



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:30 PM UTC

PDB ID : 1BL9 / pdb_00001bl9
Title : CONFORMATIONAL CHANGES OCCURRING UPON REDUCTION IN
NITRITE REDUCTASE FROM PSEUDOMONAS AERUGINOSA
Authors : Nurizzo, D.; Cambillau, C.; Tegoni, M.
Deposited on : 1998-07-20
Resolution : 2.90 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

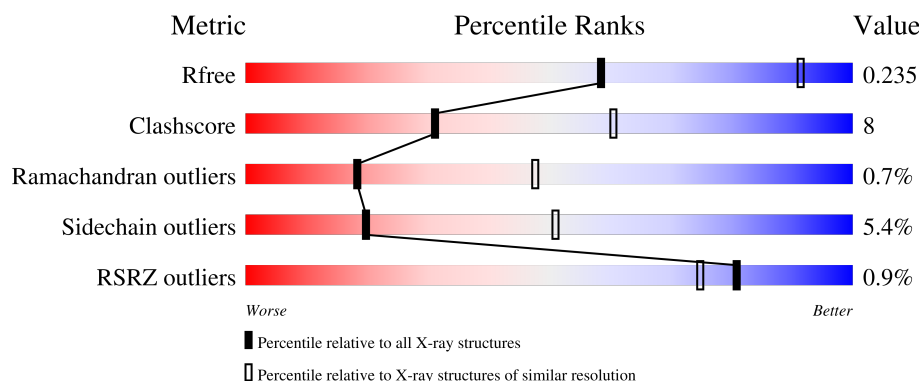
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

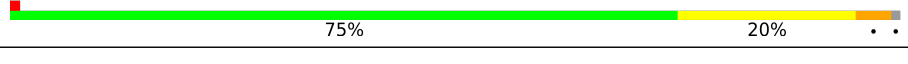
The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	543	
1	B	543	

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:

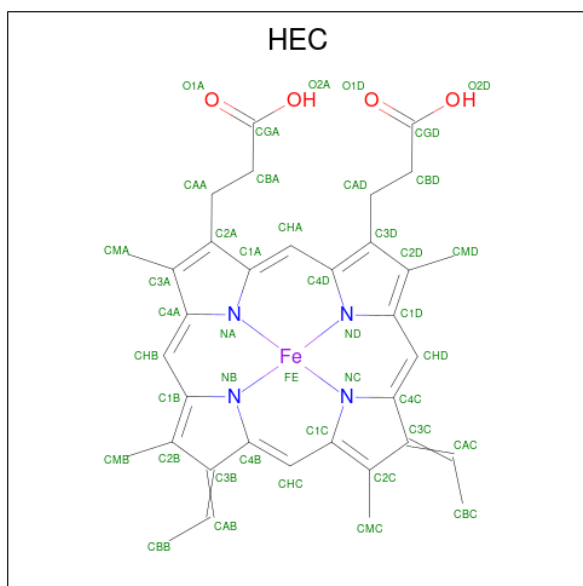
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DHE	A	602	X	-	-	-
3	DHE	B	602	X	-	-	-

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 NITRITE REDUCTASE.

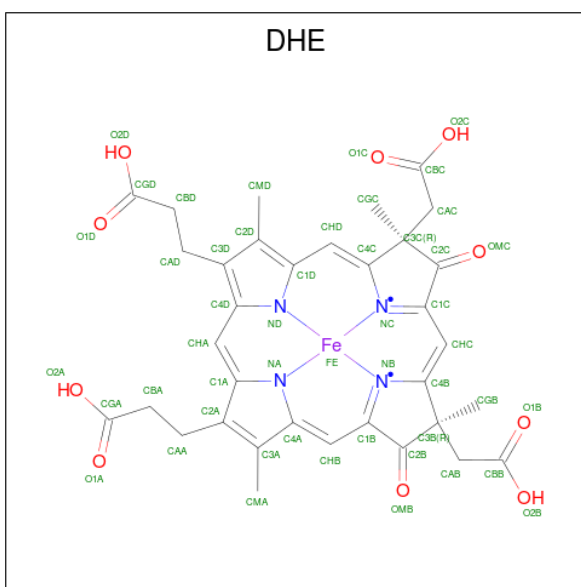
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	537	Total 4198	C 2662	N 732	O 792	S 12	0	0	0
1	B	537	Total 4198	C 2662	N 732	O 792	S 12	0	0	0

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



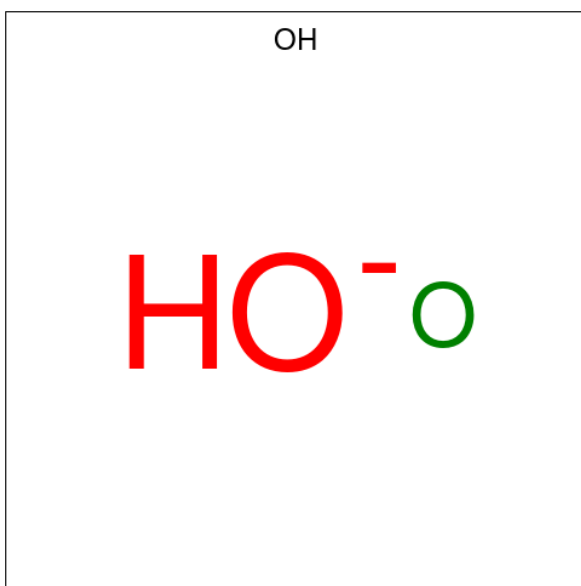
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is HEME D (CCD ID: DHE) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_{10}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total 49	C 34	Fe 1	N 4	O 10	0	0
3	B	1	Total 49	C 34	Fe 1	N 4	O 10	0	0

- Molecule 4 is HYDROXIDE ION (CCD ID: OH) (formula: HO).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O 1 1	0	0

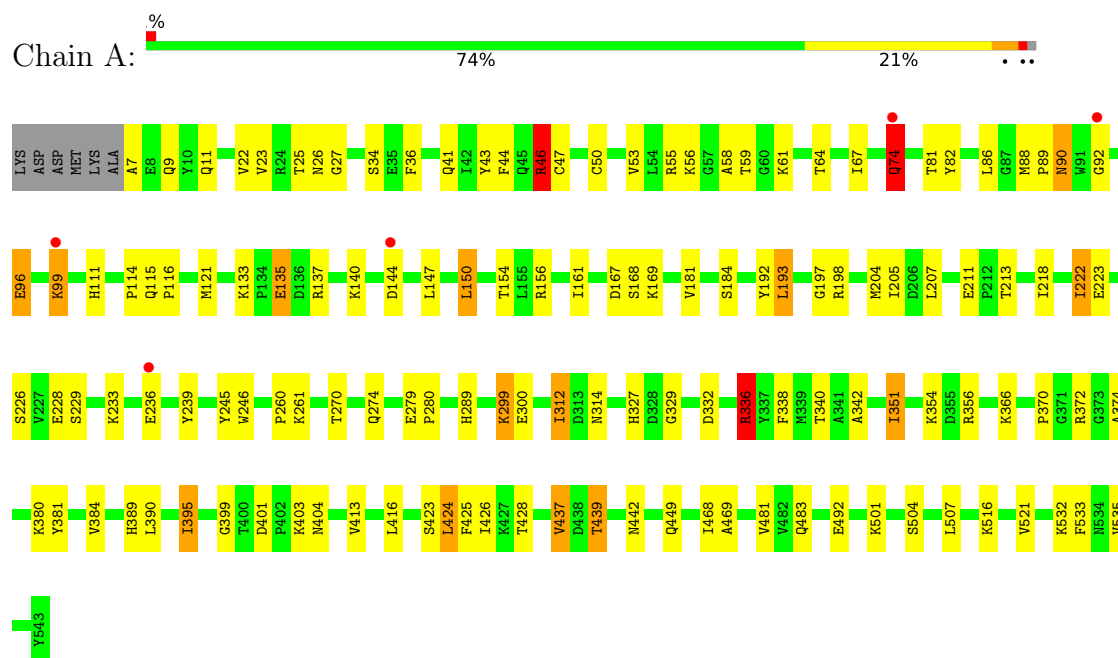
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total 36	O 36	0	0
5	B	42	Total 42	O 42	0	0

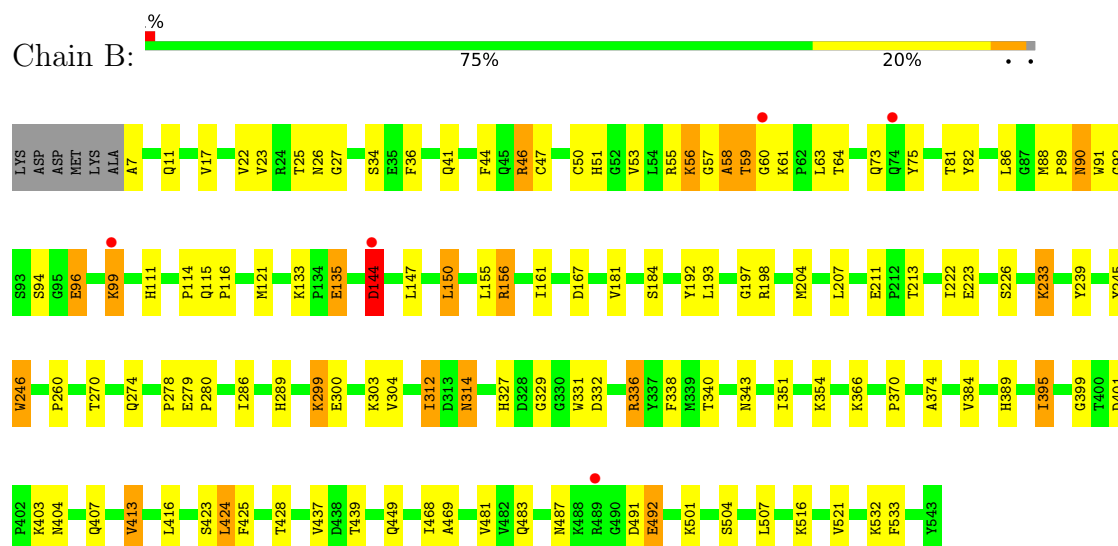
3 Residue-property plots

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: NITRITE REDUCTASE



• Molecule 1: NITRITE REDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	166.61Å 89.00Å 112.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.90 12.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (12.00-2.90) 97.0 (12.00-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.92Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.211 , 0.233 0.206 , 0.235	Depositor DCC
R_{free} test set	856 reflections (2.33%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8659	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.4536e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: DHE, OH, 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	A	0.81	11/4303 (0.3%)	1.13	25/5847 (0.4%)
1	B	0.75	11/4303 (0.3%)	1.14	32/5847 (0.5%)
All	All	0.78	22/8606 (0.3%)	1.14	57/11694 (0.5%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	74	GLN	CD-NE2	-15.09	1.01	1.33
1	A	9	GLN	CD-NE2	-12.87	1.06	1.33
1	B	90	ASN	CG-ND2	-11.95	1.08	1.33
1	A	90	ASN	CG-ND2	-11.56	1.08	1.33
1	A	314	ASN	CG-OD1	-9.92	1.04	1.23
1	A	41	GLN	CD-NE2	-9.85	1.12	1.33
1	B	314	ASN	CG-OD1	-9.82	1.04	1.23
1	B	90	ASN	CG-OD1	-9.80	1.04	1.23
1	A	90	ASN	CG-OD1	-9.24	1.05	1.23
1	A	314	ASN	CG-ND2	-9.15	1.14	1.33
1	B	314	ASN	CG-ND2	-8.43	1.15	1.33
1	A	9	GLN	CD-OE1	-7.55	1.09	1.23
1	B	41	GLN	CD-NE2	-6.67	1.19	1.33
1	B	193	LEU	CG-CD2	-6.24	1.31	1.52
1	B	403	LYS	CG-CD	-6.11	1.34	1.52
1	A	193	LEU	CG-CD2	-6.00	1.32	1.52
1	A	289	HIS	CG-CD2	-5.86	1.29	1.35
1	B	60	GLY	N-CA	5.76	1.50	1.44
1	A	90	ASN	CB-CG	5.49	1.65	1.52
1	B	437	VAL	CB-CG1	-5.46	1.34	1.52
1	B	437	VAL	CB-CG2	-5.23	1.35	1.52
1	B	246	TRP	NE1-CE2	-5.11	1.31	1.37

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59	THR	N-CA-C	-8.56	102.03	111.36
1	B	403	LYS	CD-CE-NZ	-8.36	85.15	111.90
1	A	23	VAL	N-CA-C	8.31	121.09	108.71
1	B	336	ARG	NE-CZ-NH2	8.22	126.60	119.20
1	B	23	VAL	N-CA-C	8.16	120.88	108.71
1	A	193	LEU	CD1-CG-CD2	-8.06	93.06	110.80
1	A	336	ARG	NE-CZ-NH2	7.81	126.23	119.20
1	B	193	LEU	CD1-CG-CD2	-7.64	94.00	110.80
1	B	58	ALA	N-CA-C	-7.52	101.53	108.75
1	B	27	GLY	N-CA-C	-7.51	103.70	116.01
1	A	27	GLY	N-CA-C	-7.30	104.04	116.01
1	B	403	LYS	CG-CD-CE	6.99	127.39	111.30
1	B	343	ASN	O-C-N	-6.97	114.62	122.08
1	A	74	GLN	N-CA-C	6.80	118.35	111.07
1	B	289	HIS	ND1-CE1-NE2	-6.76	101.64	108.40
1	A	144	ASP	CB-CA-C	-6.70	100.68	111.06
1	B	46	ARG	NE-CZ-NH2	6.67	125.21	119.20
1	A	535	VAL	N-CA-C	6.67	117.16	110.23
1	B	111	HIS	ND1-CE1-NE2	-6.64	101.76	108.40
1	B	437	VAL	CG1-CB-CG2	-6.63	96.22	110.80
1	A	289	HIS	ND1-CE1-NE2	-6.56	101.84	108.40
1	A	111	HIS	ND1-CE1-NE2	-6.45	101.95	108.40
1	A	226	SER	N-CA-C	6.45	120.42	110.42
1	A	11	GLN	N-CA-C	-6.41	105.33	112.57
1	B	226	SER	N-CA-C	6.41	120.35	110.42
1	B	11	GLN	N-CA-C	-6.39	105.35	112.57
1	B	370	PRO	CB-CA-C	-6.30	102.92	112.11
1	A	336	ARG	NH1-CZ-NH2	-6.20	111.25	119.30
1	A	332	ASP	N-CA-C	-6.17	101.83	110.35
1	B	332	ASP	N-CA-C	-6.16	101.86	110.35
1	B	167	ASP	N-CA-C	6.06	117.97	111.36
1	A	370	PRO	CB-CA-C	-5.98	103.39	112.11
1	A	342	ALA	N-CA-C	-5.93	101.35	109.71
1	A	46	ARG	NE-CZ-NH2	5.88	124.50	119.20
1	B	300	GLU	N-CA-C	5.86	119.25	111.75
1	A	44	PHE	CE1-CZ-CE2	-5.85	109.47	120.00
1	A	167	ASP	N-CA-C	5.80	117.68	111.36
1	B	47	CYS	N-CA-C	5.78	120.34	113.12
1	A	47	CYS	N-CA-C	5.69	120.23	113.12
1	B	336	ARG	NH1-CZ-NH2	-5.65	111.96	119.30
1	B	155	LEU	N-CA-C	-5.64	101.76	109.71
1	B	144	ASP	N-CA-CB	5.62	119.45	111.25
1	A	300	GLU	N-CA-C	5.61	118.92	111.75

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	233	LYS	CB-CA-C	-5.59	102.92	109.80
1	B	56	LYS	N-CA-C	-5.59	106.17	112.87
1	B	44	PHE	CE1-CZ-CE2	-5.45	110.18	120.00
1	B	413	VAL	N-CA-C	5.40	117.80	111.05
1	A	115	GLN	N-CA-C	5.37	117.19	109.04
1	B	115	GLN	N-CA-C	5.34	117.16	109.04
1	A	205	ILE	N-CA-C	5.24	115.45	108.11
1	A	390	LEU	N-CA-C	-5.23	107.44	113.88
1	B	403	LYS	CB-CG-CD	-5.17	99.41	111.30
1	B	135	GLU	CB-CA-C	-5.10	102.32	110.79
1	B	64	THR	CA-C-N	5.10	126.22	119.84
1	B	64	THR	C-N-CA	5.10	126.22	119.84
1	A	372	ARG	NE-CZ-NH2	5.03	123.73	119.20
1	B	437	VAL	CB-CA-C	-5.03	103.28	110.12

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	4198	0	4153	68	0
1	B	4198	0	4153	76	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
3	A	49	0	24	1	0
3	B	49	0	24	2	0
4	B	1	0	0	0	0
5	A	36	0	0	2	0
5	B	42	0	0	3	0
All	All	8659	0	8414	140	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 8.

All (140) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:ARG:HH11	1:A:354:LYS:HB3	1.29	0.97
1:A:114:PRO:HB2	1:B:22:VAL:HG12	1.57	0.86
1:A:22:VAL:HG12	1:B:114:PRO:HB2	1.66	0.77
1:B:336:ARG:NH1	1:B:354:LYS:HD3	1.99	0.77
1:B:53:VAL:HG11	1:B:116:PRO:HG3	1.68	0.76
1:A:426:ILE:HG13	1:A:437:VAL:HG12	1.68	0.74
1:A:236:GLU:HG3	5:A:611:HOH:O	1.90	0.71
1:B:50:CYS:O	1:B:58:ALA:HB3	1.93	0.68
1:A:336:ARG:NH1	1:A:354:LYS:HB3	2.06	0.68
1:A:96:GLU:HA	1:A:96:GLU:OE1	1.94	0.66
1:B:96:GLU:HA	1:B:96:GLU:OE1	1.96	0.65
1:A:56:LYS:HE3	1:A:64:THR:HG21	1.77	0.65
1:A:121:MET:SD	1:A:260:PRO:HB2	2.37	0.65
1:B:223:GLU:HG2	1:B:245:TYR:HB2	1.78	0.65
1:B:56:LYS:HG3	1:B:278:PRO:CG	2.26	0.65
1:B:46:ARG:HH11	1:B:91:TRP:HZ3	1.44	0.64
1:B:61:LYS:HE2	2:B:601:HEC:O2D	1.96	0.64
1:A:223:GLU:HG2	1:A:245:TYR:HB2	1.82	0.61
1:A:53:VAL:HG11	1:A:116:PRO:HG3	1.81	0.61
1:A:46:ARG:NH1	1:A:96:GLU:HG3	2.15	0.61
1:B:99:LYS:HE2	1:B:99:LYS:HA	1.82	0.61
1:A:7:ALA:N	5:A:636:HOH:O	2.33	0.61
1:A:181:VAL:HA	1:A:197:GLY:HA2	1.81	0.61
1:B:7:ALA:N	5:B:640:HOH:O	2.33	0.61
1:B:181:VAL:HA	1:B:197:GLY:HA2	1.82	0.60
1:A:99:LYS:HA	1:A:99:LYS:HE2	1.82	0.60
1:B:133:LYS:HB3	1:B:135:GLU:OE1	2.02	0.60
1:A:423:SER:HA	1:A:439:THR:HA	1.84	0.60
1:B:55:ARG:CD	1:B:63:LEU:HB2	2.32	0.59
1:A:43:TYR:OH	1:A:55:ARG:HG2	2.03	0.59
1:B:90:ASN:ND2	1:B:94:SER:HB3	2.18	0.58
1:A:61:LYS:HG3	2:A:601:HEC:HAD2	1.85	0.58
1:B:304:VAL:HG11	1:B:351:ILE:HG13	1.86	0.57
2:B:601:HEC:HBC3	2:B:601:HEC:HMC3	1.87	0.57
1:A:261:LYS:HB3	1:A:312:ILE:HD11	1.87	0.56
1:A:211:GLU:O	1:A:213:THR:HG23	2.05	0.56
1:A:116:PRO:HG2	1:A:246:TRP:CE2	2.41	0.55
1:B:116:PRO:HG2	1:B:246:TRP:CE2	2.42	0.55
1:A:50:CYS:O	1:A:58:ALA:HB3	2.06	0.55
1:B:211:GLU:O	1:B:213:THR:HG23	2.06	0.55
1:A:218:ILE:HD11	1:A:260:PRO:HG3	1.88	0.55
1:B:239:TYR:CZ	1:B:312:ILE:HG21	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:ARG:HD2	1:B:63:LEU:HB2	1.89	0.54
1:B:121:MET:SD	1:B:260:PRO:HB2	2.48	0.54
1:B:46:ARG:HD2	1:B:91:TRP:CZ3	2.42	0.53
1:B:279:GLU:N	1:B:280:PRO:HD3	2.22	0.53
1:A:279:GLU:N	1:A:280:PRO:HD3	2.23	0.53
1:A:81:THR:HG23	1:A:92:GLY:HA3	1.92	0.52
1:B:144:ASP:N	1:B:144:ASP:OD1	2.43	0.52
1:A:380:LYS:HE2	1:A:381:TYR:CE1	2.44	0.52
1:B:239:TYR:CE1	1:B:312:ILE:HG21	2.45	0.52
1:A:468:ILE:HB	1:A:481:VAL:HG21	1.92	0.52
1:B:338:PHE:HB3	1:B:351:ILE:HB	1.93	0.51
1:B:468:ILE:HB	1:B:481:VAL:HG21	1.92	0.51
1:B:55:ARG:C	1:B:57:GLY:N	2.66	0.51
1:B:384:VAL:HG12	1:B:399:GLY:HA2	1.93	0.51
1:A:384:VAL:HG12	1:A:399:GLY:HA2	1.93	0.50
1:B:86:LEU:HB2	2:B:601:HEC:O1D	2.12	0.50
1:A:336:ARG:NH1	1:A:354:LYS:HD3	2.26	0.50
1:A:239:TYR:CZ	1:A:312:ILE:HG21	2.46	0.49
1:B:82:TYR:O	1:B:90:ASN:HB3	2.12	0.49
1:B:423:SER:HA	1:B:439:THR:HA	1.94	0.49
1:B:424:LEU:HB3	1:B:425:PHE:CD2	2.48	0.48
1:B:449:GLN:HB3	1:B:469:ALA:HB3	1.95	0.48
1:A:424:LEU:HB3	1:A:425:PHE:CD2	2.47	0.48
1:A:192:TYR:CD1	1:A:204:MET:HE2	2.48	0.48
1:A:449:GLN:HB3	1:A:469:ALA:HB3	1.96	0.48
1:B:192:TYR:CD1	1:B:204:MET:HE2	2.49	0.48
1:B:487:ASN:CG	1:B:492:GLU:HG3	2.39	0.48
1:B:81:THR:HG23	1:B:92:GLY:HA3	1.96	0.47
1:B:395:ILE:HB	1:B:416:LEU:HB2	1.97	0.47
1:B:46:ARG:NH1	1:B:91:TRP:HZ3	2.11	0.47
1:A:184:SER:HB2	1:A:533:PHE:CD2	2.50	0.47
1:A:198:ARG:HH22	3:A:602:DHE:CBB	2.27	0.47
1:A:389:HIS:O	1:A:423:SER:HB3	2.15	0.47
1:B:374:ALA:HB1	1:B:428:THR:HG22	1.97	0.47
1:A:395:ILE:HB	1:A:416:LEU:HB2	1.98	0.46
1:A:507:LEU:HB2	1:A:521:VAL:HB	1.97	0.46
1:B:389:HIS:O	1:B:423:SER:HB3	2.16	0.46
1:B:184:SER:HB2	1:B:533:PHE:CD2	2.51	0.46
1:B:51:HIS:O	1:B:55:ARG:HA	2.15	0.45
1:A:114:PRO:HB2	1:B:22:VAL:CG1	2.39	0.45
1:B:55:ARG:C	1:B:57:GLY:H	2.25	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:532:LYS:HE2	1:B:532:LYS:HB2	1.79	0.45
1:A:374:ALA:HB1	1:A:428:THR:HG22	1.99	0.45
1:A:270:THR:O	1:A:274:GLN:HA	2.17	0.45
1:B:90:ASN:ND2	1:B:90:ASN:O	2.50	0.45
1:A:46:ARG:HH11	1:A:96:GLU:HG3	1.81	0.44
1:A:82:TYR:O	1:A:90:ASN:HB3	2.16	0.44
1:B:507:LEU:HB2	1:B:521:VAL:HB	1.98	0.44
1:B:56:LYS:HG3	1:B:278:PRO:HG3	1.99	0.44
1:A:222:ILE:CG2	1:B:17:VAL:HG22	2.48	0.44
1:A:99:LYS:HA	1:A:99:LYS:CE	2.46	0.44
1:B:75:TYR:C	1:B:75:TYR:CD1	2.96	0.44
1:A:532:LYS:HE2	1:A:532:LYS:HB2	1.79	0.44
1:B:61:LYS:HB3	5:B:638:HOH:O	2.18	0.44
1:B:116:PRO:HG2	1:B:246:TRP:NE1	2.32	0.44
1:B:156:ARG:HD3	5:B:618:HOH:O	2.16	0.44
1:A:147:LEU:HD22	1:A:207:LEU:HB3	1.99	0.43
1:A:150:LEU:HD12	1:A:150:LEU:HA	1.84	0.43
1:B:99:LYS:HA	1:B:99:LYS:CE	2.48	0.43
1:A:133:LYS:HB3	1:A:135:GLU:OE1	2.17	0.43
1:A:36:PHE:HZ	1:A:114:PRO:HG3	1.83	0.43
1:B:329:GLY:HA3	1:B:340:THR:HA	2.00	0.43
1:A:239:TYR:CE1	1:A:312:ILE:HG21	2.53	0.43
1:A:116:PRO:HG2	1:A:246:TRP:NE1	2.32	0.43
1:B:270:THR:O	1:B:274:GLN:HA	2.18	0.43
1:B:88:MET:HB2	2:B:601:HEC:C4D	2.48	0.43
1:B:198:ARG:HH22	3:B:602:DHE:CBB	2.31	0.43
1:B:401:ASP:OD2	1:B:404:ASN:HB2	2.18	0.43
1:A:439:THR:OG1	1:A:442:ASN:HB2	2.18	0.43
1:B:25:THR:O	1:B:26:ASN:HB2	2.18	0.43
1:B:56:LYS:HG3	1:B:278:PRO:CD	2.49	0.43
1:B:150:LEU:HD12	1:B:150:LEU:HA	1.84	0.43
1:A:401:ASP:OD2	1:A:404:ASN:HB2	2.19	0.42
1:B:36:PHE:HZ	1:B:114:PRO:HG3	1.84	0.42
1:A:88:MET:HA	1:A:89:PRO:HD2	1.89	0.42
1:B:286:ILE:HD11	1:B:331:TRP:CD1	2.55	0.42
1:B:55:ARG:HD3	1:B:63:LEU:HB2	2.00	0.42
1:B:198:ARG:NH2	3:B:602:DHE:O2B	2.52	0.42
1:A:25:THR:O	1:A:26:ASN:HB2	2.19	0.42
1:A:86:LEU:HB2	2:A:601:HEC:O1D	2.20	0.42
1:A:354:LYS:O	1:A:356:ARG:HG3	2.19	0.42
1:B:491:ASP:OD1	1:B:492:GLU:HG2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:MET:HA	1:B:89:PRO:HD2	1.88	0.41
1:A:228:GLU:HG3	1:A:229:SER:N	2.35	0.41
1:B:46:ARG:HA	1:B:46:ARG:HD3	1.94	0.41
1:B:55:ARG:NH1	1:B:63:LEU:O	2.52	0.41
1:A:133:LYS:O	1:A:137:ARG:HG3	2.19	0.41
1:B:147:LEU:HD22	1:B:207:LEU:HB3	2.02	0.41
2:A:601:HEC:HMC1	2:A:601:HEC:HBC3	2.01	0.41
1:A:299:LYS:NZ	1:A:327:HIS:HD2	2.19	0.41
1:A:222:ILE:HG21	1:B:17:VAL:HG22	2.02	0.41
1:B:299:LYS:NZ	1:B:327:HIS:HD2	2.20	0.40
1:A:338:PHE:HB3	1:A:351:ILE:HB	2.02	0.40
1:A:74:GLN:H	1:A:74:GLN:HG2	1.46	0.40
1:A:22:VAL:HG22	1:B:116:PRO:HB3	2.03	0.40
1:A:154:THR:HG21	1:A:181:VAL:O	2.21	0.40
1:A:168:SER:O	1:A:169:LYS:HB2	2.21	0.40
1:A:329:GLY:HA3	1:A:340:THR:HA	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	535/543 (98%)	496 (93%)	36 (7%)	3 (1%)	21	51
1	B	535/543 (98%)	494 (92%)	37 (7%)	4 (1%)	18	48
All	All	1070/1086 (98%)	990 (92%)	73 (7%)	7 (1%)	18	48

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	LYS
1	B	299	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	156	ARG
1	A	156	ARG
1	B	59	THR
1	A	483	GLN
1	B	483	GLN

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	453/458 (99%)	426 (94%)	27 (6%)	17	47
1	B	453/458 (99%)	431 (95%)	22 (5%)	22	54
All	All	906/916 (99%)	857 (95%)	49 (5%)	20	51

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	SER
1	A	46	ARG
1	A	67	ILE
1	A	74	GLN
1	A	96	GLU
1	A	99	LYS
1	A	135	GLU
1	A	140	LYS
1	A	150	LEU
1	A	161	ILE
1	A	193	LEU
1	A	222	ILE
1	A	233	LYS
1	A	312	ILE
1	A	336	ARG
1	A	351	ILE
1	A	366	LYS
1	A	395	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	403	LYS
1	A	413	VAL
1	A	424	LEU
1	A	437	VAL
1	A	439	THR
1	A	492	GLU
1	A	501	LYS
1	A	504	SER
1	A	516	LYS
1	B	34	SER
1	B	59	THR
1	B	73	GLN
1	B	96	GLU
1	B	99	LYS
1	B	144	ASP
1	B	150	LEU
1	B	161	ILE
1	B	222	ILE
1	B	233	LYS
1	B	303	LYS
1	B	312	ILE
1	B	314	ASN
1	B	366	LYS
1	B	395	ILE
1	B	407	GLN
1	B	413	VAL
1	B	424	LEU
1	B	492	GLU
1	B	501	LYS
1	B	504	SER
1	B	516	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	110	GLN
1	A	111	HIS
1	A	115	GLN
1	A	160	GLN
1	A	327	HIS
1	A	344	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	434	HIS
1	A	502	ASN
1	A	540	HIS
1	B	73	GLN
1	B	110	GLN
1	B	115	GLN
1	B	160	GLN
1	B	289	HIS
1	B	314	ASN
1	B	327	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 ⓘ

Of 5 ligands modelled in this entry, 1 is modelled with single atom - leaving 4 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	A	601	1	46,50,50	1.56	4 (8%)	58,82,82	1.13	4 (6%)
2	HEC	B	601	1	46,50,50	1.45	2 (4%)	58,82,82	1.30	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DHE	B	602	1,4	52,56,56	1.92	9 (17%)	68,94,94	1.78	14 (20%)
3	DHE	A	602	1	52,56,56	1.88	9 (17%)	68,94,94	1.83	12 (17%)

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	A	601	1	-	8/14/54/54	-
2	HEC	B	601	1	-	8/14/54/54	-
3	DHE	B	602	1,4	1/1/15/19	9/20/108/108	-
3	DHE	A	602	1	1/1/15/19	7/20/108/108	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	DHE	CBD-CAD	-6.74	1.28	1.51
3	A	602	DHE	CBD-CAD	-6.63	1.29	1.51
2	A	601	HEC	CAC-C3C	5.59	1.53	1.35
2	A	601	HEC	CAB-C3B	5.43	1.52	1.35
2	B	601	HEC	CAB-C3B	5.25	1.52	1.35
3	B	602	DHE	FE-NB	4.98	2.10	1.94
3	A	602	DHE	FE-NB	4.79	2.09	1.94
2	B	601	HEC	CAC-C3C	4.67	1.50	1.35
3	B	602	DHE	CGC-C3C	4.25	1.62	1.54
3	B	602	DHE	FE-NC	4.20	2.07	1.94
3	A	602	DHE	FE-NC	4.11	2.07	1.94
3	A	602	DHE	FE-NA	3.86	2.07	1.95
3	A	602	DHE	CGC-C3C	3.86	1.61	1.54
3	B	602	DHE	FE-NA	3.67	2.07	1.95
3	B	602	DHE	CGB-C3B	3.58	1.60	1.54
3	A	602	DHE	CGB-C3B	3.50	1.60	1.54
3	A	602	DHE	FE-ND	3.22	2.05	1.95
3	B	602	DHE	FE-ND	2.83	2.04	1.95
2	A	601	HEC	C3B-C4B	-2.62	1.41	1.46
2	A	601	HEC	CMB-C2B	2.33	1.55	1.50
3	A	602	DHE	CAC-C3C	-2.23	1.48	1.54
3	B	602	DHE	CAC-C3C	-2.09	1.48	1.54
3	B	602	DHE	CAB-C3B	-2.09	1.48	1.54
3	A	602	DHE	CAB-C3B	-2.06	1.48	1.54

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	DHE	CBD-CAD-C3D	5.59	127.99	112.53
3	A	602	DHE	CBD-CAD-C3D	5.43	127.54	112.53
3	A	602	DHE	C1C-NC-C4C	4.94	111.05	105.21
3	A	602	DHE	C4B-NB-C1B	4.85	110.95	105.21
3	B	602	DHE	C1C-NC-C4C	4.64	110.70	105.21
3	B	602	DHE	CAD-CBD-CGD	4.62	125.91	113.67
3	A	602	DHE	CAD-CBD-CGD	4.51	125.64	113.67
3	B	602	DHE	C4B-NB-C1B	4.31	110.31	105.21
3	A	602	DHE	C3B-C4B-CHC	4.17	126.14	122.44
2	A	601	HEC	CBB-CAB-C3B	-4.02	119.40	127.43
3	B	602	DHE	C3B-C4B-CHC	3.79	125.81	122.44
2	B	601	HEC	CBC-CAC-C3C	-3.67	120.11	127.43
2	B	601	HEC	CAA-C2A-C3A	-3.48	121.36	127.87
2	B	601	HEC	CAA-C2A-C1A	3.29	131.54	124.85
2	B	601	HEC	CBB-CAB-C3B	-3.22	121.00	127.43
3	A	602	DHE	C3C-C4C-CHD	3.13	125.22	122.44
3	A	602	DHE	C2A-C1A-NA	-3.02	107.41	110.32
3	B	602	DHE	CHC-C1C-NC	2.95	127.60	124.42
3	A	602	DHE	C3D-C4D-ND	-2.85	106.99	110.15
3	A	602	DHE	CHA-C1A-C2A	2.65	129.05	124.86
3	A	602	DHE	CHB-C1B-NB	2.62	127.24	124.42
3	B	602	DHE	C2A-C1A-NA	-2.54	107.87	110.32
3	B	602	DHE	C3C-C4C-CHD	2.53	124.69	122.44
2	A	601	HEC	CBC-CAC-C3C	-2.52	122.39	127.43
3	B	602	DHE	CHA-C1A-C2A	2.51	128.83	124.86
3	B	602	DHE	C4D-ND-C1D	2.26	109.51	105.82
3	A	602	DHE	C1C-CHC-C4B	2.24	128.79	125.23
3	B	602	DHE	CHB-C1B-NB	2.20	126.79	124.42
2	A	601	HEC	CAD-C3D-C4D	2.14	129.12	124.94
3	B	602	DHE	C3D-C4D-ND	-2.10	107.83	110.15
2	A	601	HEC	CMD-C2D-C1D	2.05	128.54	125.42
3	B	602	DHE	C4A-NA-C1A	2.04	109.15	105.82
3	A	602	DHE	CHC-C1C-NC	2.04	126.62	124.42
3	B	602	DHE	C1C-CHC-C4B	2.02	128.44	125.23

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	602	DHE	NA
3	B	602	DHE	NA

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	HEC	C2B-C3B-CAB-CBB
2	A	601	HEC	C4B-C3B-CAB-CBB
2	A	601	HEC	C2C-C3C-CAC-CBC
2	A	601	HEC	C4C-C3C-CAC-CBC
2	B	601	HEC	C2B-C3B-CAB-CBB
2	B	601	HEC	C4B-C3B-CAB-CBB
2	B	601	HEC	C2C-C3C-CAC-CBC
2	B	601	HEC	C4C-C3C-CAC-CBC
3	B	602	DHE	C2D-C3D-CAD-CBD
3	B	602	DHE	C4D-C3D-CAD-CBD
3	A	602	DHE	C2D-C3D-CAD-CBD
3	A	602	DHE	C4D-C3D-CAD-CBD
3	A	602	DHE	C3C-CAC-CBC-O2C
3	B	602	DHE	C3C-CAC-CBC-O2C
3	A	602	DHE	C3C-CAC-CBC-O1C
3	B	602	DHE	C3C-CAC-CBC-O1C
2	A	601	HEC	CAA-CBA-CGA-O2A
2	A	601	HEC	CAA-CBA-CGA-O1A
2	B	601	HEC	CAA-CBA-CGA-O2A
3	B	602	DHE	CAA-CBA-CGA-O2A
2	B	601	HEC	CAA-CBA-CGA-O1A
3	A	602	DHE	C3B-CAB-CBB-O1B
3	B	602	DHE	C3B-CAB-CBB-O1B
3	B	602	DHE	CAA-CBA-CGA-O1A
2	B	601	HEC	CAD-CBD-CGD-O1D
2	A	601	HEC	CAD-CBD-CGD-O2D
3	A	602	DHE	C3B-CAB-CBB-O2B
3	B	602	DHE	C3B-CAB-CBB-O2B
2	A	601	HEC	CAD-CBD-CGD-O1D
2	B	601	HEC	CAD-CBD-CGD-O2D
3	B	602	DHE	CAD-CBD-CGD-O2D
3	A	602	DHE	CAD-CBD-CGD-O2D

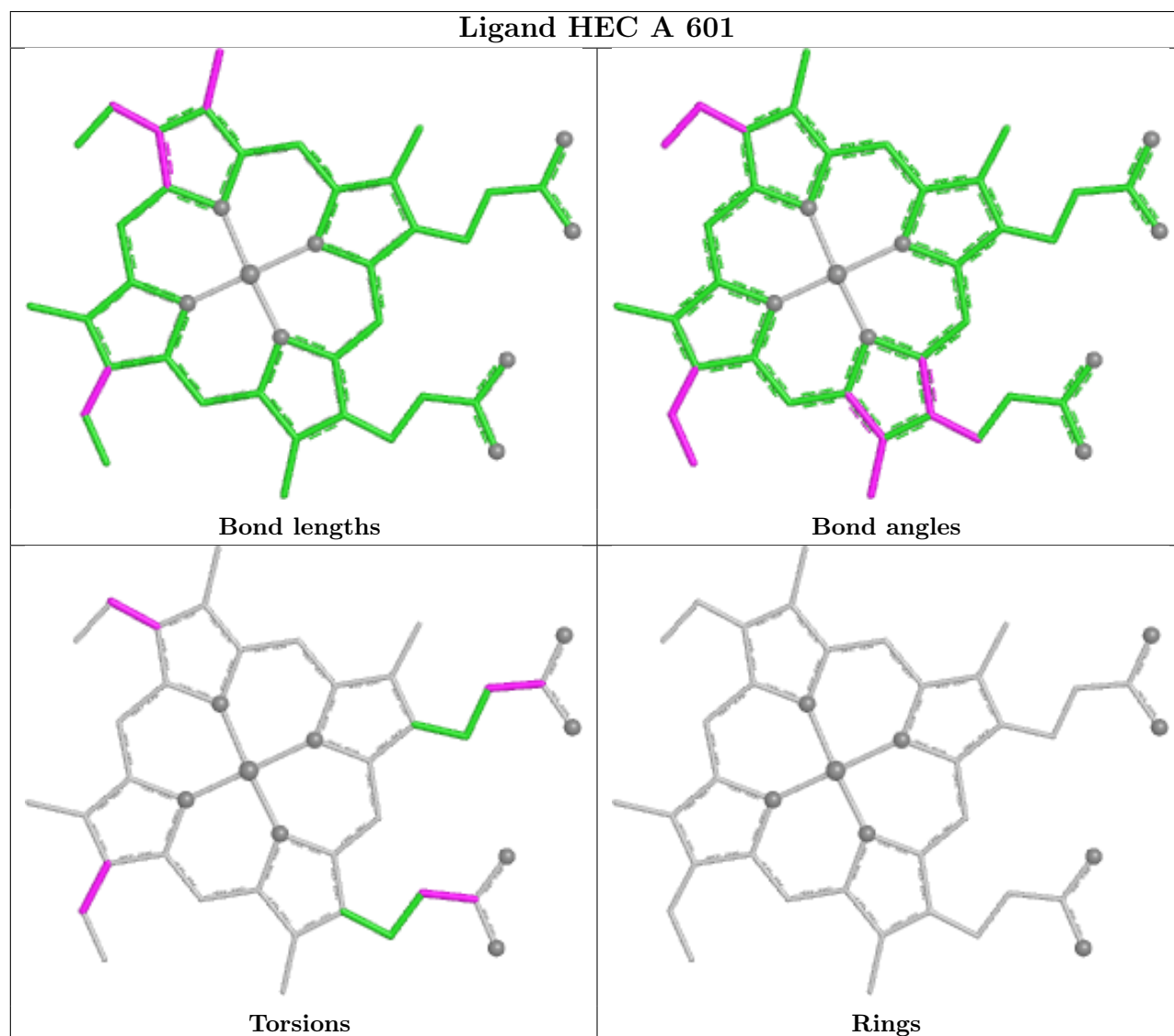
There are no ring outliers.

4 monomers are involved in 10 short contacts:

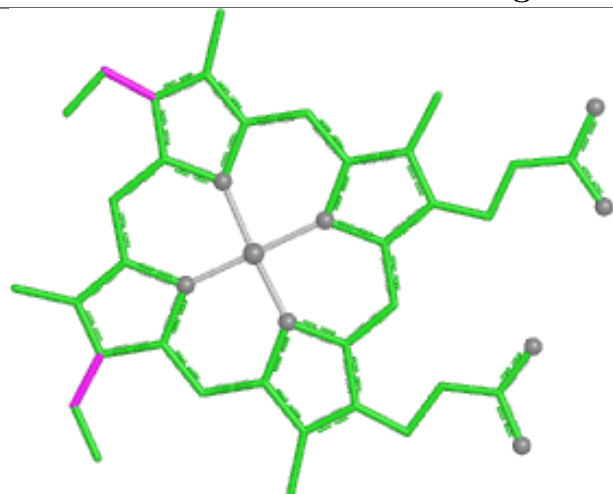
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEC	3	0
2	B	601	HEC	4	0
3	B	602	DHE	2	0
3	A	602	DHE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

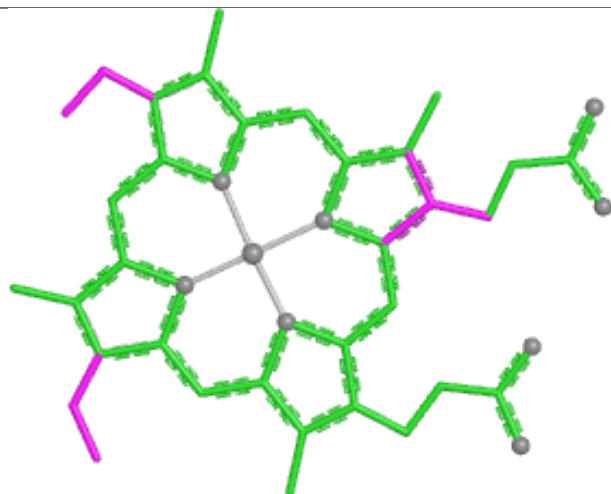
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.



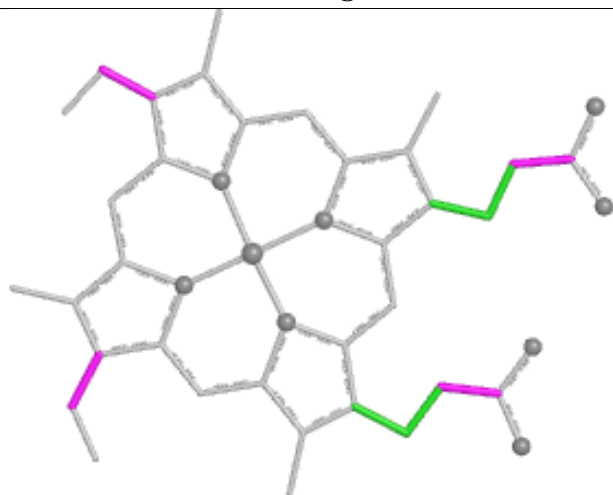
Ligand HEC B 601



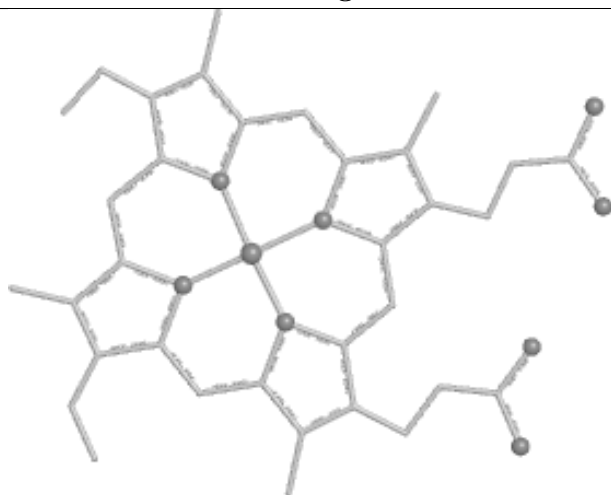
Bond lengths



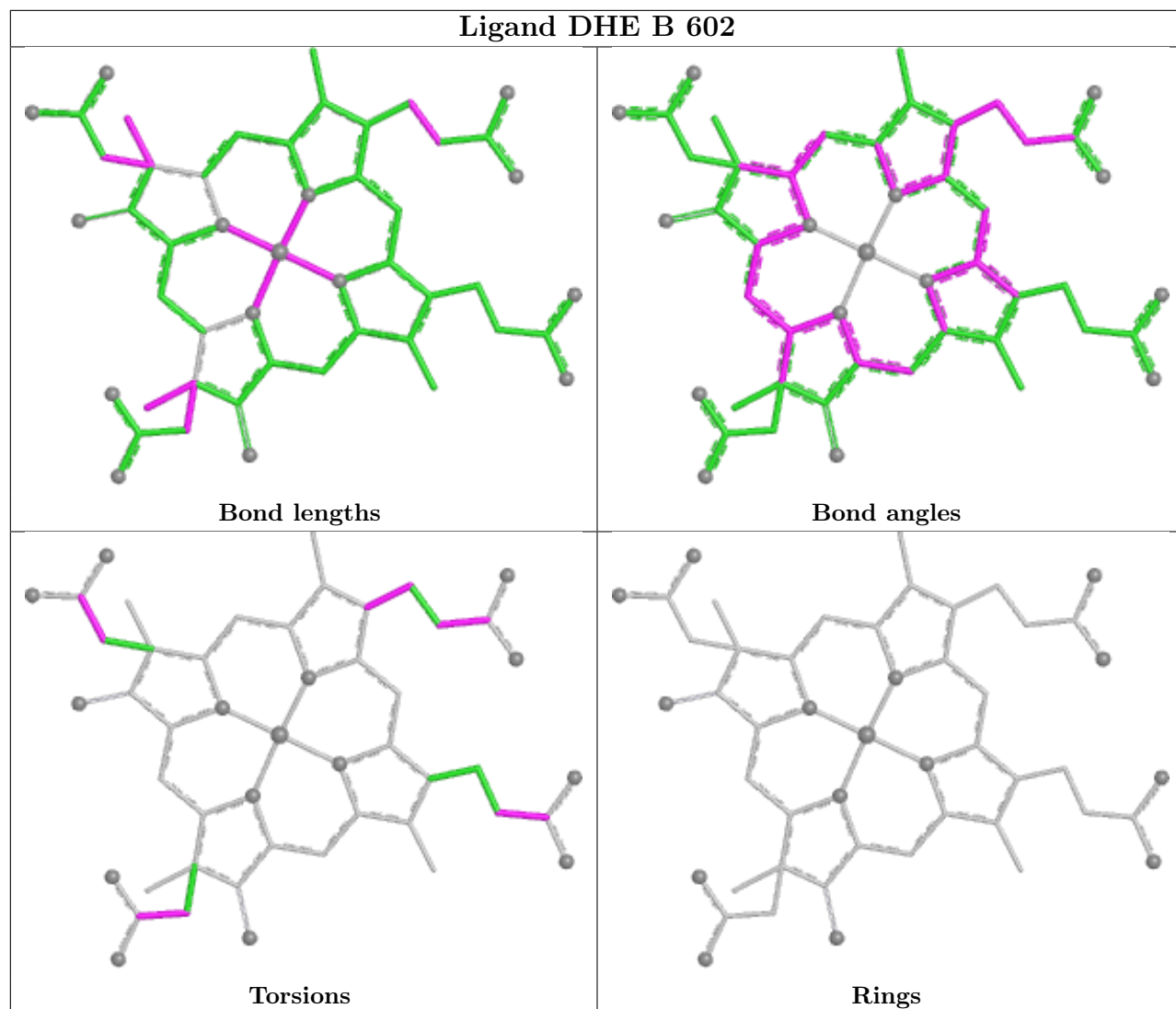
Bond angles

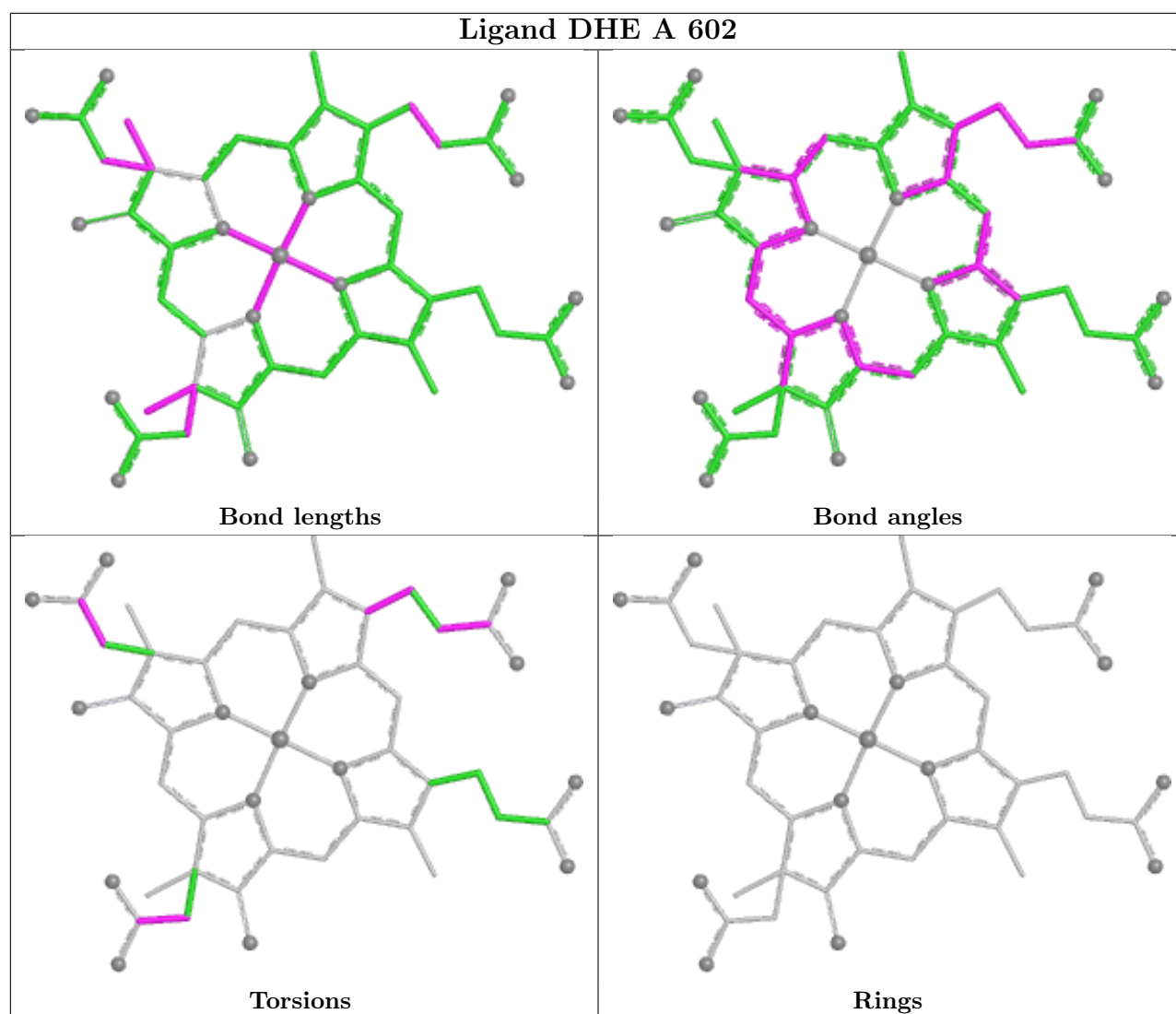


Torsions



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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	537/543 (98%)	-0.37	5 (0%) 81 75	15, 39, 65, 84	0
1	B	537/543 (98%)	-0.39	5 (0%) 81 75	21, 38, 65, 83	0
All	All	1074/1086 (98%)	-0.38	10 (0%) 81 75	15, 38, 65, 84	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	60	GLY	6.6
1	A	99	LYS	3.6
1	A	74	GLN	3.0
1	B	99	LYS	3.0
1	B	74	GLN	2.7
1	A	236	GLU	2.7
1	A	92	GLY	2.4
1	B	489	ARG	2.3
1	B	144	ASP	2.2
1	A	144	ASP	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](#)

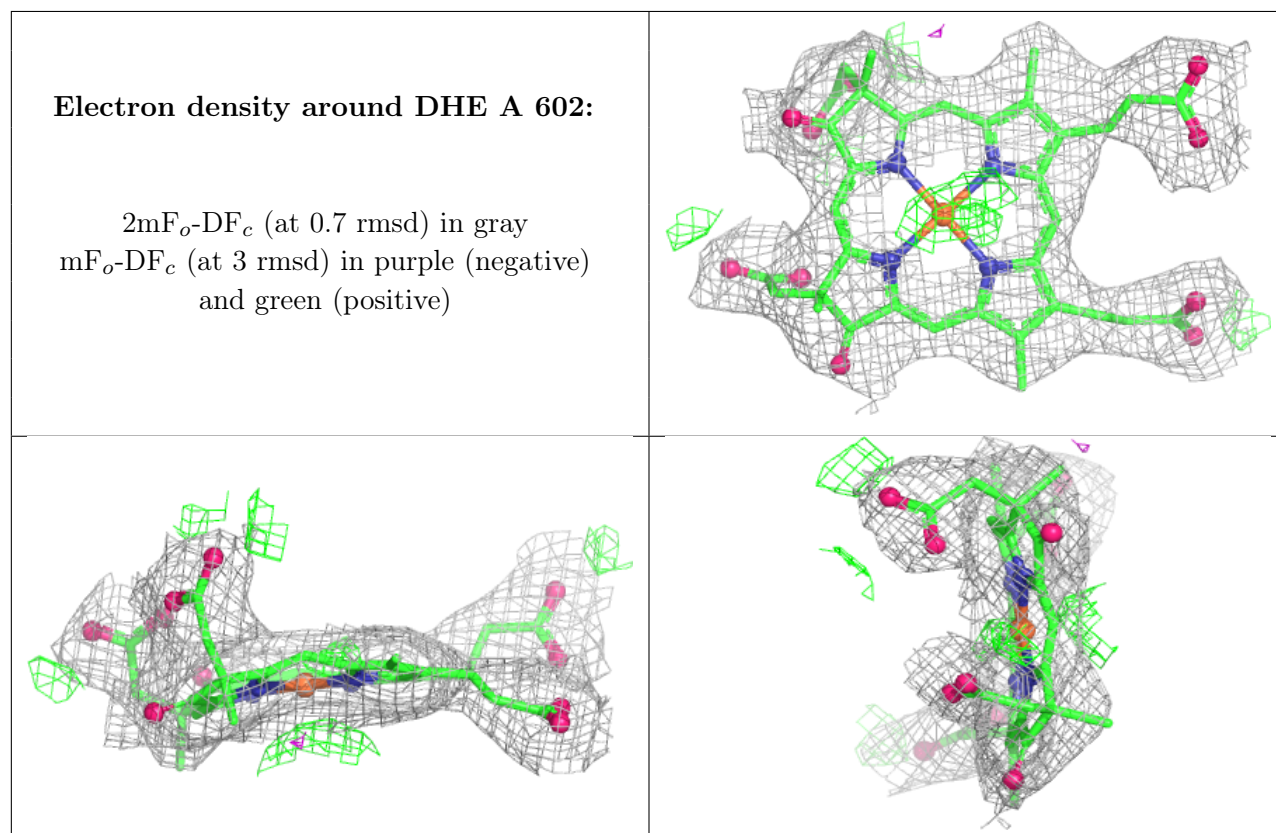
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

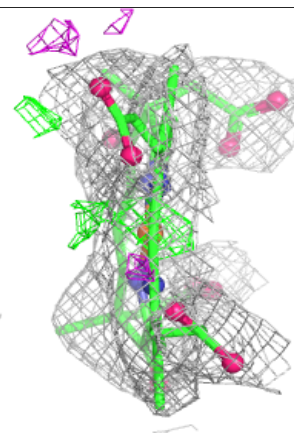
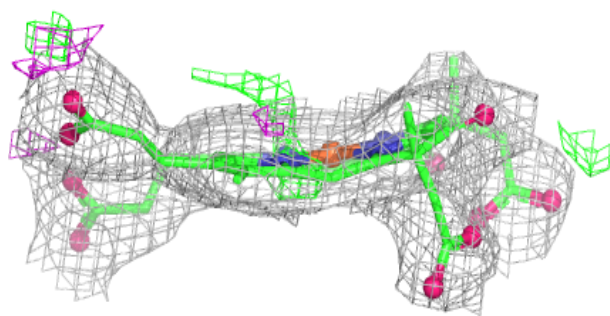
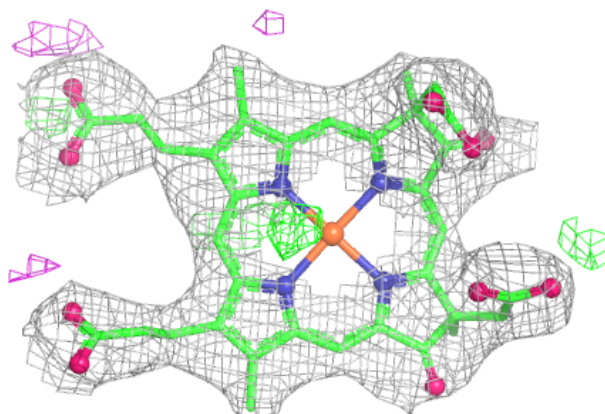
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	OH	B	603	1/1	0.94	0.27	42,42,42,42	0
3	DHE	A	602	49/49	0.97	0.07	24,32,43,45	0
3	DHE	B	602	49/49	0.97	0.06	16,29,42,47	0
2	HEC	B	601	43/43	0.97	0.07	26,34,45,47	0
2	HEC	A	601	43/43	0.98	0.07	19,35,56,65	0

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.



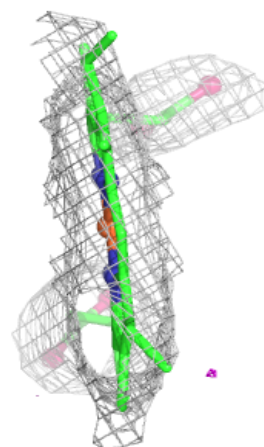
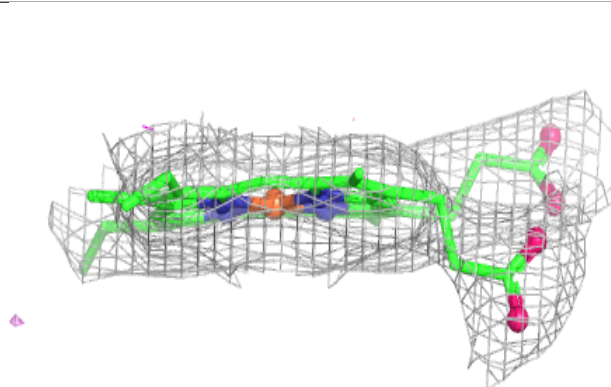
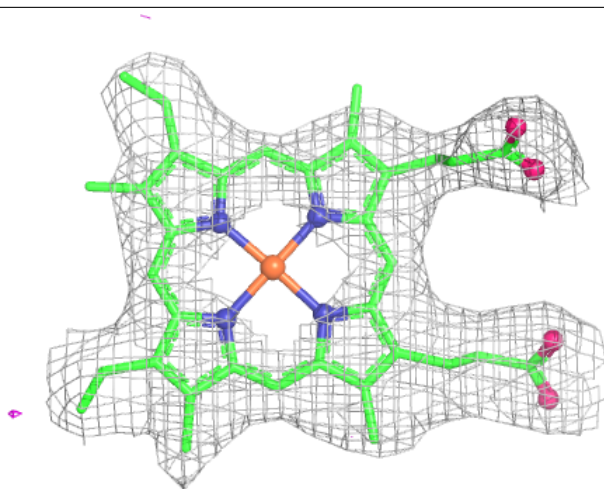
Electron density around DHE B 602:

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



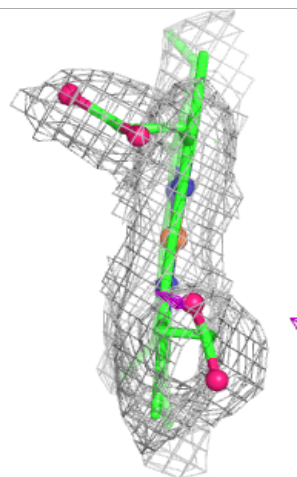
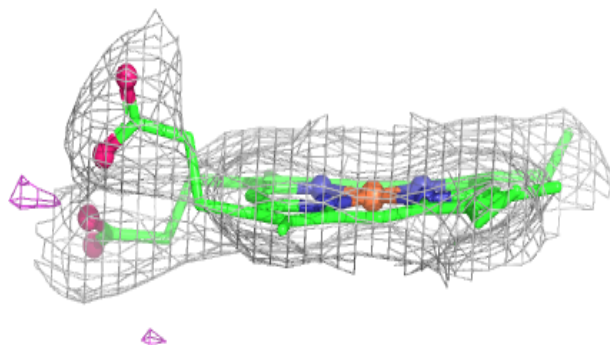
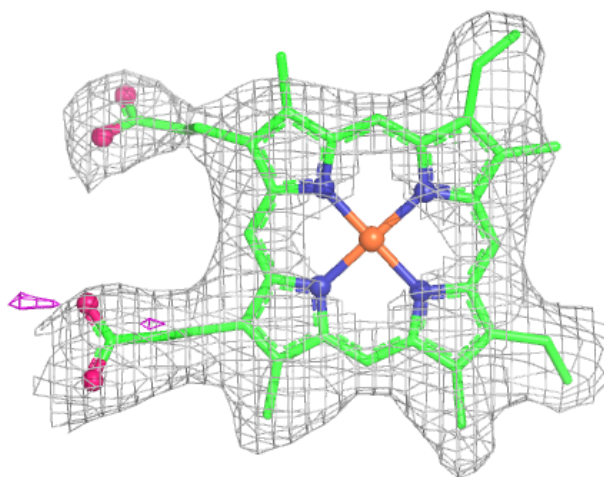
Electron density around HEC B 601:

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



Electron density around HEC A 601:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.