



Full wwPDB X-ray Structure Validation Report ⓘ

May 19, 2020 – 12:37 am BST

PDB ID : 1QW5
Title : Murine inducible nitric oxide synthase oxygenase domain in complex with W1400 inhibitor.
Authors : Fedorov, R.; Hartmann, E.; Ghosh, D.K.; Schlichting, I.
Deposited on : 2003-08-31
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

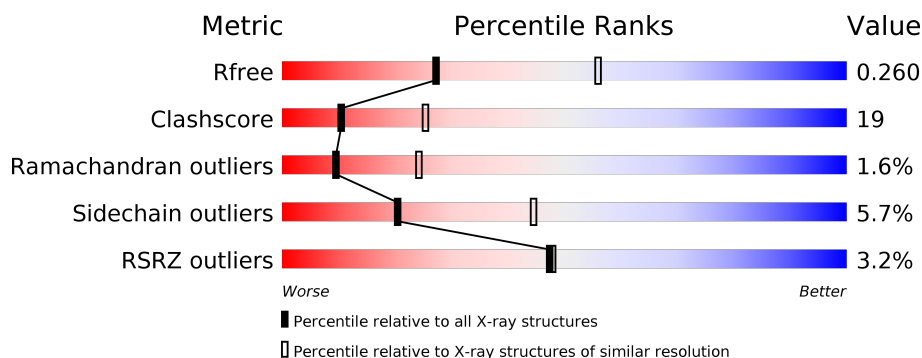
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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

Mol	Chain	Length	Quality of chain
1	A	419	<div> <div>4%</div> <div> <div></div> <div>67%</div> <div>29%</div> <div>.</div> </div> </div>
1	B	419	<div> <div>3%</div> <div> <div></div> <div>67%</div> <div>29%</div> <div>.</div> </div> </div>

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.

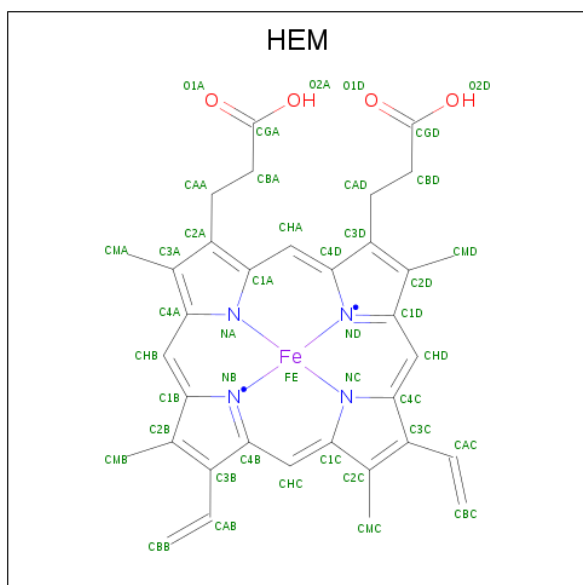
- Molecule 1 is a protein called Nitric oxide synthase, inducible.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total 3415	C 2189	N 588	O 617	S 21	0	0	0
1	B	419	Total 3415	C 2189	N 588	O 617	S 21	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



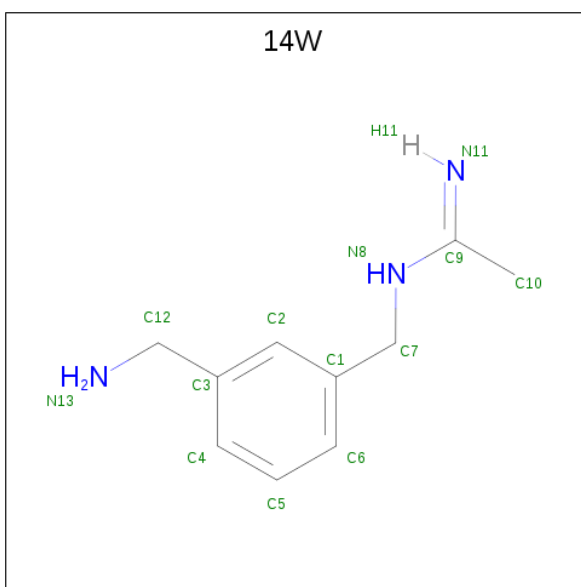
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is N-(3-(AMINOMETHYL)BENZYL)ACETAMIDINE (three-letter code: 14W) (formula: $C_{10}H_{15}N_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			13	10	3		
5	B	1	Total	C	N	0	0
			13	10	3		

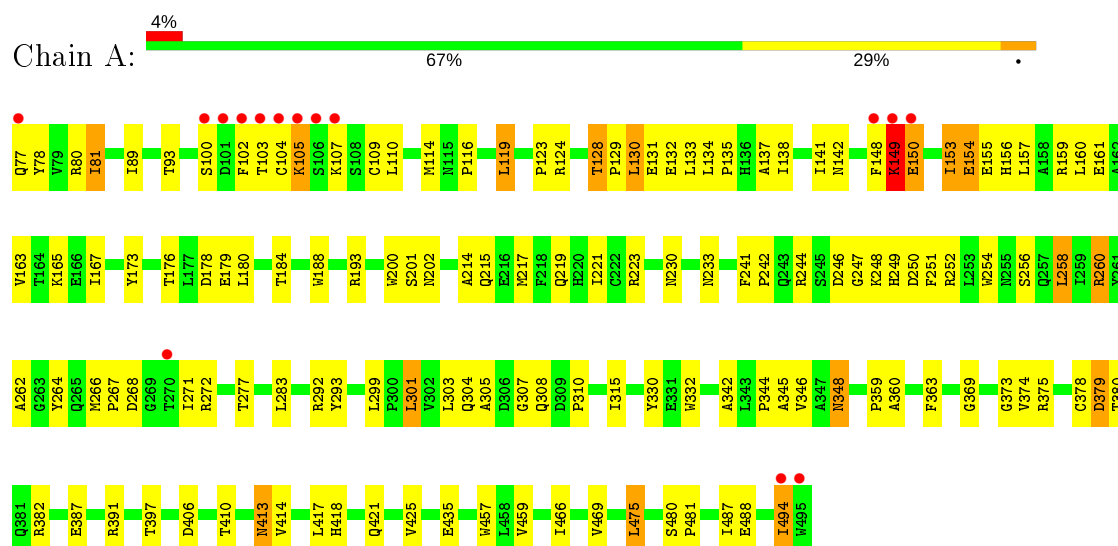
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	135	Total	O	0	0
			135	135		
6	B	128	Total	O	0	0
			128	128		

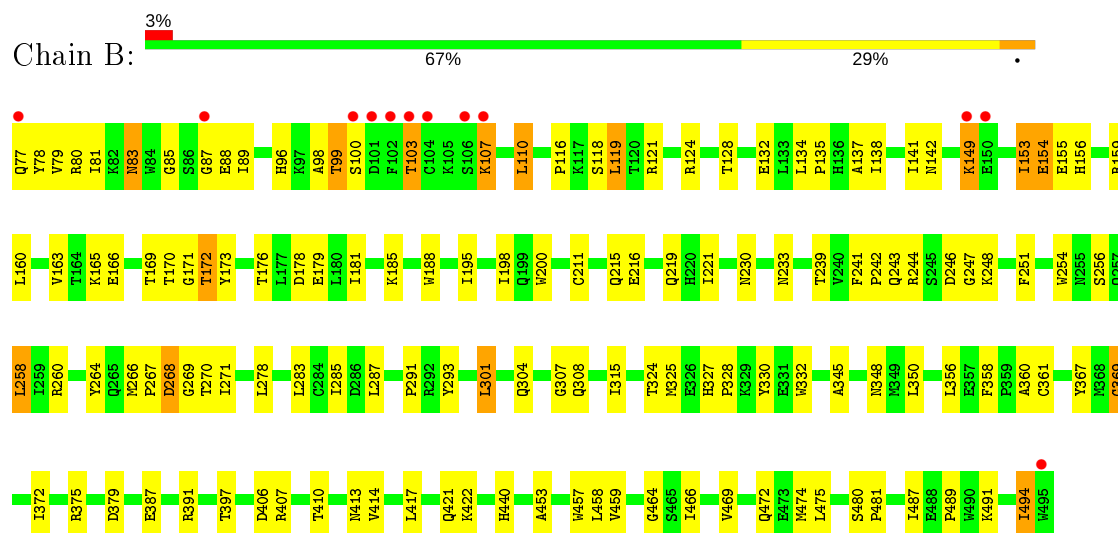
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Nitric oxide synthase, inducible



- Molecule 1: Nitric oxide synthase, inducible



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	214.56 Å 214.56 Å 117.39 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.70 19.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.70) 99.7 (19.69-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.71 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.211 , 0.264 0.210 , 0.260	Depositor DCC
R_{free} test set	2107 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	51.6	Xtriage
Anisotropy	0.579	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7241	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, H4B, 14W

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	0.39	0/3515	0.63	1/4778 (0.0%)
1	B	0.39	0/3515	0.63	0/4778
All	All	0.39	0/7030	0.63	1/9556 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	LYS	N-CA-C	-5.32	96.65	111.00

There are no chirality outliers.

There are no planarity outliers.

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	A	3415	0	3313	135	0
1	B	3415	0	3313	115	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	43	0	30	3	0
3	B	43	0	30	2	0
4	A	17	0	15	0	0
4	B	17	0	15	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	13	0	14	1	0
5	B	13	0	14	0	0
6	A	135	0	0	3	0
6	B	128	0	0	6	0
All	All	7241	0	6744	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 19.

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)
1:B:153:ILE:H	1:B:153:ILE:HD12	1.13	1.14
1:A:153:ILE:HD12	1:A:153:ILE:H	1.28	0.96
1:B:285:ILE:HD11	1:B:291:PRO:HB3	1.53	0.91
1:B:494:ILE:H	1:B:494:ILE:HD12	1.36	0.91
1:A:494:ILE:H	1:A:494:ILE:HD12	1.34	0.91
1:A:80:ARG:HE	1:A:89:ILE:HG21	1.38	0.89
1:A:77:GLN:HG2	1:A:78:TYR:H	1.37	0.88
1:A:81:ILE:HD11	1:A:475:LEU:HD13	1.61	0.83
1:A:134:LEU:O	1:A:138:ILE:HG12	1.80	0.81
1:B:153:ILE:H	1:B:153:ILE:CD1	1.90	0.80
1:A:103:THR:HG22	1:A:110:LEU:HB2	1.63	0.79
1:B:83:ASN:ND2	1:B:85:GLY:H	1.81	0.79
1:B:301:LEU:HD13	1:B:315:ILE:HD11	1.66	0.78
1:B:83:ASN:HD22	1:B:83:ASN:C	1.87	0.78
1:B:83:ASN:HD22	1:B:85:GLY:H	1.34	0.76
1:B:103:THR:HG21	1:B:116:PRO:HB2	1.66	0.76
1:B:387:GLU:OE1	1:B:397:THR:HG21	1.86	0.75
1:B:387:GLU:OE2	1:B:391:ARG:HD2	1.85	0.75
1:A:149:LYS:O	1:A:150:GLU:HG2	1.86	0.75
1:A:77:GLN:HG2	1:A:78:TYR:N	2.01	0.75
1:B:107:LYS:HB3	1:B:107:LYS:NZ	2.03	0.74
1:A:130:LEU:HD13	1:A:167:ILE:HG22	1.69	0.74
1:A:221:ILE:HG21	1:A:301:LEU:HD21	1.68	0.73
1:B:494:ILE:N	1:B:494:ILE:HD12	2.03	0.73
1:A:129:PRO:HB2	1:A:132:GLU:HG3	1.72	0.71
1:B:110:LEU:HD23	1:B:110:LEU:N	2.05	0.70
1:A:104:CYS:HA	1:A:110:LEU:HD12	1.74	0.70
1:A:134:LEU:HB3	1:A:135:PRO:HD3	1.74	0.70
1:B:103:THR:O	1:B:110:LEU:HG	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LYS:O	1:B:169:THR:HG23	1.93	0.69
1:A:159:ARG:O	1:A:163:VAL:HG23	1.93	0.69
1:A:154:GLU:H	1:A:154:GLU:CD	1.96	0.68
1:A:104:CYS:HA	1:A:110:LEU:CD1	2.24	0.67
1:A:188:TRP:CE3	1:A:200:TRP:HA	2.31	0.65
1:A:176:THR:OG1	1:A:179:GLU:HG3	1.96	0.65
1:B:375:ARG:O	1:B:379:ASP:HB2	1.96	0.65
1:A:138:ILE:HG22	1:A:142:ASN:HD21	1.62	0.65
1:A:262:ALA:HB2	1:A:299:LEU:CD2	2.27	0.64
1:B:153:ILE:N	1:B:153:ILE:HD12	1.98	0.64
1:A:387:GLU:O	1:A:391:ARG:HG3	1.98	0.63
1:A:138:ILE:HG23	1:A:160:LEU:HD22	1.81	0.63
1:A:215:GLN:HG3	1:A:219:GLN:NE2	2.14	0.62
1:B:110:LEU:HD23	1:B:110:LEU:H	1.62	0.62
1:A:252:ARG:HD3	1:A:359:PRO:HB2	1.80	0.62
1:A:330:TYR:HB3	1:A:332:TRP:CE2	2.34	0.62
1:B:260:ARG:HG3	6:B:986:HOH:O	1.99	0.62
1:B:88:GLU:C	1:B:89:ILE:HD12	2.21	0.61
1:A:271:ILE:HD12	1:A:271:ILE:N	2.16	0.61
1:A:375:ARG:O	1:A:379:ASP:HB2	2.00	0.61
1:B:171:GLY:O	1:B:172:THR:HB	2.01	0.61
1:B:285:ILE:HD11	1:B:291:PRO:CB	2.28	0.61
1:A:258:LEU:HB2	1:A:345:ALA:HB3	1.83	0.60
3:B:900:HEM:HMC1	3:B:900:HEM:HBC2	1.83	0.60
1:B:149:LYS:HD2	1:B:149:LYS:O	2.01	0.60
1:B:81:ILE:HD11	1:B:475:LEU:CD1	2.32	0.59
1:A:132:GLU:O	1:A:135:PRO:HD2	2.02	0.59
1:A:116:PRO:HG2	1:A:119:LEU:HB2	1.85	0.59
1:B:264:TYR:CE2	1:B:293:TYR:HA	2.38	0.59
1:B:116:PRO:CG	1:B:119:LEU:HD22	2.33	0.59
1:A:217:MET:HB3	1:A:303:LEU:HD13	1.83	0.58
3:A:900:HEM:HBA2	6:A:963:HOH:O	2.02	0.58
1:A:266:MET:CE	1:A:272:ARG:HH11	2.15	0.58
1:A:251:PHE:O	1:A:360:ALA:HB2	2.02	0.58
1:A:103:THR:HG23	1:A:116:PRO:HB3	1.84	0.58
1:A:494:ILE:N	1:A:494:ILE:HD12	2.13	0.58
1:A:103:THR:HG22	1:A:110:LEU:CB	2.34	0.57
1:B:407:ARG:HD3	6:B:983:HOH:O	2.05	0.57
1:B:188:TRP:CE3	1:B:200:TRP:HA	2.39	0.57
1:B:166:GLU:OE2	1:B:173:TYR:HA	2.05	0.57
1:A:417:LEU:O	1:A:421:GLN:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:GLU:HG2	1:A:155:GLU:H	1.71	0.56
1:A:271:ILE:HD12	1:A:271:ILE:H	1.71	0.56
1:A:223:ARG:HG2	1:A:223:ARG:HH11	1.70	0.56
1:A:254:TRP:HE3	1:A:283:LEU:HD21	1.70	0.56
1:A:163:VAL:HG13	1:A:173:TYR:CD2	2.41	0.56
1:A:230:ASN:HB3	1:A:233:ASN:O	2.06	0.56
1:B:304:GLN:HG3	1:B:308:GLN:O	2.06	0.56
1:B:103:THR:CG2	1:B:116:PRO:HB2	2.35	0.55
1:A:138:ILE:HG23	1:A:160:LEU:CD2	2.36	0.55
1:A:303:LEU:O	1:A:310:PRO:HA	2.07	0.55
1:B:107:LYS:HZ3	1:B:107:LYS:HB3	1.70	0.55
1:B:254:TRP:HE3	1:B:283:LEU:HD21	1.72	0.55
1:A:124:ARG:HH22	1:A:128:THR:HG22	1.72	0.55
1:B:137:ALA:O	1:B:141:ILE:HG12	2.07	0.55
1:A:153:ILE:O	1:A:157:LEU:HG	2.07	0.55
1:B:153:ILE:O	1:B:156:HIS:HB3	2.06	0.55
1:B:176:THR:OG1	1:B:179:GLU:HG3	2.06	0.55
1:A:133:LEU:HD22	1:A:167:ILE:HD13	1.88	0.55
1:A:105:LYS:HG3	1:A:110:LEU:HD11	1.88	0.54
1:A:131:GLU:O	1:A:135:PRO:HG2	2.07	0.54
1:B:301:LEU:CD1	1:B:315:ILE:HD11	2.36	0.54
1:A:344:PRO:HB2	5:A:902:14W:H6	1.90	0.54
1:B:103:THR:HG23	1:B:118:SER:HB3	1.90	0.54
1:B:283:LEU:O	1:B:287:LEU:HG	2.08	0.54
1:A:459:VAL:HG22	1:A:469:VAL:HG23	1.90	0.53
1:B:116:PRO:HG2	1:B:119:LEU:HD22	1.90	0.53
1:B:221:ILE:HG21	1:B:301:LEU:HD21	1.89	0.53
1:B:241:PHE:HB3	1:B:242:PRO:CD	2.38	0.53
1:A:107:LYS:HB2	1:A:107:LYS:NZ	2.22	0.53
1:B:134:LEU:O	1:B:138:ILE:HG13	2.08	0.53
1:B:83:ASN:C	1:B:83:ASN:ND2	2.60	0.52
1:A:246:ASP:OD2	1:A:248:LYS:HB2	2.09	0.52
1:B:78:TYR:CD1	1:B:78:TYR:C	2.83	0.52
1:A:342:ALA:HB1	1:A:425:VAL:HG11	1.92	0.52
1:B:244:ARG:HA	6:B:1002:HOH:O	2.10	0.51
1:B:330:TYR:HD2	1:B:332:TRP:NE1	2.08	0.51
1:B:124:ARG:HB2	1:B:247:GLY:HA3	1.92	0.51
1:B:251:PHE:O	1:B:360:ALA:HB2	2.10	0.51
1:A:104:CYS:CB	1:A:109:CYS:HA	2.40	0.51
1:A:138:ILE:O	1:A:142:ASN:ND2	2.43	0.51
1:B:198:ILE:HB	1:B:440:HIS:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ARG:NH2	1:A:128:THR:HG22	2.25	0.51
1:B:417:LEU:O	1:B:421:GLN:HG3	2.11	0.51
1:B:81:ILE:HD11	1:B:475:LEU:HD12	1.93	0.51
1:A:148:PHE:N	1:A:148:PHE:CD2	2.79	0.51
1:A:153:ILE:HG22	1:A:157:LEU:HD11	1.92	0.50
1:A:330:TYR:CD2	1:A:330:TYR:N	2.76	0.50
1:B:132:GLU:O	1:B:135:PRO:HD2	2.11	0.50
1:B:266:MET:HB3	1:B:267:PRO:HD2	1.93	0.50
1:A:410:THR:O	1:A:414:VAL:HG23	2.12	0.50
1:B:268:ASP:O	1:B:270:THR:N	2.37	0.50
1:A:241:PHE:HB3	1:A:242:PRO:HD2	1.93	0.50
1:B:138:ILE:HG22	1:B:142:ASN:HD21	1.77	0.50
1:B:327:HIS:ND1	1:B:328:PRO:HD2	2.27	0.50
1:B:330:TYR:HD2	1:B:332:TRP:HE1	1.58	0.50
1:B:215:GLN:HG3	1:B:219:GLN:NE2	2.27	0.50
1:B:410:THR:O	1:B:414:VAL:HG23	2.11	0.49
1:A:104:CYS:HA	1:A:110:LEU:H	1.76	0.49
1:A:241:PHE:HB3	1:A:242:PRO:CD	2.42	0.49
1:A:262:ALA:HB2	1:A:299:LEU:HD21	1.91	0.49
1:B:154:GLU:CD	1:B:154:GLU:N	2.66	0.49
1:B:246:ASP:OD2	1:B:248:LYS:HB2	2.12	0.49
1:A:180:LEU:O	1:A:184:THR:HG23	2.12	0.49
1:A:130:LEU:CD1	1:A:167:ILE:HG22	2.42	0.49
1:B:489:PRO:C	1:B:491:LYS:H	2.16	0.48
1:B:453:ALA:HB1	1:B:458:LEU:CD1	2.43	0.48
1:A:264:TYR:CD2	1:A:293:TYR:HA	2.47	0.48
1:A:305:ALA:O	1:A:308:GLN:HB2	2.14	0.48
1:B:110:LEU:CD2	1:B:110:LEU:N	2.75	0.48
1:B:215:GLN:HG3	1:B:219:GLN:HE22	1.79	0.48
1:A:153:ILE:HD12	1:A:153:ILE:N	2.11	0.48
1:A:379:ASP:HB3	1:A:382:ARG:HG2	1.94	0.48
1:B:173:TYR:CE1	1:B:356:LEU:HD21	2.48	0.48
1:A:304:GLN:HG3	1:A:308:GLN:O	2.13	0.48
1:A:301:LEU:HD13	1:A:315:ILE:HD11	1.96	0.48
1:A:494:ILE:CD1	1:A:494:ILE:H	2.11	0.48
1:B:195:ILE:N	6:B:1021:HOH:O	2.44	0.48
1:B:271:ILE:HD13	1:B:278:LEU:HD11	1.96	0.48
1:A:132:GLU:C	1:A:135:PRO:HD2	2.33	0.47
1:B:124:ARG:HG3	1:B:244:ARG:HD3	1.96	0.47
1:B:267:PRO:HG2	1:B:268:ASP:OD1	2.14	0.47
1:A:138:ILE:HG22	1:A:142:ASN:ND2	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:ARG:CD	1:A:359:PRO:HB2	2.44	0.47
1:A:104:CYS:HB2	1:A:109:CYS:HA	1.96	0.47
1:A:379:ASP:CB	1:A:382:ARG:HG2	2.44	0.47
1:B:239:THR:O	1:B:361:CYS:HA	2.15	0.47
1:A:81:ILE:HD12	1:A:475:LEU:HD22	1.97	0.47
1:A:102:PHE:CG	1:A:103:THR:N	2.82	0.47
1:A:457:TRP:HZ3	6:A:963:HOH:O	1.97	0.47
1:B:241:PHE:HB3	1:B:242:PRO:HD2	1.96	0.47
1:B:98:ALA:O	1:B:99:THR:O	2.32	0.47
1:B:487:ILE:HD12	1:B:487:ILE:N	2.30	0.46
1:A:161:GLU:OE2	1:A:165:LYS:NZ	2.47	0.46
1:A:254:TRP:CE3	1:A:283:LEU:HD21	2.50	0.46
3:A:900:HEM:HBD1	6:A:963:HOH:O	2.15	0.46
1:B:230:ASN:HB3	1:B:233:ASN:O	2.16	0.46
1:A:348:ASN:ND2	1:A:348:ASN:H	2.14	0.46
1:B:154:GLU:CD	1:B:155:GLU:H	2.18	0.46
1:B:80:ARG:NH2	6:B:1042:HOH:O	2.44	0.46
1:B:83:ASN:HB2	1:B:472:GLN:OE1	2.15	0.46
1:B:89:ILE:HD12	1:B:89:ILE:N	2.31	0.46
3:A:900:HEM:HHC	3:A:900:HEM:HBB2	1.97	0.45
1:A:264:TYR:CE2	1:A:293:TYR:HA	2.52	0.45
1:A:103:THR:HG23	1:A:116:PRO:CB	2.47	0.45
1:A:249:HIS:HA	1:A:307:GLY:HA3	1.99	0.45
1:A:114:MET:HE2	1:A:457:TRP:HZ2	1.82	0.45
1:B:466:ILE:O	1:B:466:ILE:HG22	2.16	0.45
1:B:387:GLU:CD	1:B:391:ARG:HD2	2.36	0.45
1:B:79:VAL:HG11	1:B:475:LEU:HD11	1.98	0.45
1:A:330:TYR:HB3	1:A:332:TRP:NE1	2.32	0.45
1:B:258:LEU:HD22	1:B:345:ALA:HB1	1.98	0.44
1:B:83:ASN:ND2	1:B:85:GLY:N	2.59	0.44
1:B:264:TYR:CD2	1:B:293:TYR:HA	2.52	0.44
3:B:900:HEM:CMC	3:B:900:HEM:HBC2	2.46	0.44
1:A:78:TYR:CD1	1:A:78:TYR:C	2.91	0.44
1:A:104:CYS:HA	1:A:110:LEU:HD13	1.99	0.44
1:A:137:ALA:O	1:A:141:ILE:HG12	2.17	0.44
1:A:134:LEU:HD11	1:A:138:ILE:HD11	1.99	0.44
1:A:116:PRO:CG	1:A:119:LEU:HD22	2.48	0.44
1:B:181:ILE:O	1:B:185:LYS:HG3	2.17	0.44
1:A:130:LEU:HD13	1:A:167:ILE:CG2	2.44	0.44
1:A:131:GLU:O	1:A:135:PRO:CD	2.65	0.44
1:A:103:THR:CG2	1:A:116:PRO:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:VAL:HB	1:A:363:PHE:CZ	2.53	0.43
1:B:350:LEU:HD23	1:B:350:LEU:C	2.38	0.43
1:A:154:GLU:N	1:A:154:GLU:CD	2.69	0.43
1:A:244:ARG:HG3	1:A:250:ASP:OD1	2.18	0.43
1:A:262:ALA:CB	1:A:299:LEU:HD21	2.48	0.43
1:A:373:GLY:HA3	1:A:413:ASN:ND2	2.34	0.43
1:B:258:LEU:HB2	1:B:345:ALA:HB3	1.99	0.43
1:B:327:HIS:ND1	1:B:328:PRO:CD	2.80	0.43
1:B:480:SER:HA	1:B:481:PRO:C	2.39	0.43
1:B:494:ILE:CD1	1:B:494:ILE:H	2.17	0.43
1:A:131:GLU:O	1:A:135:PRO:CG	2.67	0.43
1:B:327:HIS:CG	1:B:328:PRO:HD2	2.53	0.43
1:A:80:ARG:HG3	1:A:89:ILE:CG2	2.49	0.43
1:B:138:ILE:HG23	1:B:160:LEU:HD22	2.01	0.43
1:A:148:PHE:N	1:A:148:PHE:HD2	2.17	0.42
1:A:202:ASN:HD22	1:A:202:ASN:N	2.16	0.42
1:A:154:GLU:HG2	1:A:155:GLU:N	2.34	0.42
1:B:159:ARG:O	1:B:163:VAL:HG23	2.19	0.42
1:A:114:MET:CE	1:A:457:TRP:HZ2	2.32	0.42
1:A:466:ILE:O	1:A:466:ILE:HG22	2.18	0.42
1:A:123:PRO:HD2	1:A:487:ILE:HD12	2.01	0.42
1:A:260:ARG:HD2	1:A:277:THR:HG21	2.02	0.42
1:B:367:TYR:CD2	1:B:372:ILE:HD11	2.54	0.42
1:A:266:MET:HB3	1:A:267:PRO:HD2	2.02	0.42
1:A:266:MET:HE2	1:A:272:ARG:HH11	1.82	0.42
1:A:344:PRO:O	1:A:344:PRO:HG2	2.19	0.42
1:B:327:HIS:CE1	1:B:330:TYR:HD1	2.37	0.42
1:A:103:THR:HG21	1:A:110:LEU:O	2.20	0.41
1:B:256:SER:HA	1:B:348:ASN:ND2	2.35	0.41
1:B:459:VAL:HG22	1:B:469:VAL:HG23	2.01	0.41
1:B:121:ARG:HD3	1:B:121:ARG:HA	1.90	0.41
1:B:375:ARG:HH12	4:B:903:H4B:C4	2.33	0.41
1:A:153:ILE:O	1:A:156:HIS:HB3	2.21	0.41
1:B:166:GLU:O	1:B:170:THR:OG1	2.31	0.41
1:A:193:ARG:HD3	1:A:457:TRP:CD2	2.56	0.41
1:A:330:TYR:HD1	1:A:332:TRP:CZ2	2.38	0.41
1:A:413:ASN:HA	1:A:413:ASN:HD22	1.56	0.41
1:A:248:LYS:HE3	1:A:248:LYS:HB3	1.81	0.41
1:B:422:LYS:HB3	1:B:422:LYS:NZ	2.36	0.41
1:A:266:MET:HE1	1:A:272:ARG:HD3	2.03	0.41
1:B:83:ASN:O	1:B:87:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:GLN:O	1:B:96:HIS:HE1	2.02	0.41
1:A:214:ALA:O	1:A:217:MET:HB2	2.20	0.41
1:B:103:THR:HG23	1:B:118:SER:CB	2.50	0.41
1:B:195:ILE:O	1:B:195:ILE:HG12	2.20	0.41
1:B:211:CYS:SG	1:B:216:GLU:HB3	2.60	0.41
1:A:330:TYR:HD2	1:A:330:TYR:N	2.17	0.41
1:A:110:LEU:HD12	1:A:110:LEU:N	2.35	0.41
1:A:330:TYR:CD1	1:A:332:TRP:CZ2	3.09	0.41
1:A:418:HIS:HA	1:A:421:GLN:OE1	2.21	0.41
1:B:457:TRP:HA	4:B:903:H4B:N1	2.36	0.41
1:A:494:ILE:CD1	1:A:494:ILE:N	2.79	0.40
1:B:116:PRO:HG2	1:B:119:LEU:HB2	2.02	0.40
1:A:78:TYR:HB3	1:A:93:THR:HG22	2.04	0.40
1:B:243:GLN:HB3	1:B:358:PHE:CE2	2.56	0.40
1:B:369:GLY:HA3	6:B:1004:HOH:O	2.21	0.40
1:A:134:LEU:CD1	1:A:138:ILE:HD11	2.50	0.40
1:A:244:ARG:HG3	1:A:247:GLY:HA2	2.04	0.40
1:A:480:SER:HA	1:A:481:PRO:C	2.41	0.40
1:A:374:VAL:O	1:A:378:CYS:HB2	2.21	0.40
1:B:103:THR:HG21	1:B:116:PRO:CB	2.46	0.40
1:B:138:ILE:O	1:B:142:ASN:ND2	2.55	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	417/419 (100%)	374 (90%)	37 (9%)	6 (1%)	11	28
1	B	417/419 (100%)	376 (90%)	34 (8%)	7 (2%)	9	23
All	All	834/838 (100%)	750 (90%)	71 (8%)	13 (2%)	9	24

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	SER
1	A	105	LYS
1	B	99	THR
1	B	172	THR
1	B	269	GLY
1	A	150	GLU
1	A	369	GLY
1	A	397	THR
1	B	100	SER
1	A	268	ASP
1	B	464	GLY
1	B	307	GLY
1	B	369	GLY

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	367/367 (100%)	344 (94%)	23 (6%)	18	40
1	B	367/367 (100%)	348 (95%)	19 (5%)	23	49
All	All	734/734 (100%)	692 (94%)	42 (6%)	20	44

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	ILE
1	A	119	LEU
1	A	128	THR
1	A	130	LEU
1	A	149	LYS
1	A	153	ILE
1	A	154	GLU
1	A	178	ASP
1	A	201	SER
1	A	256	SER

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Mol	Chain	Res	Type
1	A	258	LEU
1	A	260	ARG
1	A	292	ARG
1	A	301	LEU
1	A	348	ASN
1	A	379	ASP
1	A	380	THR
1	A	406	ASP
1	A	413	ASN
1	A	435	GLU
1	A	475	LEU
1	A	488	GLU
1	A	494	ILE
1	B	83	ASN
1	B	103	THR
1	B	107	LYS
1	B	110	LEU
1	B	119	LEU
1	B	128	THR
1	B	149	LYS
1	B	153	ILE
1	B	154	GLU
1	B	178	ASP
1	B	258	LEU
1	B	268	ASP
1	B	301	LEU
1	B	324	THR
1	B	325	MET
1	B	406	ASP
1	B	413	ASN
1	B	474	MET
1	B	494	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	142	ASN
1	A	174	GLN
1	A	202	ASN
1	A	215	GLN
1	A	219	GLN

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Mol	Chain	Res	Type
1	A	231	ASN
1	A	348	ASN
1	A	413	ASN
1	B	83	ASN
1	B	96	HIS
1	B	142	ASN
1	B	143	GLN
1	B	174	GLN
1	B	202	ASN
1	B	215	GLN
1	B	219	GLN
1	B	231	ASN
1	B	249	HIS
1	B	486	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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
3	HEM	B	900	1	27,50,50	1.46	4 (14%)	17,82,82	1.17	2 (11%)
5	14W	A	902	-	13,13,13	1.38	2 (15%)	13,16,16	1.44	2 (15%)
3	HEM	A	900	1	27,50,50	1.65	3 (11%)	17,82,82	1.44	4 (23%)
4	H4B	A	901	-	16,18,18	2.08	5 (31%)	11,26,26	4.27	8 (72%)
4	H4B	B	903	-	16,18,18	2.29	5 (31%)	11,26,26	4.23	7 (63%)
5	14W	B	904	-	13,13,13	1.40	2 (15%)	13,16,16	1.26	1 (7%)

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
3	HEM	B	900	1	-	0/6/54/54	-
5	14W	A	902	-	-	3/6/7/7	0/1/1/1
3	HEM	A	900	1	-	0/6/54/54	-
4	H4B	A	901	-	-	0/8/17/17	0/2/2/2
4	H4B	B	903	-	-	0/8/17/17	0/2/2/2
5	14W	B	904	-	-	1/6/7/7	0/1/1/1

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	903	H4B	C4-N3	6.20	1.43	1.33
4	A	901	H4B	C4-N3	5.45	1.42	1.33
4	B	903	H4B	C4A-N5	4.20	1.46	1.38
3	B	900	HEM	C3C-CAC	-3.97	1.39	1.47
4	A	901	H4B	C4A-N5	3.69	1.45	1.38
3	A	900	HEM	C3C-CAC	-3.68	1.40	1.47
3	A	900	HEM	C3C-C2C	-3.44	1.35	1.40
3	A	900	HEM	C3B-CAB	-3.33	1.41	1.47
4	B	903	H4B	C6-N5	3.10	1.52	1.45
4	A	901	H4B	C6-N5	3.01	1.51	1.45
4	A	901	H4B	C8A-N1	2.77	1.39	1.34
3	B	900	HEM	C3B-CAB	-2.74	1.42	1.47
3	B	900	HEM	C1C-C2C	2.72	1.48	1.42
4	B	903	H4B	C8A-N1	2.56	1.39	1.34
5	A	902	14W	C2-C3	2.48	1.43	1.39
5	B	904	14W	C6-C1	2.28	1.43	1.38
5	B	904	14W	C5-C4	2.13	1.43	1.38
4	A	901	H4B	C7-N8	2.11	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	903	H4B	C7-N8	2.08	1.48	1.44
3	B	900	HEM	C1D-CHD	-2.08	1.35	1.41
5	A	902	14W	C6-C1	2.02	1.43	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	H4B	C4-C4A-C8A	9.01	122.57	114.57
4	B	903	H4B	C4-C4A-C8A	8.73	122.33	114.57
4	B	903	H4B	C4-N3-C2	6.07	125.57	115.93
4	A	901	H4B	C4-N3-C2	5.89	125.29	115.93
4	A	901	H4B	N3-C2-N1	-5.30	117.11	125.42
4	B	903	H4B	N3-C2-N1	-5.01	117.57	125.42
5	A	902	14W	C10-C9-N8	4.56	120.08	114.24
5	B	904	14W	C10-C9-N8	3.88	119.22	114.24
4	B	903	H4B	C4A-C4-N3	-3.78	113.25	124.01
4	A	901	H4B	N2-C2-N1	3.67	122.96	117.25
4	A	901	H4B	C2-N1-C8A	3.55	122.49	114.54
4	B	903	H4B	N2-C2-N1	3.54	122.75	117.25
4	B	903	H4B	C2-N1-C8A	3.53	122.46	114.54
4	A	901	H4B	C4A-C4-N3	-3.47	114.15	124.01
4	B	903	H4B	C4A-N5-C6	-3.37	112.00	121.16
4	A	901	H4B	C4A-N5-C6	-3.02	112.95	121.16
3	A	900	HEM	C4C-C3C-C2C	-2.59	105.09	106.90
3	B	900	HEM	C3B-C4B-NB	2.48	112.41	109.21
5	A	902	14W	C1-C7-N8	-2.24	108.25	113.05
3	A	900	HEM	C1D-C2D-C3D	-2.22	105.45	107.00
3	A	900	HEM	C3B-C4B-NB	2.20	112.05	109.21
3	A	900	HEM	CBD-CAD-C3D	-2.10	108.60	112.48
4	A	901	H4B	C4-C4A-N5	-2.07	117.39	119.12
3	B	900	HEM	C4C-C3C-C2C	-2.06	105.46	106.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

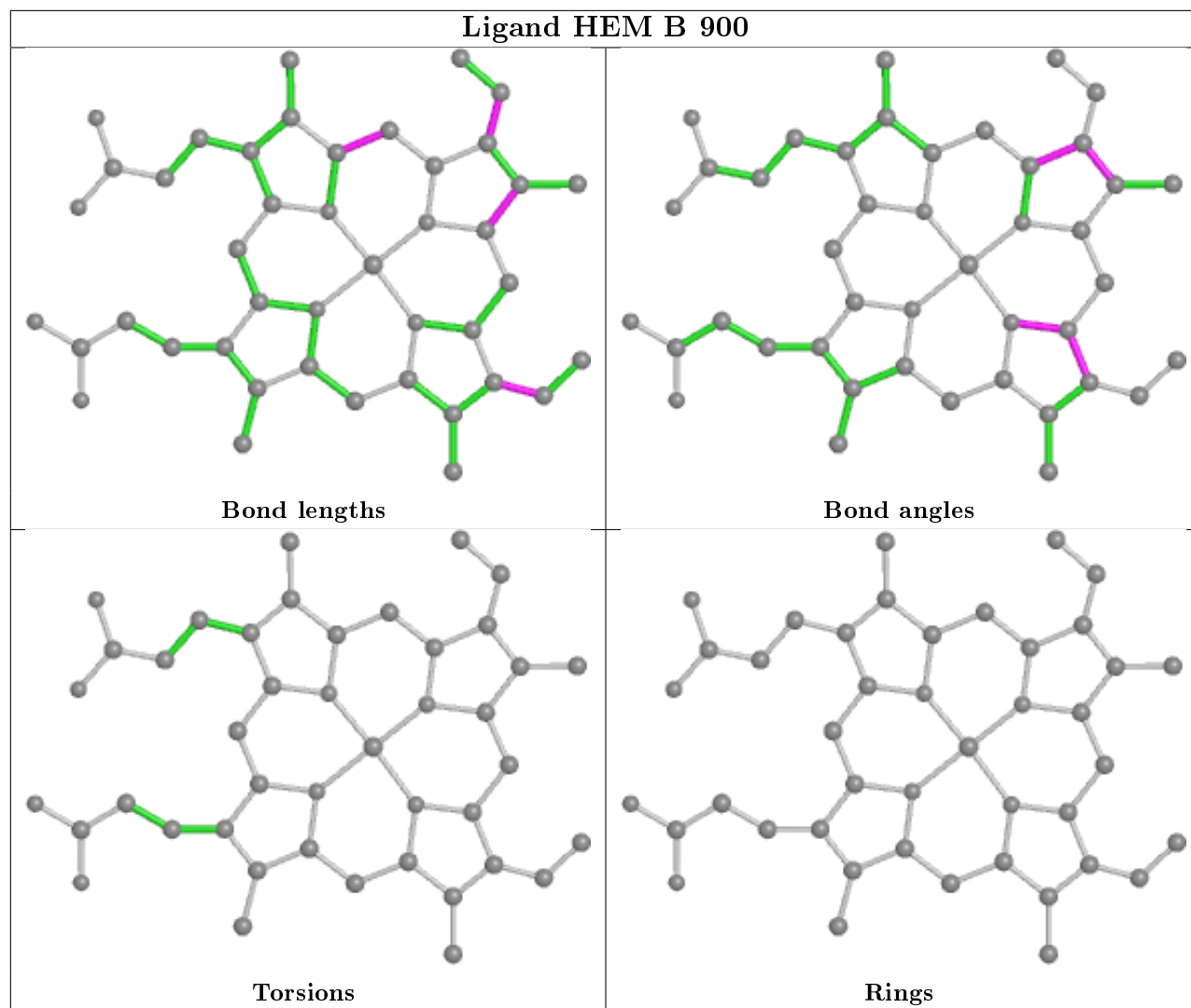
Mol	Chain	Res	Type	Atoms
5	A	902	14W	C1-C7-N8-C9
5	B	904	14W	C1-C7-N8-C9
5	A	902	14W	N13-C12-C3-C2
5	A	902	14W	N13-C12-C3-C4

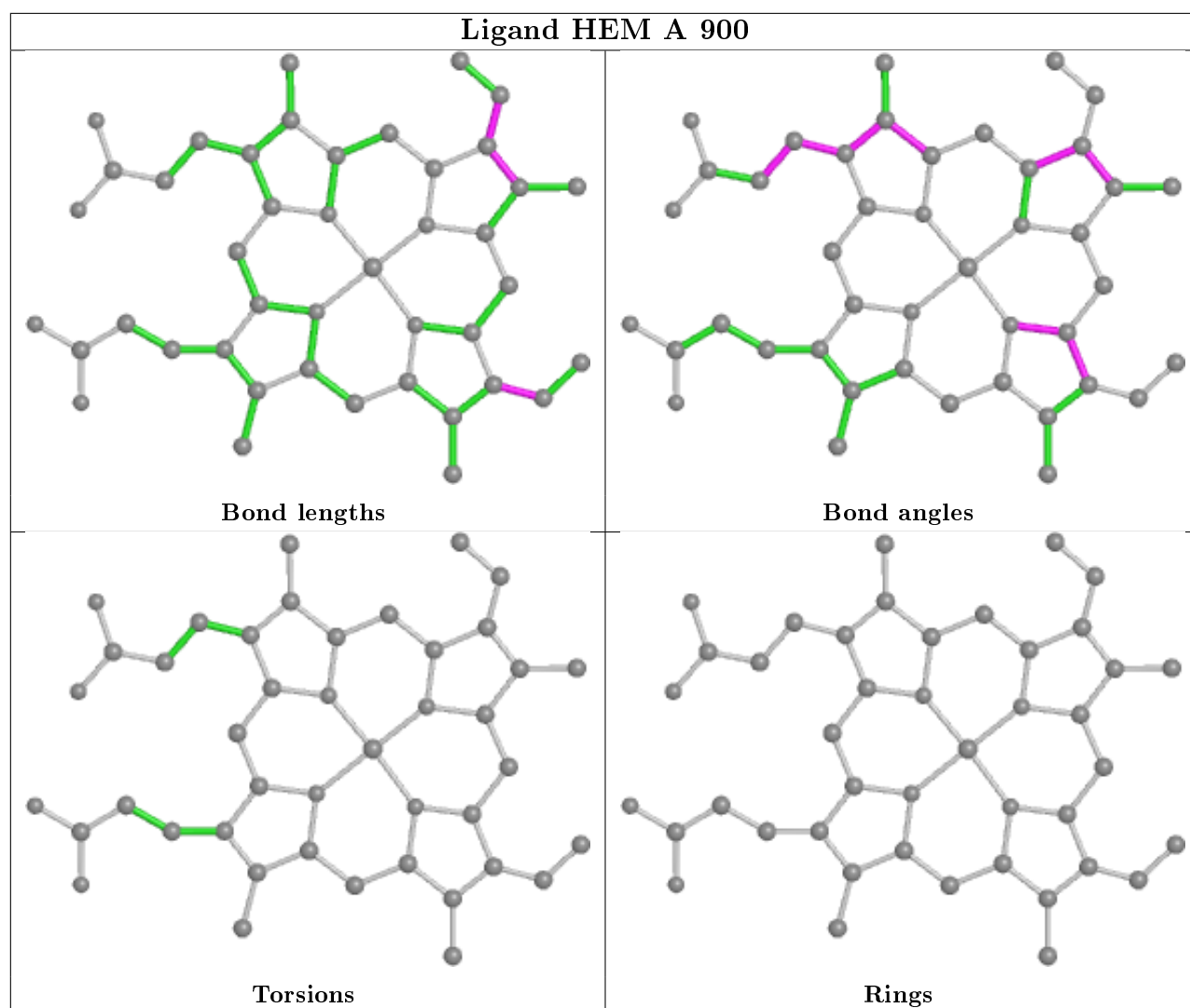
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	900	HEM	2	0
5	A	902	14W	1	0
3	A	900	HEM	3	0
4	B	903	H4B	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	419/419 (100%)	-0.17	15 (3%) 42 42	32, 49, 72, 89	0
1	B	419/419 (100%)	-0.19	12 (2%) 51 52	32, 49, 69, 93	0
All	All	838/838 (100%)	-0.18	27 (3%) 47 48	32, 49, 71, 93	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	106	SER	7.6
1	A	103	THR	7.0
1	A	104	CYS	5.8
1	A	102	PHE	5.6
1	B	103	THR	5.5
1	B	102	PHE	5.2
1	A	106	SER	4.6
1	B	101	ASP	4.3
1	B	107	LYS	3.8
1	A	150	GLU	3.5
1	A	149	LYS	3.3
1	B	150	GLU	3.1
1	A	100	SER	3.1
1	A	107	LYS	3.1
1	B	77	GLN	2.8
1	A	105	LYS	2.8
1	B	87	GLY	2.8
1	A	101	ASP	2.7
1	B	149	LYS	2.6
1	B	104	CYS	2.4
1	A	270	THR	2.4
1	A	77	GLN	2.4
1	A	495	TRP	2.4
1	B	100	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	494	ILE	2.2
1	B	495	TRP	2.1
1	A	148	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

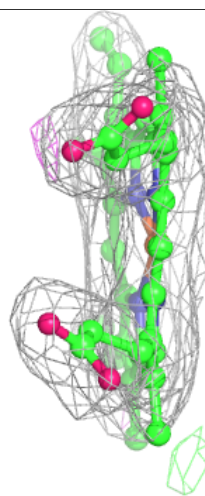
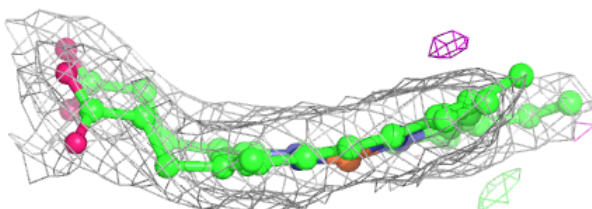
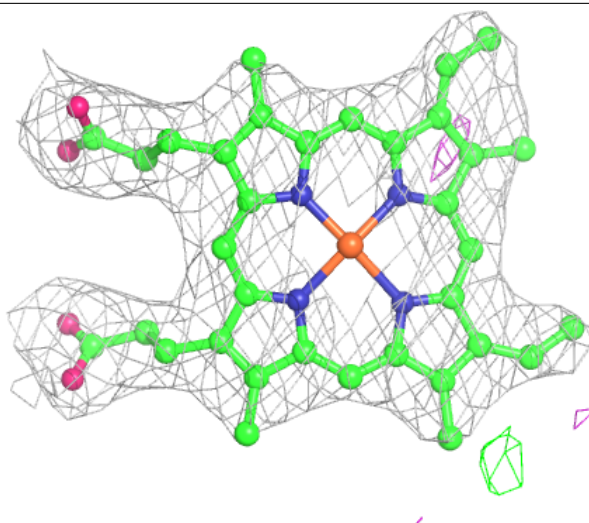
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

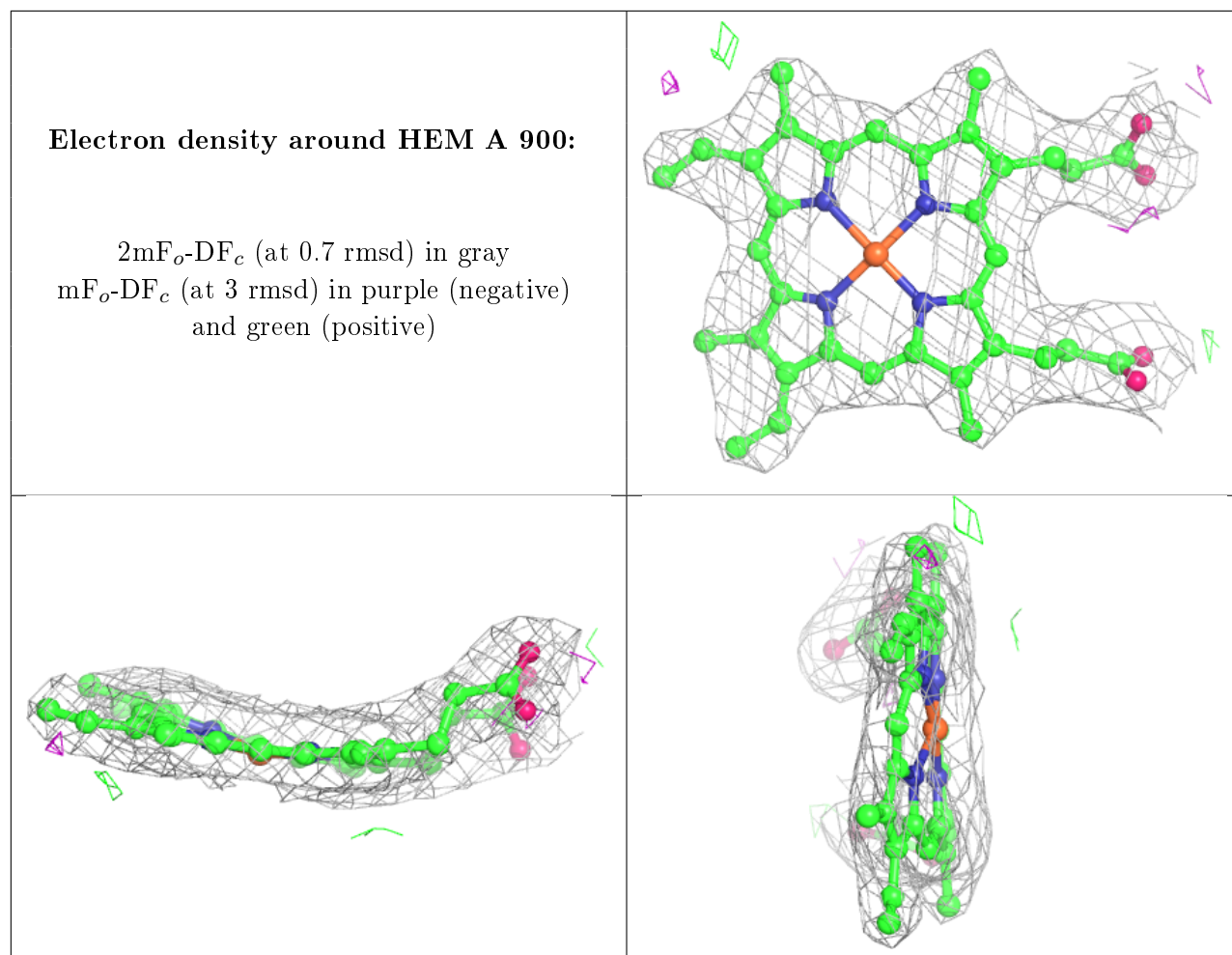
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	A	950	1/1	0.85	0.34	49,49,49,49	1
2	ZN	B	950	1/1	0.86	0.30	45,45,45,45	1
5	14W	B	904	13/13	0.94	0.22	38,40,43,43	0
5	14W	A	902	13/13	0.94	0.19	37,39,40,41	0
4	H4B	A	901	17/17	0.96	0.13	18,35,47,48	0
4	H4B	B	903	17/17	0.97	0.12	22,35,40,42	0
3	HEM	B	900	43/43	0.98	0.14	30,42,48,53	0
3	HEM	A	900	43/43	0.98	0.14	26,43,57,64	0

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

Electron density around HEM B 900:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.