR:HB	2:B:487:VAL:HG22	1.98	0.44
5:E:93:LEU:HD23	7:G:100:MET:HE1	2.00	0.44
1:A:168:HIS:HE1	9:A:302:HEC:CHA	2.30	0.44
5:E:99:TYR:O	5:E:104:ALA:N	2.49	0.44
2:B:889:SER:HB2	2:B:928:MET:HE3	1.99	0.44
2:B:913:LYS:HG2	5:E:34:GLN:HB3	2.00	0.44
2:B:924:ILE:HG12	2:B:925:ARG:H	1.83	0.44
6:F:235:LEU:HB3	6:F:267:ILE:HG12	1.99	0.44
2:B:79:GLN:HG2	2:B:80:PRO:HD2	1.99	0.44
2:B:147:GLU:HG3	2:B:469:HIS:CE1	2.52	0.44
2:B:617:LEU:HD13	2:B:715:VAL:HG11	1.99	0.44
3:C:101:GLY:HA2	3:C:123:ALA:HB1	2.00	0.44
2:B:478:ARG:HH21	2:B:482:GLY:HA3	1.82	0.44
3:C:251:LEU:O	3:C:255:ILE:HG12	2.18	0.44
8:I:11:VAL:O	8:I:14:VAL:HG22	2.18	0.44
2:B:280:LYS:HG2	2:B:790:ASN:HD22	1.83	0.43
2:B:875:ASN:ND2	10:B:1103:SF4:S3	2.92	0.43
3:C:178:TYR:HB2	3:C:245:VAL:HG21	2.00	0.43
3:C:448:PHE:HA	3:C:451:ARG:HG2	1.99	0.43
2:B:288:MET:HE1	2:B:1017:VAL:O	2.19	0.43
2:B:682:TYR:HB3	2:B:695:GLY:HA3	1.99	0.43
3:C:121:ARG:HD3	3:C:186:TRP:HE1	1.82	0.43
5:E:38:THR:O	5:E:51:SER:OG	2.36	0.43
2:B:422:MET:HB2	2:B:449:HIS:CD2	2.51	0.43
3:C:163:GLN:C	3:C:165:ARG:H	2.25	0.43
3:C:188:VAL:O	3:C:227:TYR:OH	2.31	0.43
2:B:738:ILE:HA	2:B:1001:LEU:HD21	2.00	0.43
5:E:107:HIS:CD2	9:E:301:HEC:NB	2.86	0.43
2:B:275:PHE:CE2	2:B:279:ARG:HD2	2.53	0.43
3:C:24:THR:H	3:C:27:SER:HB2	1.82	0.43
2:B:965:GLN:HB2	2:B:970:GLN:HE21	1.83	0.43
2:B:142:LEU:HD12	2:B:591:LEU:HD22	2.01	0.43
3:C:42:LYS:HE2	3:C:42:LYS:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:239:THR:HB	3:C:240:PRO:HD3	2.00	0.43
6:F:55:MET:HE1	6:F:157:PHE:CE1	2.53	0.43
6:F:101:ALA:HA	6:F:104:TYR:CE2	2.53	0.43
2:B:655:GLU:HA	2:B:659:GLY:O	2.19	0.42
2:B:888:CYS:SG	11:B:1104:F3S:S4	3.14	0.42
3:C:245:VAL:O	3:C:249:ILE:HG12	2.19	0.42
4:D:158:ASP:HB2	4:D:162:THR:OG1	2.19	0.42
2:B:597:PRO:C	2:B:599:THR:H	2.27	0.42
2:B:759:TYR:CD2	2:B:768:PRO:HD3	2.54	0.42
6:F:46:SER:OG	6:F:370:ASP:OD1	2.29	0.42
1:A:58:HIS:HB3	1:A:64:ILE:HD12	2.01	0.42
3:C:102:THR:OG1	3:C:178:TYR:OH	2.27	0.42
2:B:282:ARG:H	2:B:285:SER:HB2	1.84	0.42
1:A:161:MET:HG3	9:A:301:HEC:C1D	2.50	0.42
3:C:198:ARG:HB3	3:C:210:TYR:HB2	2.00	0.42
6:F:68:GLN:HE22	6:F:80:ARG:NE	2.17	0.42
2:B:221:GLN:HG2	2:B:397:ARG:HH21	1.85	0.42
2:B:449:HIS:ND1	2:B:451:SER:HB2	2.35	0.42
3:C:201:ALA:HB3	3:C:207:LYS:HG3	2.02	0.42
6:F:378:ILE:O	6:F:382:ILE:HG12	2.20	0.42
2:B:280:LYS:HG2	2:B:790:ASN:ND2	2.35	0.42
2:B:436:ARG:HA	2:B:436:ARG:HD2	1.86	0.42
2:B:602:VAL:HG22	2:B:725:VAL:HG23	2.02	0.42
1:A:95:LYS:HD3	1:A:95:LYS:HA	1.93	0.41
3:C:103:LEU:HD12	3:C:107:ILE:HD12	2.00	0.41
2:B:595:PRO:HG3	2:B:727:THR:HG21	2.02	0.41
2:B:635:ARG:NH2	2:B:734:GLU:HB3	2.36	0.41
6:F:108:TYR:C	6:F:110:ALA:H	2.27	0.41
1:A:147:VAL:HA	1:A:150:MET:SD	2.60	0.41
2:B:136:SER:O	2:B:138:GLY:N	2.53	0.41
2:B:733:LEU:HD23	2:B:733:LEU:H	1.85	0.41
2:B:853:CYS:HB2	2:B:856:ALA:HA	2.03	0.41
2:B:858:CYS:SG	2:B:897:ARG:NH1	2.93	0.41
2:B:187:GLN:HB2	2:B:216:GLN:CG	2.51	0.41
2:B:86:PRO:O	5:E:49:ARG:HD3	2.21	0.41
2:B:475:GLY:HA2	2:B:519:VAL:HG11	2.02	0.41
5:E:106:CYS:HB3	9:E:301:HEC:CMC	2.51	0.41
6:F:235:LEU:HD23	6:F:235:LEU:HA	1.96	0.41
1:A:72:SER:HB2	2:B:96:PRO:HD2	2.02	0.41
2:B:759:TYR:CZ	2:B:768:PRO:HG3	2.56	0.41
3:C:446:ASN:ND2	3:C:449:GLU:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:GLN:HE21	2:B:90:GLN:HB3	1.73	0.41
2:B:669:PRO:HB2	2:B:841:PRO:HG3	2.02	0.41
2:B:824:MET:HE3	2:B:824:MET:HB3	1.92	0.41
2:B:851:MET:HA	2:B:1011:THR:HB	2.03	0.41
1:A:94:ILE:HD11	5:E:117:VAL:HG13	2.03	0.41
2:B:293:VAL:HG13	2:B:308:ARG:HG3	2.02	0.41
8:I:23:MET:O	8:I:27:LEU:HG	2.21	0.41
1:A:38:ASN:HB2	7:G:57:PRO:HD2	2.03	0.40
2:B:252:GLN:CD	2:B:278:ARG:HH22	2.28	0.40
4:D:9:MET:CE	4:D:132:VAL:HG13	2.50	0.40
1:A:183:ASN:O	1:A:186:TYR:HB3	2.21	0.40
2:B:187:GLN:HB3	2:B:215:PRO:HD2	2.03	0.40
5:E:107:HIS:HD1	9:E:301:HEC:C4C	2.34	0.40
6:F:90:LEU:N	6:F:91:PRO:HD2	2.37	0.40
6:F:375:ILE:HA	6:F:378:ILE:HG22	2.02	0.40
1:A:161:MET:HE1	3:C:160:MET:HG2	2.03	0.40
2:B:133:HIS:ND1	2:B:134:PRO:O	2.55	0.40
6:F:101:ALA:HA	6:F:104:TYR:CZ	2.56	0.40
6:F:352:ALA:O	6:F:357:PRO:HD3	2.22	0.40
1:A:10:ASN:ND2	4:D:129:TYR:O	2.50	0.40
2:B:524:LEU:C	2:B:526:GLN:H	2.28	0.40
2:B:667:LEU:HD23	2:B:667:LEU:HA	1.89	0.40
4:D:12:PHE:HZ	4:D:169:LEU:HB3	1.85	0.40
4:D:35:ALA:HB3	4:D:44:VAL:HG11	2.02	0.40
5:E:83:MET:HE3	5:E:175:TRP:HB3	2.04	0.40
6:F:27:ILE:O	6:F:31:VAL:HG12	2.22	0.40
7:G:40:LEU:HD11	8:I:24:VAL:HG11	2.03	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	A	216/219 (99%)	205 (95%)	11 (5%)	0	100	100
2	B	950/1029 (92%)	882 (93%)	64 (7%)	4 (0%)	30	59
3	C	447/486 (92%)	425 (95%)	20 (4%)	2 (0%)	30	59
4	D	173/179 (97%)	160 (92%)	12 (7%)	1 (1%)	21	51
5	E	162/205 (79%)	151 (93%)	11 (7%)	0	100	100
6	F	394/411 (96%)	376 (95%)	17 (4%)	1 (0%)	36	66
7	G	78/112 (70%)	75 (96%)	3 (4%)	0	100	100
8	I	25/37 (68%)	23 (92%)	2 (8%)	0	100	100
All	All	2445/2678 (91%)	2297 (94%)	140 (6%)	8 (0%)	36	66

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	833	PHE
3	C	202	LYS
4	D	171	PRO
2	B	220	TYR
6	F	395	LEU
2	B	482	GLY
3	C	219	GLY
2	B	80	PRO

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	198/199 (100%)	198 (100%)	0	100	100
2	B	769/830 (93%)	769 (100%)	0	100	100
3	C	382/405 (94%)	382 (100%)	0	100	100
4	D	143/147 (97%)	143 (100%)	0	100	100
5	E	135/171 (79%)	135 (100%)	0	100	100
6	F	317/330 (96%)	317 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	68/95 (72%)	68 (100%)	0	100	100
8	I	23/32 (72%)	23 (100%)	0	100	100
All	All	2035/2209 (92%)	2035 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN
1	A	168	HIS
2	B	90	GLN
2	B	206	GLN
2	B	375	HIS
2	B	386	GLN
2	B	452	GLN
2	B	464	HIS
2	B	588	ASN
2	B	790	ASN
2	B	808	ASN
3	C	257	GLN
4	D	143	GLN
5	E	28	GLN
6	F	404	GLN
7	G	93	HIS

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

10 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
9	HEC	E	301	5	50,50,50	1.88	5 (10%)	68,82,82	1.45	5 (7%)
9	HEC	A	303	1	50,50,50	1.83	5 (10%)	68,82,82	1.49	9 (13%)
10	SF4	B	1102	2	0,12,12	-	-	-	-	-
9	HEC	A	305	1	50,50,50	1.82	5 (10%)	68,82,82	1.46	8 (11%)
9	HEC	A	304	1	50,50,50	1.80	5 (10%)	68,82,82	1.46	8 (11%)
9	HEC	A	302	1	50,50,50	1.81	5 (10%)	68,82,82	1.40	6 (8%)
10	SF4	B	1103	2	0,12,12	-	-	-	-	-
11	F3S	B	1104	2	0,9,9	-	-	-	-	-
9	HEC	A	301	1	50,50,50	1.85	6 (12%)	68,82,82	1.46	8 (11%)
10	SF4	B	1101	2	0,12,12	-	-	-	-	-

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
9	HEC	E	301	5	1/1/3/7	2/14/54/54	-
9	HEC	A	303	1	-	4/14/54/54	-
10	SF4	B	1102	2	-	-	0/6/5/5
9	HEC	A	305	1	1/1/3/7	1/14/54/54	-
9	HEC	A	304	1	-	5/14/54/54	-
9	HEC	A	302	1	1/1/3/7	5/14/54/54	-
10	SF4	B	1103	2	-	-	0/6/5/5
11	F3S	B	1104	2	-	-	0/3/3/3
9	HEC	A	301	1	-	2/14/54/54	-
10	SF4	B	1101	2	-	-	0/6/5/5

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	305	HEC	C3D-C2D	8.11	1.54	1.36
9	A	304	HEC	C3D-C2D	8.06	1.53	1.36
9	A	303	HEC	C3D-C2D	8.05	1.53	1.36
9	A	301	HEC	C3D-C2D	8.04	1.53	1.36
9	E	301	HEC	C3D-C2D	8.04	1.53	1.36
9	A	302	HEC	C3D-C2D	7.99	1.53	1.36
9	E	301	HEC	FE-ND	5.50	2.11	1.94
9	A	305	HEC	FE-ND	4.92	2.10	1.94
9	A	303	HEC	FE-NB	4.85	2.09	1.94
9	A	301	HEC	FE-NB	4.67	2.09	1.94
9	A	302	HEC	FE-ND	4.52	2.08	1.94
9	A	304	HEC	FE-ND	4.47	2.08	1.94
9	E	301	HEC	FE-NB	4.21	2.07	1.94
9	A	301	HEC	FE-ND	4.16	2.07	1.94
9	E	301	HEC	FE-NC	4.10	2.09	1.95
9	A	301	HEC	FE-NC	3.90	2.08	1.95
9	A	303	HEC	FE-ND	3.89	2.06	1.94
9	A	302	HEC	FE-NB	3.77	2.06	1.94
9	A	304	HEC	FE-NC	3.68	2.07	1.95
9	A	304	HEC	FE-NB	3.57	2.05	1.94
9	A	302	HEC	FE-NA	3.55	2.07	1.95
9	A	305	HEC	FE-NC	3.49	2.07	1.95
9	A	305	HEC	FE-NB	3.45	2.05	1.94
9	A	303	HEC	FE-NC	3.33	2.06	1.95
9	A	302	HEC	FE-NC	3.27	2.06	1.95
9	A	303	HEC	FE-NA	3.19	2.06	1.95
9	A	301	HEC	FE-NA	3.14	2.05	1.95
9	A	305	HEC	FE-NA	3.04	2.05	1.95
9	A	304	HEC	FE-NA	2.95	2.05	1.95
9	E	301	HEC	FE-NA	2.35	2.03	1.95
9	A	301	HEC	CMB-C2B	2.09	1.55	1.50

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	301	HEC	C1D-ND-C4D	6.65	111.94	105.07
9	A	303	HEC	C1D-ND-C4D	6.60	111.89	105.07
9	E	301	HEC	C1D-ND-C4D	6.45	111.73	105.07
9	A	302	HEC	C1D-ND-C4D	6.28	111.56	105.07
9	A	304	HEC	C1D-ND-C4D	6.26	111.54	105.07
9	A	305	HEC	C1D-ND-C4D	6.16	111.44	105.07
9	E	301	HEC	C4A-NA-C1A	3.07	108.35	105.35
9	A	305	HEC	C4B-NB-C1B	3.02	108.19	105.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	305	HEC	C4C-NC-C1C	2.85	108.14	105.35
9	A	305	HEC	C4A-NA-C1A	2.78	108.08	105.35
9	A	304	HEC	C4C-NC-C1C	2.78	108.07	105.35
9	A	304	HEC	C4A-NA-C1A	2.78	108.07	105.35
9	A	303	HEC	C4A-NA-C1A	2.76	108.05	105.35
9	A	303	HEC	C4C-NC-C1C	2.76	108.05	105.35
9	A	303	HEC	C4B-NB-C1B	2.76	107.92	105.07
9	A	304	HEC	C4B-NB-C1B	2.75	107.92	105.07
9	E	301	HEC	C2A-C1A-NA	-2.71	107.69	110.32
9	A	305	HEC	C2A-C1A-NA	-2.67	107.73	110.32
9	A	301	HEC	C2A-C1A-NA	-2.65	107.74	110.32
9	A	302	HEC	C4B-NB-C1B	2.64	107.80	105.07
9	A	303	HEC	CAC-C3C-C4C	2.61	128.53	124.92
9	A	302	HEC	C4A-NA-C1A	2.59	107.89	105.35
9	E	301	HEC	C4B-NB-C1B	2.58	107.74	105.07
9	A	304	HEC	C2A-C1A-NA	-2.57	107.83	110.32
9	A	301	HEC	C4A-NA-C1A	2.51	107.81	105.35
9	A	301	HEC	C4C-NC-C1C	2.48	107.78	105.35
9	A	302	HEC	C2A-C1A-NA	-2.46	107.93	110.32
9	A	303	HEC	C2A-C1A-NA	-2.38	108.01	110.32
9	A	302	HEC	C4C-NC-C1C	2.34	107.64	105.35
9	A	301	HEC	C3C-C4C-NC	-2.32	107.55	110.15
9	A	303	HEC	C3C-C4C-NC	-2.31	107.57	110.15
9	A	301	HEC	C4B-NB-C1B	2.28	107.43	105.07
9	A	301	HEC	CAC-C3C-C4C	2.20	127.97	124.92
9	A	305	HEC	C3B-C4B-NB	-2.17	107.75	110.17
9	A	305	HEC	CAD-CBD-CGD	-2.09	109.11	113.60
9	A	304	HEC	CAC-C3C-C4C	2.07	127.79	124.92
9	E	301	HEC	C3C-C4C-NC	-2.07	107.83	110.15
9	A	305	HEC	C3C-C4C-NC	-2.06	107.84	110.15
9	A	302	HEC	C3C-C4C-NC	-2.04	107.86	110.15
9	A	304	HEC	C3B-C4B-NB	-2.04	107.89	110.17
9	A	303	HEC	CAC-C3C-C2C	-2.04	123.60	126.86
9	A	303	HEC	CAB-C3B-C4B	2.02	127.43	124.81
9	A	304	HEC	C3C-C4C-NC	-2.01	107.90	110.15
9	A	301	HEC	CBA-CAA-C2A	-2.01	107.05	112.63

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	A	302	HEC	NA
9	A	305	HEC	NA

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Mol	Chain	Res	Type	Atom
9	E	301	HEC	NA

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	302	HEC	C2A-CAA-CBA-CGA
9	A	303	HEC	C4C-C3C-CAC-CBC
9	A	303	HEC	C2C-C3C-CAC-CBC
9	A	304	HEC	C2C-C3C-CAC-CBC
9	A	304	HEC	C4C-C3C-CAC-CBC
9	A	303	HEC	C2B-C3B-CAB-CBB
9	A	305	HEC	C2C-C3C-CAC-CBC
9	A	304	HEC	C1A-C2A-CAA-CBA
9	A	301	HEC	C2B-C3B-CAB-CBB
9	A	302	HEC	C2C-C3C-CAC-CBC
9	E	301	HEC	CAD-CBD-CGD-O2D
9	E	301	HEC	CAD-CBD-CGD-O1D
9	A	304	HEC	C3D-CAD-CBD-CGD
9	A	301	HEC	C4B-C3B-CAB-CBB
9	A	302	HEC	C1A-C2A-CAA-CBA
9	A	304	HEC	C3A-C2A-CAA-CBA
9	A	302	HEC	CAD-CBD-CGD-O2D
9	A	303	HEC	CAD-CBD-CGD-O2D
9	A	302	HEC	CAD-CBD-CGD-O1D

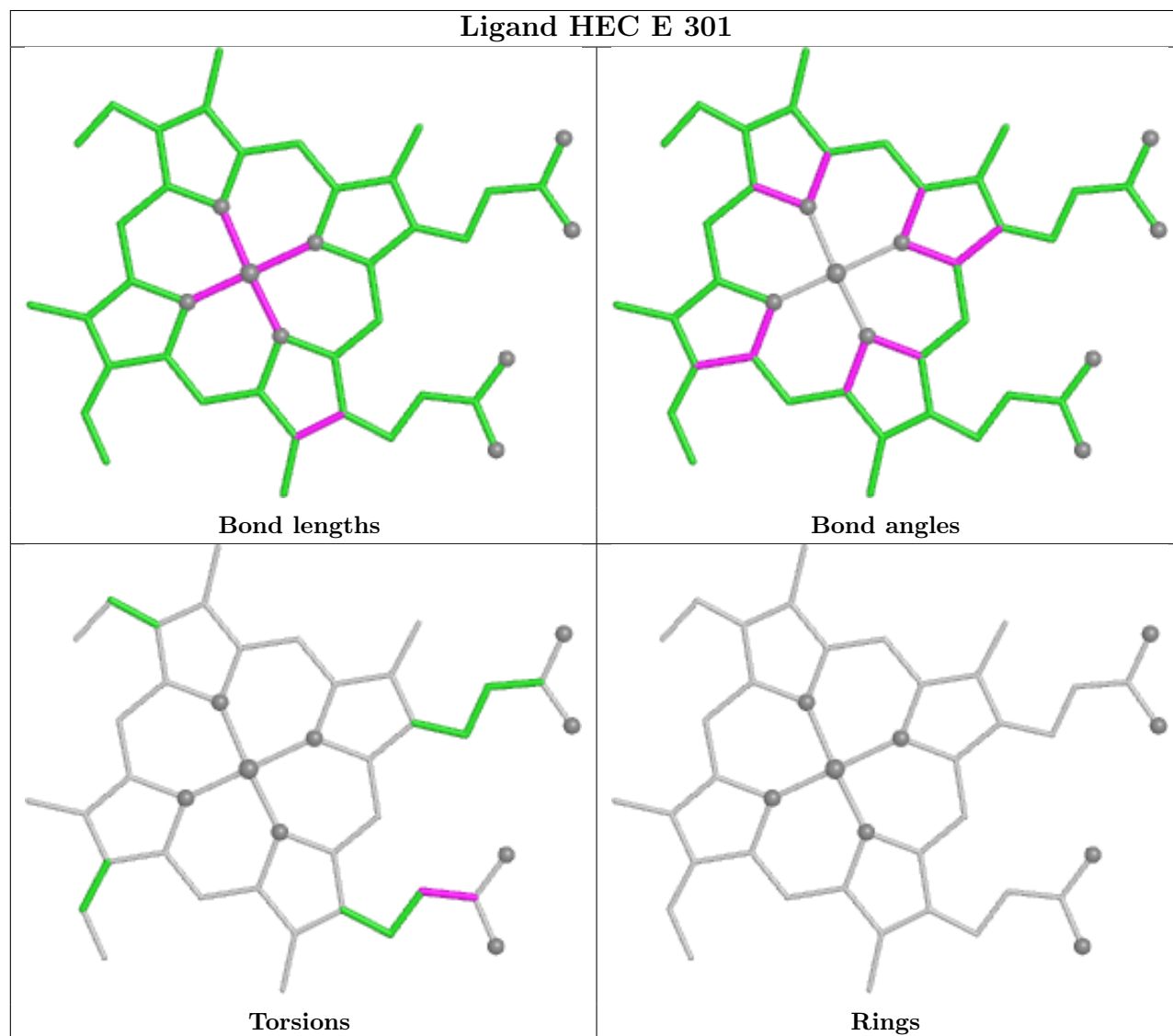
There are no ring outliers.

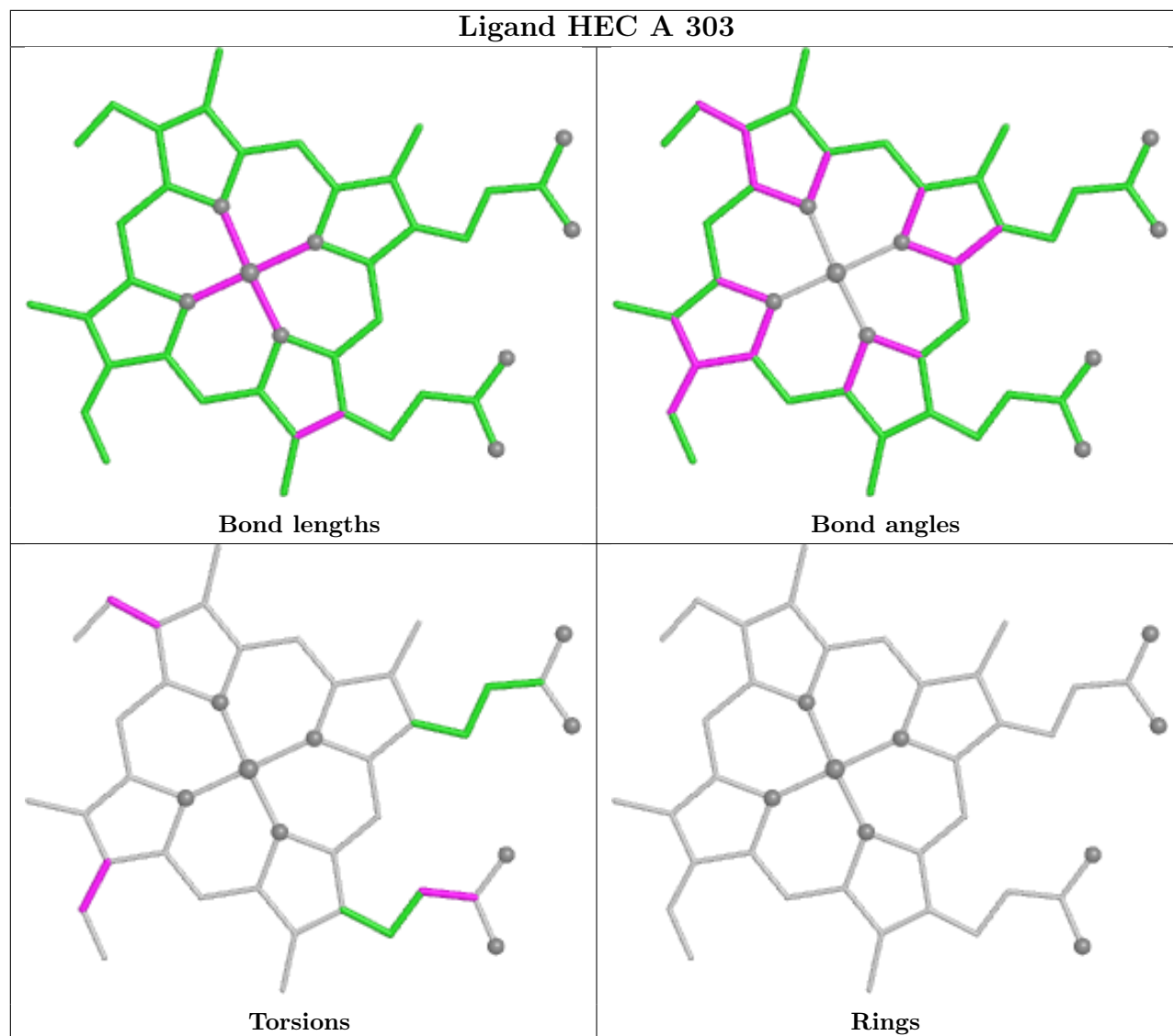
7 monomers are involved in 24 short contacts:

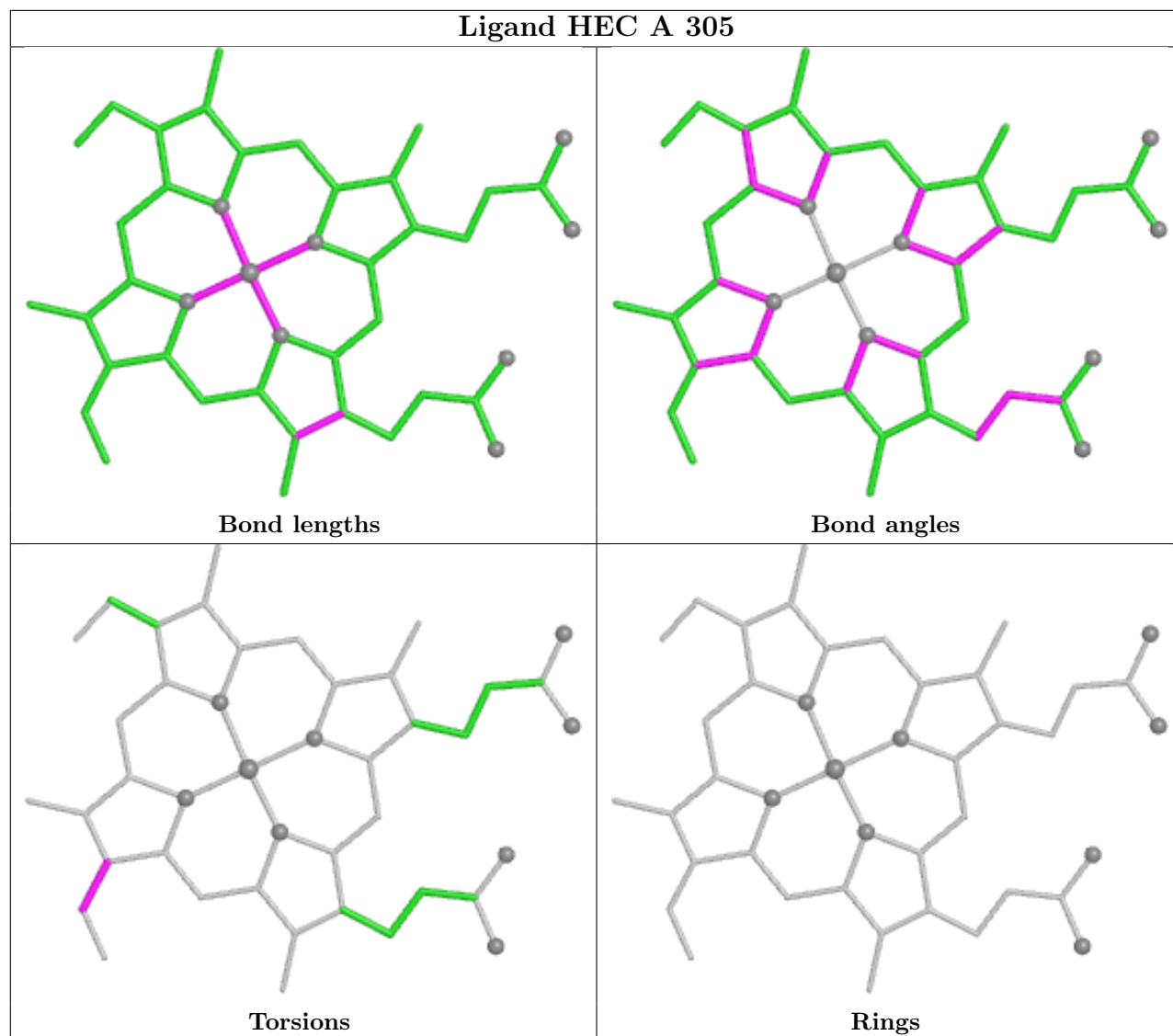
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	301	HEC	6	0
9	A	303	HEC	2	0
9	A	304	HEC	2	0
9	A	302	HEC	6	0
10	B	1103	SF4	1	0
11	B	1104	F3S	5	0
9	A	301	HEC	2	0

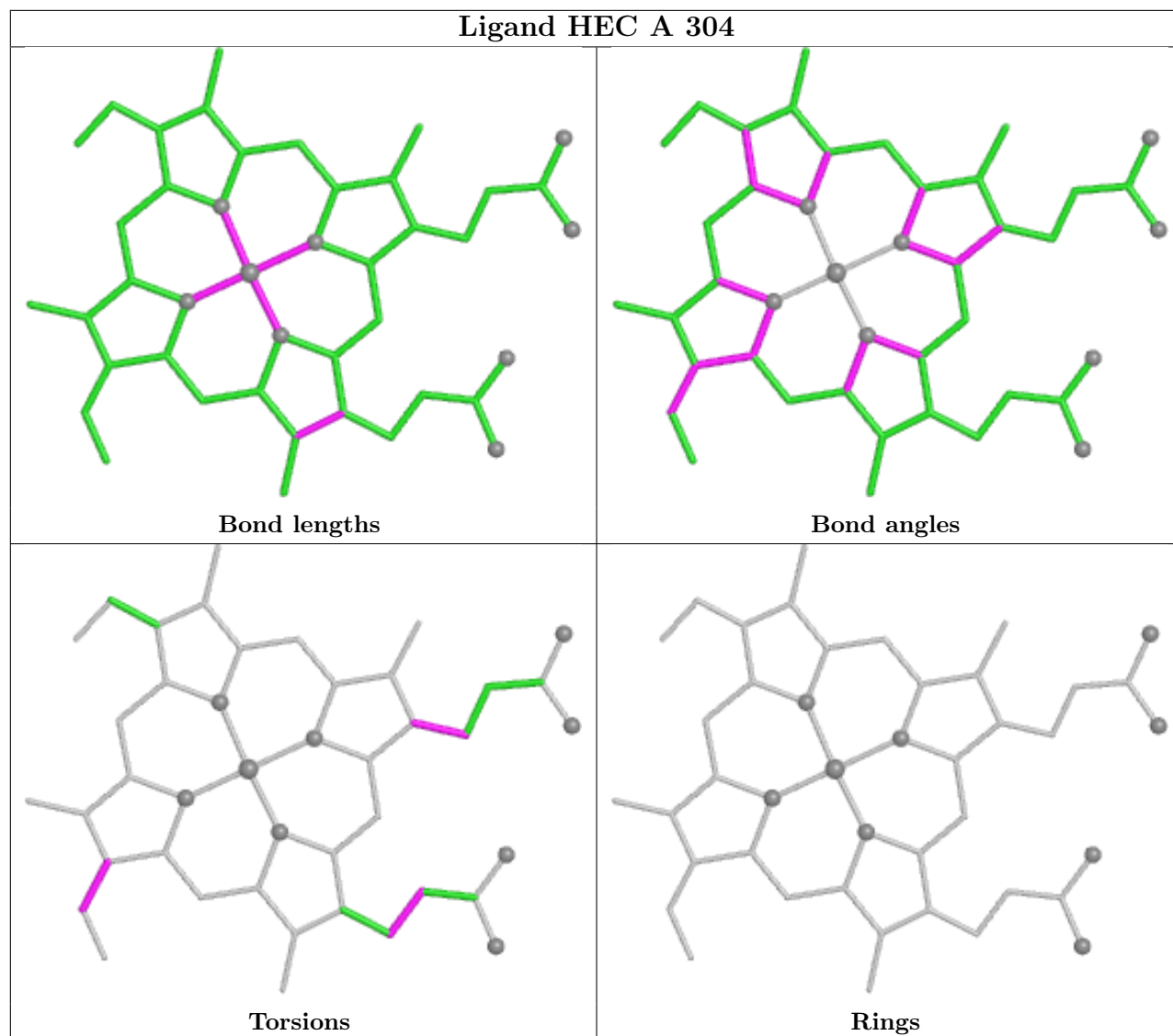
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

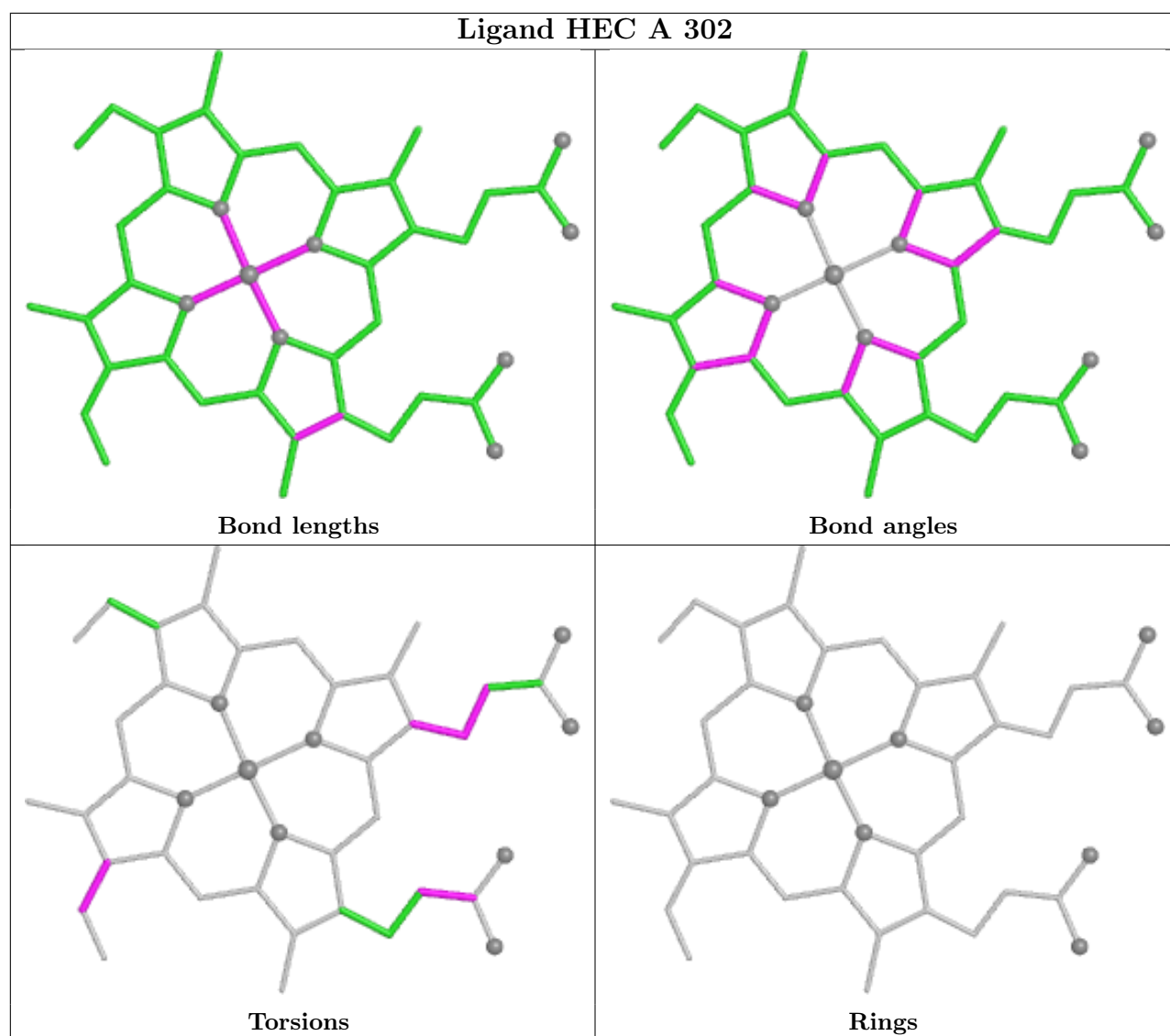
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

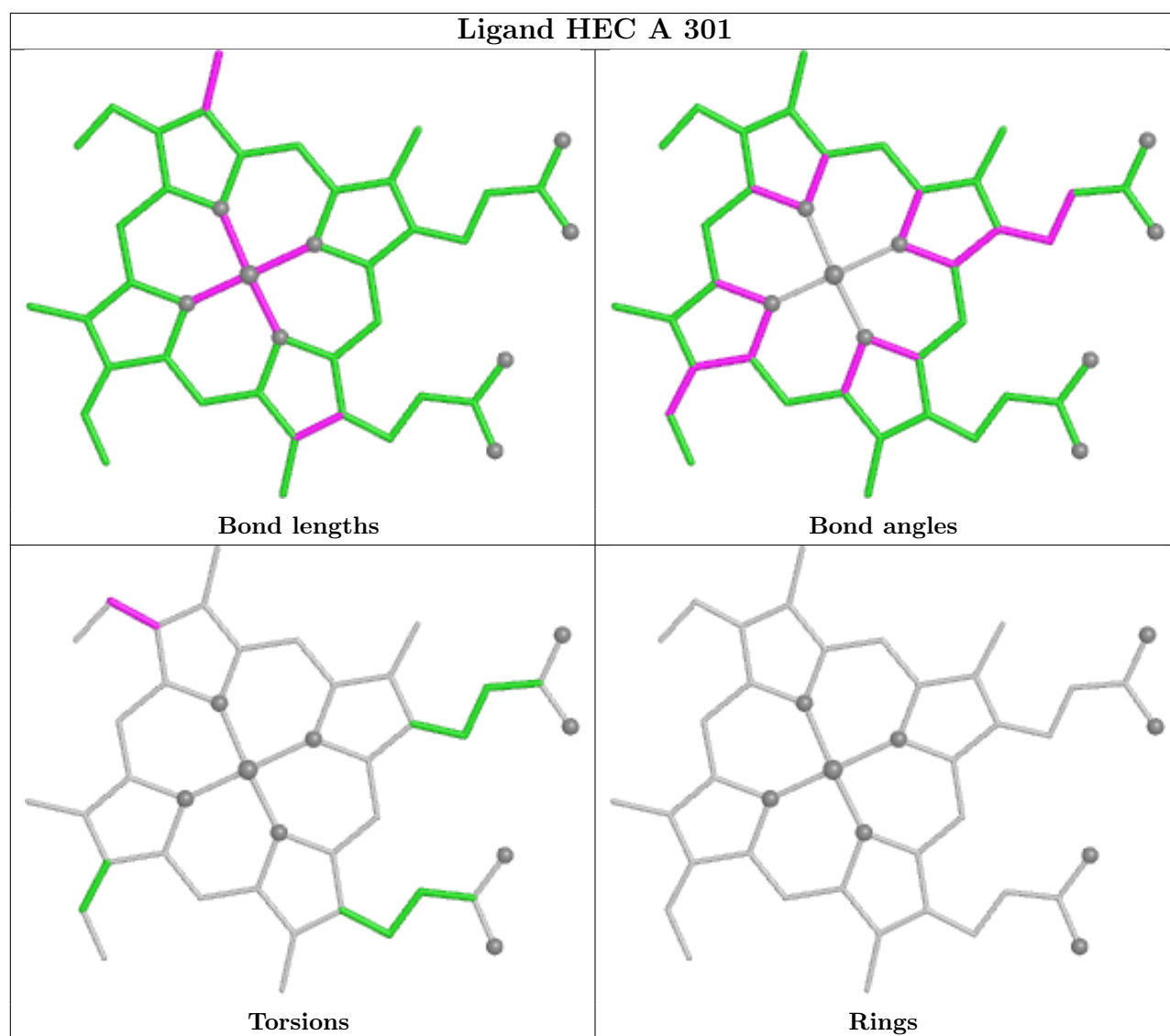












5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	218/219 (99%)	0.19	8 (3%)	45	30	37, 77, 127, 160	0
2	B	952/1029 (92%)	0.09	16 (1%)	69	50	29, 77, 126, 193	0
3	C	449/486 (92%)	0.17	11 (2%)	59	40	49, 92, 142, 214	0
4	D	175/179 (97%)	0.14	5 (2%)	53	36	39, 109, 166, 218	0
5	E	164/205 (80%)	0.28	5 (3%)	52	35	48, 87, 160, 232	0
6	F	396/411 (96%)	0.16	15 (3%)	44	29	54, 107, 172, 224	0
7	G	80/112 (71%)	0.33	5 (6%)	26	18	66, 103, 172, 241	0
8	I	27/37 (72%)	0.42	1 (3%)	45	30	71, 118, 168, 188	0
All	All	2461/2678 (91%)	0.15	66 (2%)	56	38	29, 88, 150, 241	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	181	VAL	4.8
3	C	143	GLY	4.5
6	F	395	LEU	4.4
5	E	106	CYS	4.3
2	B	481	ASP	3.8
3	C	171	ASP	3.7
3	C	410	SER	3.6
7	G	56	LEU	3.5
3	C	252	ASP	3.4
1	A	182	TYR	3.2
4	D	39	PHE	3.2
1	A	180	GLU	3.1
6	F	115	HIS	3.1
6	F	78	THR	3.1
5	E	109	GLU	3.0
6	F	11	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
6	F	251	PHE	2.9
3	C	100	ALA	2.9
6	F	222	TYR	2.8
2	B	939	SER	2.8
3	C	405	ASP	2.8
5	E	149	VAL	2.8
7	G	92	VAL	2.8
4	D	40	PRO	2.8
6	F	119	GLU	2.7
2	B	162	ARG	2.6
2	B	425	GLY	2.6
5	E	69	PHE	2.6
5	E	161	SER	2.6
6	F	394	LEU	2.6
1	A	51	VAL	2.6
8	I	37	TRP	2.5
2	B	319	PHE	2.5
2	B	543	GLU	2.5
3	C	22	GLY	2.5
2	B	483	THR	2.4
1	A	79	ALA	2.3
6	F	74	ALA	2.3
7	G	96	ILE	2.3
3	C	19	LEU	2.3
4	D	42	GLU	2.2
2	B	335	THR	2.2
2	B	867	THR	2.2
3	C	163	GLN	2.2
7	G	91	LYS	2.2
2	B	463	TRP	2.2
1	A	86	THR	2.2
2	B	242	VAL	2.2
1	A	102	GLU	2.2
3	C	160	MET	2.2
2	B	1015	ALA	2.2
2	B	172	PHE	2.1
4	D	82	TYR	2.1
1	A	123	PRO	2.1
4	D	41	ILE	2.1
6	F	47	TYR	2.1
2	B	330	GLY	2.1
6	F	75	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	80	ILE	2.1
7	G	67	GLY	2.1
2	B	503	LEU	2.0
6	F	255	VAL	2.0
6	F	185	THR	2.0
2	B	264	PRO	2.0
6	F	253	GLU	2.0
6	F	397	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

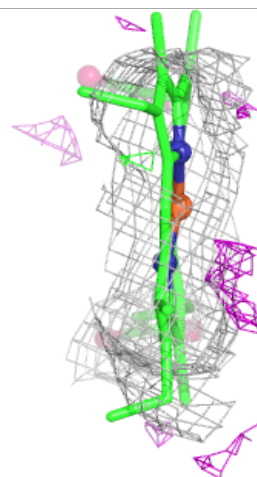
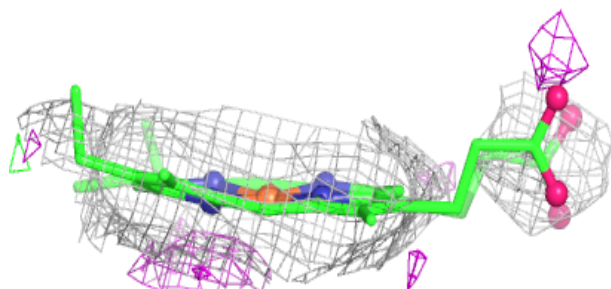
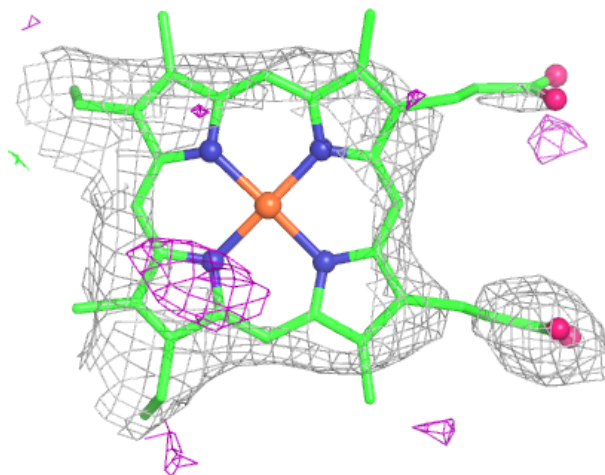
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	HEC	E	301	43/43	0.95	0.12	80,96,106,108	0
9	HEC	A	302	43/43	0.96	0.13	63,68,71,72	0
9	HEC	A	301	43/43	0.96	0.11	53,62,65,65	0
9	HEC	A	304	43/43	0.97	0.10	56,66,70,71	0
9	HEC	A	305	43/43	0.97	0.10	69,77,86,90	0
9	HEC	A	303	43/43	0.97	0.09	52,59,63,64	0
10	SF4	B	1101	8/8	0.97	0.05	68,71,74,74	0
11	F3S	B	1104	7/7	0.97	0.07	74,96,109,150	0
10	SF4	B	1103	8/8	0.99	0.04	45,46,48,49	0
10	SF4	B	1102	8/8	0.99	0.04	51,53,55,56	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.

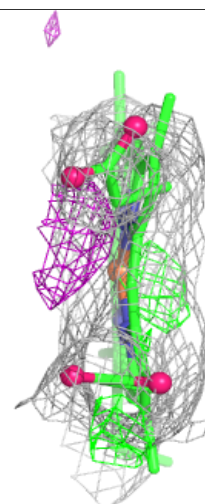
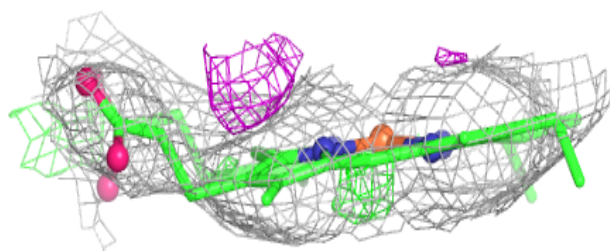
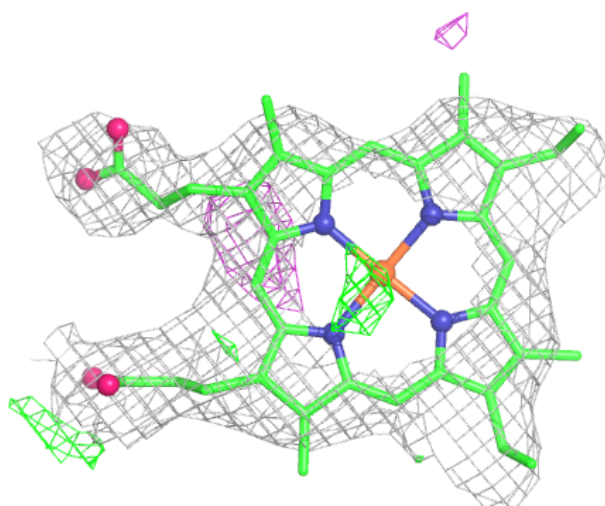
Electron density around HEC E 301:

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



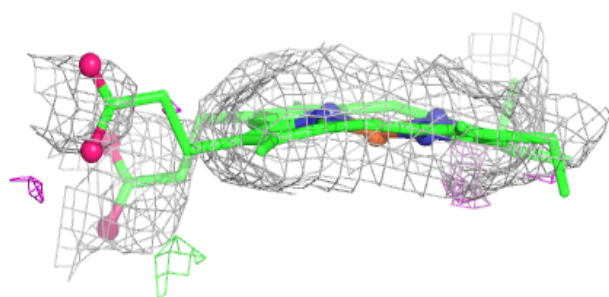
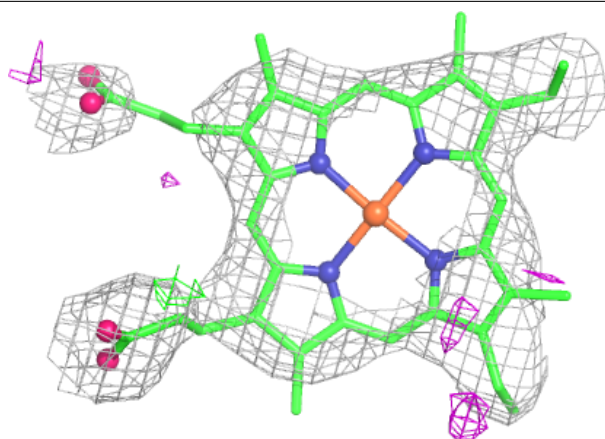
Electron density around HEC A 302:

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



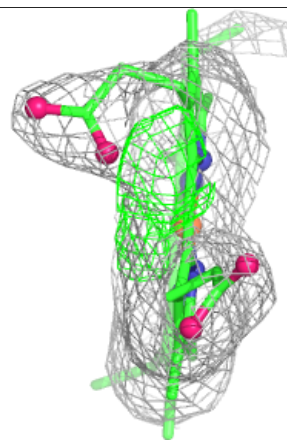
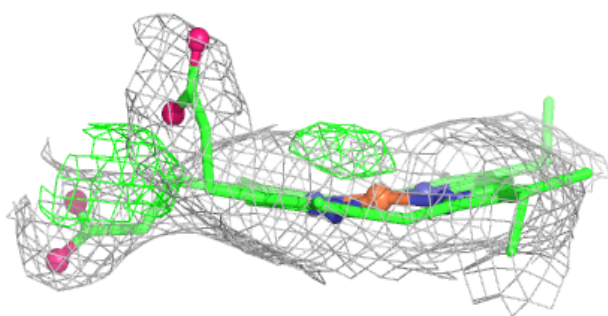
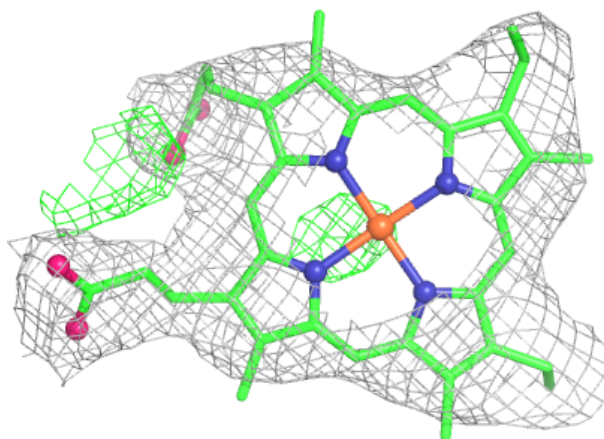
Electron density around HEC A 301:

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



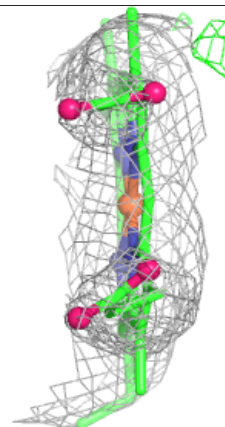
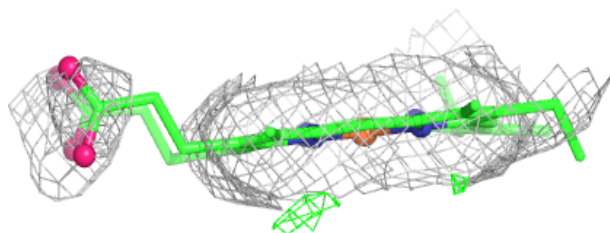
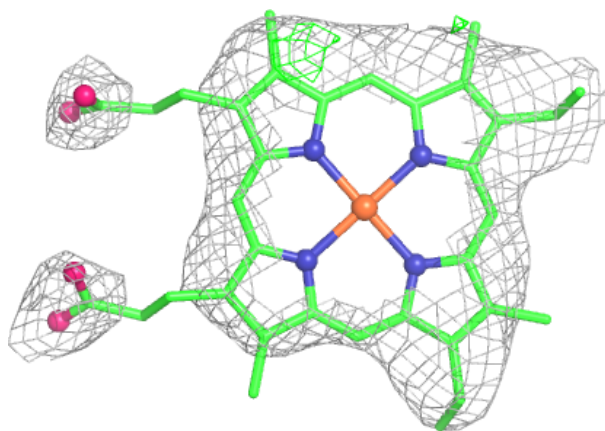
Electron density around HEC A 304:

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



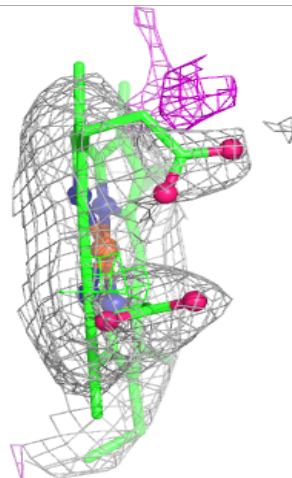
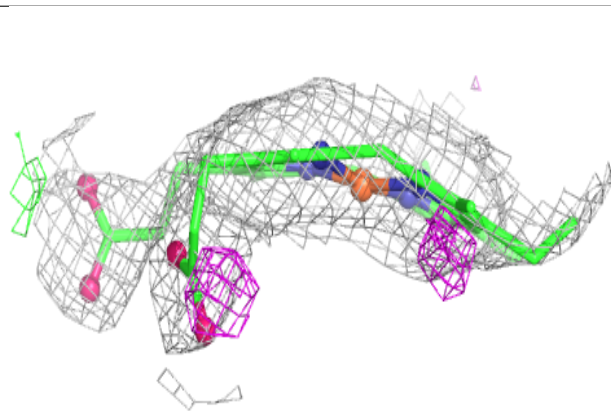
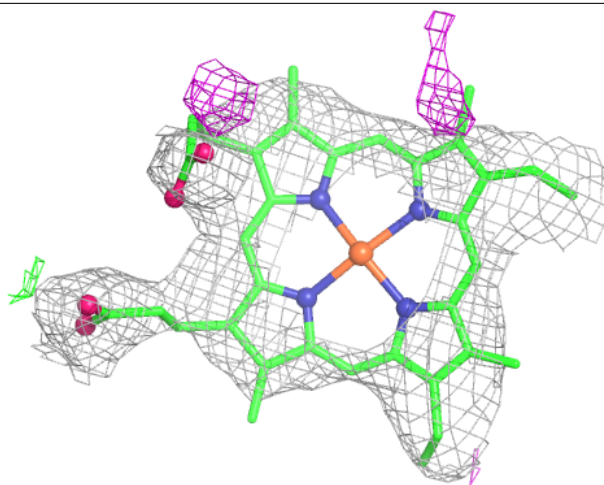
Electron density around HEC A 305:

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



Electron density around HEC A 303:

$2mF_o-DF_c$ (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.