



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 08:38 PM EDT

PDB ID : 3JWW / pdb_00003jww
Title : Structure of endothelial nitric oxide synthase heme domain complexed with N
1-[(3'S,4'S)-4'-((6"-amino-4"-methylpyridin-2"-yl)methyl)pyrrolidin-3'-yl]-N2
- (3'-fluorophenethyl)ethane-1,2-diamine tetrahydrochloride
Authors : Delker, S.L.; Li, H.; Poulos, T.L.
Deposited on : 2009-09-18
Resolution : 2.20 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	:	9.0.015 (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

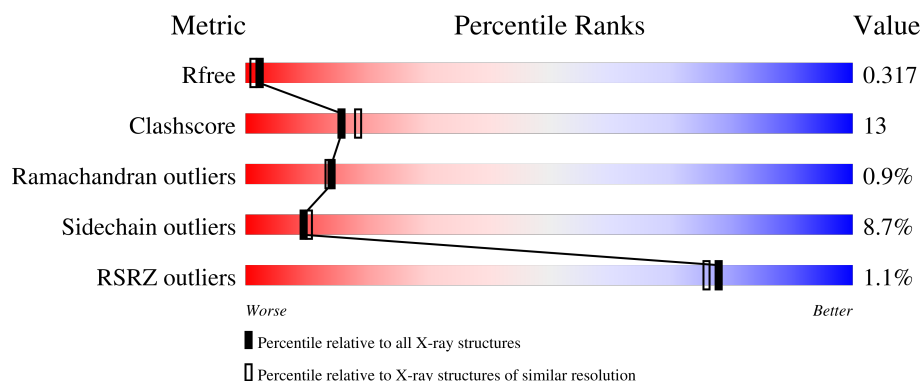
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	444	
1	B	444	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 6863 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 Nitric oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3213	2042	567	588	16			
1	B	403	Total	C	N	O	S	0	3	0
			3242	2058	577	591	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ARG	CYS	SEE REMARK 999	UNP P29473
B	100	ARG	CYS	SEE REMARK 999	UNP P29473

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (CCD ID: H4B) (formula: $C_9H_{15}N_5O_3$).



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

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

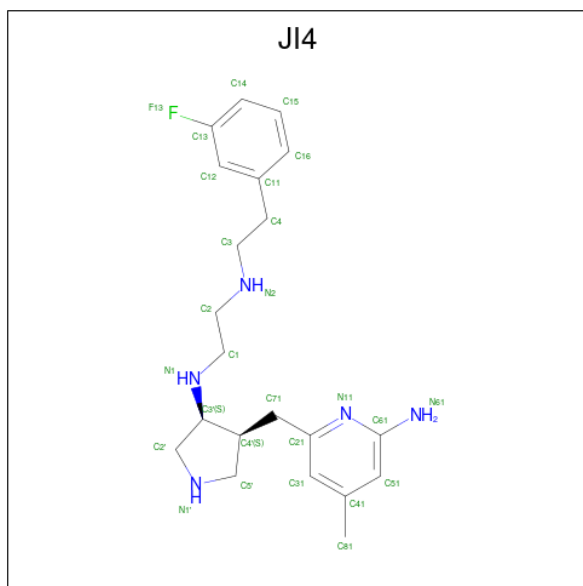
- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

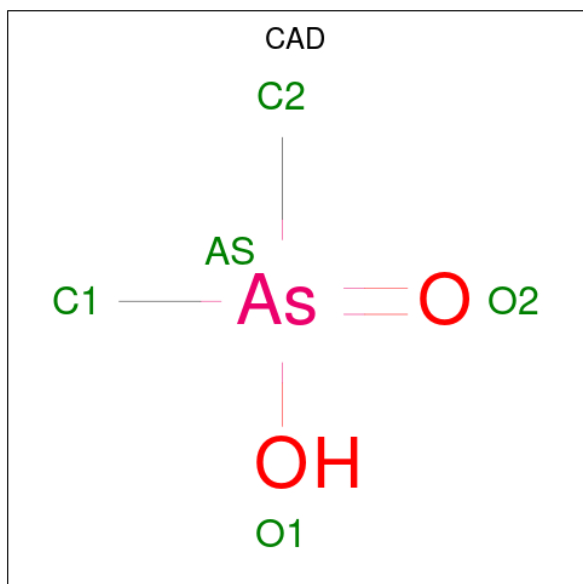
- Molecule 6 is N-{(3S,4S)-4-[(6-amino-4-methylpyridin-2-yl)methyl]pyrrolidin-3-yl}-N'-[2-(3-

fluorophenyl)ethyl]ethane-1,2-diamine (CCD ID: JI4) (formula: $C_{21}H_{30}FN_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	F	N	0	0
			27	21	1	5		
6	B	1	Total	C	F	N	0	0
			27	21	1	5		

- Molecule 7 is CACODYLIC ACID (CCD ID: CAD) (formula: $C_2H_7AsO_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	As	C	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	As	C	0	0
			3	1	2		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Zn	0	0
			1	1		

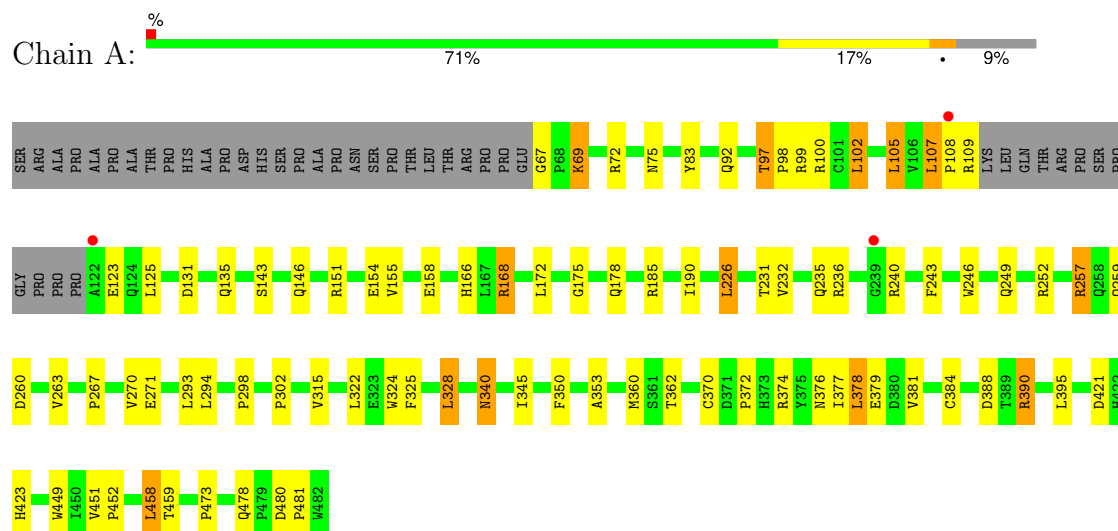
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	104	Total	O	0	0
			104	104		
9	B	107	Total	O	0	0
			107	107		

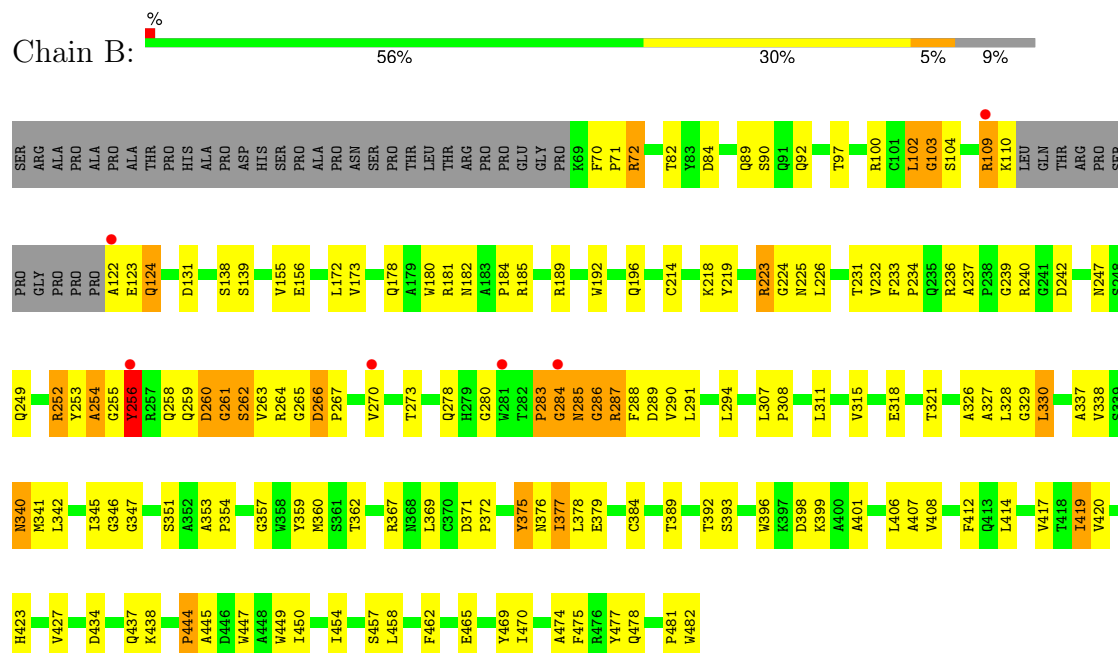
3 Residue-property plots

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: Nitric oxide synthase, endothelial



• Molecule 1: Nitric oxide synthase, endothelial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.61Å 107.13Å 157.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.43 – 2.20 39.43 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.6 (39.43-2.20) 96.5 (39.43-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0089, CNS	Depositor
R, R_{free}	0.210 , 0.284 0.263 , 0.317	Depositor DCC
R_{free} test set	2450 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.718	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6863	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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: HEM, JI4, ACT, CAD, GOL, H4B, ZN

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	1.02	1/3302 (0.0%)	1.11	10/4497 (0.2%)
1	B	1.38	23/3330 (0.7%)	1.38	39/4531 (0.9%)
All	All	1.22	24/6632 (0.4%)	1.26	49/9028 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	284	GLY	N-CA	24.40	1.80	1.45
1	B	286	GLY	N-CA	11.40	1.61	1.45
1	B	338	VAL	CA-CB	9.28	1.64	1.54
1	B	375	TYR	N-CA	7.30	1.55	1.46
1	B	445	ALA	N-CA	7.14	1.54	1.45
1	B	254	ALA	CA-CB	-6.96	1.42	1.53
1	B	261	GLY	C-O	6.89	1.33	1.23
1	B	285	ASN	CA-CB	6.44	1.64	1.53
1	B	444	PRO	CA-C	6.26	1.60	1.52
1	B	470	ILE	C-O	6.11	1.30	1.24
1	B	371	ASP	C-O	6.02	1.31	1.24
1	B	353	ALA	CA-CB	-5.94	1.46	1.53
1	A	97	THR	CA-CB	5.94	1.62	1.54
1	B	261	GLY	N-CA	5.89	1.53	1.45
1	B	256	TYR	CB-CG	5.84	1.64	1.51
1	B	97	THR	C-O	5.71	1.28	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	285	ASN	CG-ND2	5.56	1.45	1.33
1	B	185	ARG	N-CA	5.54	1.53	1.46
1	B	289	ASP	CB-CG	5.50	1.65	1.52
1	B	104	SER	N-CA	5.36	1.53	1.46
1	B	359	TYR	CA-CB	-5.16	1.45	1.53
1	B	419	ILE	CA-CB	5.12	1.61	1.55
1	B	447	TRP	C-O	-5.06	1.18	1.24
1	B	247	ASN	C-O	5.00	1.30	1.23

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	285	ASN	OD1-CG-ND2	-15.44	107.16	122.60
1	B	367	ARG	N-CA-C	9.70	121.55	110.97
1	B	254	ALA	N-CA-C	8.25	122.67	110.46
1	B	371	ASP	CA-C-N	-7.89	109.98	119.84
1	B	371	ASP	C-N-CA	-7.89	109.98	119.84
1	B	253	TYR	CA-C-N	-7.66	109.41	122.67
1	B	253	TYR	C-N-CA	-7.66	109.41	122.67
1	B	419	ILE	N-CA-C	-7.49	98.47	108.06
1	B	283	PRO	CA-C-N	-7.25	107.20	121.41
1	B	283	PRO	C-N-CA	-7.25	107.20	121.41
1	B	280	GLY	N-CA-C	7.00	123.19	114.37
1	B	237	ALA	CA-C-N	6.78	128.31	119.84
1	B	237	ALA	C-N-CA	6.78	128.31	119.84
1	B	285	ASN	CB-CG-OD1	6.70	134.20	120.80
1	B	478	GLN	CA-C-N	6.69	126.67	119.78
1	B	478	GLN	C-N-CA	6.69	126.67	119.78
1	B	70	PHE	CA-C-N	6.62	128.11	119.84
1	B	70	PHE	C-N-CA	6.62	128.11	119.84
1	A	99	ARG	N-CA-C	6.56	118.52	111.36
1	B	294	LEU	CA-C-N	-6.25	114.37	123.00
1	B	294	LEU	C-N-CA	-6.25	114.37	123.00
1	B	255	GLY	CA-C-N	-6.22	114.50	122.77
1	B	255	GLY	C-N-CA	-6.22	114.50	122.77
1	B	437	GLN	N-CA-C	-6.20	104.07	111.69
1	B	178	GLN	N-CA-C	-6.19	103.85	111.40
1	A	459	THR	CA-C-N	-6.14	113.41	120.04
1	A	459	THR	C-N-CA	-6.14	113.41	120.04
1	B	182	ASN	N-CA-C	6.10	120.56	113.18
1	B	240	ARG	N-CA-C	6.00	117.90	108.96
1	A	67	GLY	CA-C-N	5.90	126.20	119.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	GLY	C-N-CA	5.90	126.20	119.83
1	B	379	GLU	N-CA-C	-5.69	104.98	111.07
1	A	226	LEU	N-CA-C	5.59	118.55	110.28
1	B	263	VAL	CB-CA-C	-5.58	102.15	111.29
1	A	315	VAL	CA-C-N	-5.48	114.33	120.14
1	A	315	VAL	C-N-CA	-5.48	114.33	120.14
1	B	285	ASN	N-CA-CB	-5.47	101.25	110.49
1	B	100	ARG	N-CA-C	5.28	116.98	108.32
1	B	290	VAL	CB-CA-C	-5.26	104.60	110.96
1	B	450	ILE	CB-CA-C	-5.25	104.97	112.22
1	B	470	ILE	N-CA-C	5.25	115.41	107.80
1	B	444	PRO	CA-C-O	-5.23	115.20	121.48
1	B	266	ASP	CA-C-N	5.15	124.95	119.28
1	B	266	ASP	C-N-CA	5.15	124.95	119.28
1	B	329	GLY	CA-C-N	-5.15	114.14	121.50
1	B	329	GLY	C-N-CA	-5.15	114.14	121.50
1	A	107	LEU	CA-C-N	-5.14	113.42	119.84
1	A	107	LEU	C-N-CA	-5.14	113.42	119.84
1	B	247	ASN	N-CA-C	5.02	117.18	110.35

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	239	GLY	Peptide
1	B	256	TYR	Sidechain

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	3213	0	3120	59	0
1	B	3242	0	3154	111	0
2	A	43	0	30	6	0
2	B	43	0	30	6	0
3	A	17	0	15	1	0
3	B	17	0	15	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	4	0	3	0	0
5	A	6	0	8	0	0
5	B	6	0	8	0	0
6	A	27	0	30	1	0
6	B	27	0	30	4	0
7	A	3	0	0	2	0
7	B	3	0	0	1	0
8	A	1	0	0	0	0
9	A	104	0	0	2	0
9	B	107	0	0	9	0
All	All	6863	0	6443	172	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 13.

All (172) 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:284:GLY:CA	1:B:284:GLY:N	1.80	1.41
1:B:444:PRO:HB3	1:B:469:TYR:CZ	1.71	1.25
1:B:109[A]:ARG:HG3	1:B:109[A]:ARG:HH11	1.08	1.15
2:B:500:HEM:HMC2	2:B:500:HEM:HBC2	1.25	1.15
1:A:72:ARG:H	1:B:109[B]:ARG:NH2	1.45	1.14
1:B:109[A]:ARG:HH11	1:B:109[A]:ARG:CG	1.62	1.12
1:B:109[B]:ARG:HH11	1:B:109[B]:ARG:HG2	1.14	1.10
1:B:72:ARG:HH11	1:B:72:ARG:HG2	1.28	0.98
1:B:254:ALA:HB3	9:B:1102:HOH:O	1.62	0.97
1:B:444:PRO:HB3	1:B:469:TYR:CE1	2.01	0.95
1:B:254:ALA:HB2	1:B:291:LEU:HG	1.51	0.92
1:A:257:ARG:HG3	1:A:257:ARG:HH11	1.35	0.90
1:B:109[A]:ARG:HG3	1:B:109[A]:ARG:NH1	1.84	0.90
1:A:388:ASP:OD1	1:A:390:ARG:HG3	1.74	0.88
1:B:109[B]:ARG:HH11	1:B:109[B]:ARG:CG	1.86	0.87
1:B:444:PRO:HB3	1:B:469:TYR:CE2	2.10	0.86
1:B:109[A]:ARG:CG	1:B:109[A]:ARG:NH1	2.36	0.84
1:A:72:ARG:H	1:B:109[B]:ARG:HH22	1.29	0.79
1:A:72:ARG:H	1:B:109[B]:ARG:HH21	1.29	0.79
1:B:444:PRO:CB	1:B:469:TYR:CZ	2.62	0.79
2:B:500:HEM:HBB2	2:B:500:HEM:HH1	1.65	0.78
2:B:500:HEM:HBC2	2:B:500:HEM:CMC	2.08	0.77
1:B:254:ALA:HB2	1:B:291:LEU:CG	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:PRO:C	1:B:284:GLY:CA	2.57	0.77
1:A:360:MET:HE3	1:A:362:THR:OG1	1.85	0.76
1:B:249:GLN:HB2	1:B:252:ARG:HG2	1.70	0.73
1:B:231:THR:O	1:B:354:PRO:HD2	1.88	0.73
2:B:500:HEM:HMC2	2:B:500:HEM:CBC	2.13	0.72
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.73	0.71
1:B:256:TYR:CZ	9:B:1102:HOH:O	2.43	0.70
1:B:122:ALA:N	9:B:1087:HOH:O	2.26	0.69
1:B:236:ARG:HD2	1:B:242:ASP:OD1	1.93	0.69
1:A:72:ARG:N	1:B:109[B]:ARG:NH2	2.31	0.69
1:A:257:ARG:HG3	1:A:257:ARG:NH1	2.09	0.67
1:A:105:LEU:HD22	1:B:465:GLU:HG2	1.77	0.67
2:A:500:HEM:HBC2	2:A:500:HEM:CMC	2.25	0.66
1:B:423:HIS:O	1:B:427:VAL:HG23	1.95	0.66
1:B:109[B]:ARG:HG2	1:B:109[B]:ARG:NH1	1.92	0.66
1:B:258:GLN:NE2	1:B:264:ARG:HB3	2.12	0.65
1:A:235:GLN:HB3	1:A:350:PHE:CE2	2.32	0.64
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.26	0.64
1:B:341:MET:HE2	1:B:475:PHE:HB3	1.80	0.63
1:A:340:ASN:H	1:A:340:ASN:HD22	1.45	0.62
1:B:72:ARG:HG2	1:B:72:ARG:NH1	2.06	0.61
1:A:249:GLN:HB2	1:A:252:ARG:HG3	1.83	0.61
1:B:254:ALA:CB	9:B:1102:HOH:O	2.34	0.60
1:B:330:LEU:HB2	9:B:1024:HOH:O	2.01	0.60
1:B:264:ARG:HH11	1:B:287[B]:ARG:HG2	1.66	0.60
1:B:266:ASP:HB2	1:B:375:TYR:OH	2.02	0.59
1:A:72:ARG:HB3	1:B:109[B]:ARG:HH22	1.67	0.59
1:A:172:LEU:HD11	1:A:232:VAL:HG21	1.85	0.59
2:A:500:HEM:HBB2	2:A:500:HEM:HHC	1.85	0.58
1:B:254:ALA:HB1	1:B:273:THR:OG1	2.03	0.58
1:A:178:GLN:HB3	1:A:473:PRO:HG2	1.85	0.58
1:A:384:CYS:CB	7:A:950:CAD:AS	3.11	0.58
2:A:500:HEM:HBC2	2:A:500:HEM:HMC1	1.85	0.58
1:B:109[A]:ARG:HH11	1:B:109[A]:ARG:HG2	1.63	0.58
1:B:449:TRP:HA	3:B:600:H4B:N1	2.19	0.57
1:B:434:ASP:OD2	1:B:438:LYS:NZ	2.22	0.57
1:A:370:CYS:SG	1:A:378:LEU:HD13	2.45	0.57
1:A:246:TRP:CZ2	1:A:302:PRO:HG3	2.40	0.56
1:B:340:ASN:HD22	1:B:340:ASN:C	2.14	0.56
1:B:444:PRO:CB	1:B:469:TYR:CE2	2.84	0.56
1:B:412:PHE:CD2	1:B:419:ILE:HD13	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:500:HEM:HMC1	2:A:500:HEM:CBC	2.37	0.55
6:B:800:JI4:N11	6:B:800:JI4:H5'A	2.22	0.55
1:A:175:GLY:HA3	1:A:345:ILE:HD13	1.88	0.55
1:B:180:TRP:CZ3	1:B:192:TRP:HA	2.43	0.54
1:A:388:ASP:OD1	1:A:390:ARG:CG	2.52	0.54
1:B:124[A]:GLN:NE2	1:B:124[A]:GLN:HA	2.22	0.54
1:B:477:TYR:CE1	6:B:800:JI4:H15	2.42	0.54
1:A:340:ASN:O	1:A:478:GLN:NE2	2.30	0.53
1:A:378:LEU:HB2	9:A:1005:HOH:O	2.08	0.53
1:A:185:ARG:HD3	1:A:449:TRP:CD2	2.44	0.53
1:B:236:ARG:HD3	1:B:351:SER:HB3	1.91	0.53
1:A:263:VAL:HG11	1:A:267:PRO:HA	1.91	0.52
1:B:423:HIS:ND1	9:B:1090:HOH:O	2.34	0.52
1:B:265:GLY:HA2	1:B:287[A]:ARG:HA	1.90	0.52
1:B:109[B]:ARG:CG	1:B:109[B]:ARG:NH1	2.55	0.52
1:B:256:TYR:OH	1:B:284:GLY:N	2.43	0.52
1:B:360:MET:HE3	1:B:362:THR:OG1	2.10	0.52
1:A:72:ARG:N	1:B:109[B]:ARG:HH21	2.03	0.51
1:B:223:ARG:HB2	1:B:223:ARG:HH11	1.74	0.51
1:A:423:HIS:HB2	1:B:392:THR:HB	1.92	0.51
1:B:481:PRO:HD2	1:B:482:TRP:CE3	2.46	0.51
1:B:342:LEU:C	1:B:342:LEU:HD23	2.35	0.51
1:A:240:ARG:HD2	1:A:240:ARG:C	2.36	0.50
1:B:384:CYS:SG	7:B:950:CAD:C2	2.98	0.50
1:B:328:LEU:CB	1:B:330:LEU:HD22	2.42	0.50
1:B:258:GLN:HG2	1:B:262:SER:O	2.11	0.50
1:B:345:ILE:C	1:B:347:GLY:H	2.19	0.50
1:A:72:ARG:HB2	1:A:83:TYR:CE2	2.46	0.49
1:B:328:LEU:HB2	1:B:330:LEU:HD22	1.94	0.49
1:B:481:PRO:HD2	1:B:482:TRP:CZ3	2.48	0.49
2:A:500:HEM:HBA2	6:A:800:JI4:H71A	1.93	0.49
1:B:372:PRO:HA	1:B:376:ASN:HD22	1.77	0.49
1:B:184:PRO:HD2	9:B:1014:HOH:O	2.11	0.48
1:B:389:THR:HG22	1:B:396:TRP:CD2	2.49	0.48
1:B:180:TRP:O	1:B:181:ARG:C	2.53	0.48
1:B:287[A]:ARG:HB3	1:B:288:PHE:CD2	2.48	0.48
1:A:384:CYS:HB3	7:A:950:CAD:AS	2.74	0.48
1:B:328:LEU:HD12	1:B:330:LEU:CD2	2.43	0.48
1:B:477:TYR:CZ	6:B:800:JI4:H15	2.49	0.48
1:B:254:ALA:HB2	1:B:291:LEU:CD1	2.44	0.48
1:B:258:GLN:O	1:B:259:GLN:C	2.57	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:ASN:C	1:B:340:ASN:ND2	2.72	0.48
1:A:123:GLU:CD	1:A:123:GLU:H	2.23	0.47
1:A:131:ASP:OD2	1:A:135:GLN:NE2	2.48	0.47
1:B:345:ILE:C	1:B:347:GLY:N	2.69	0.47
1:B:233:PHE:HB3	1:B:234:PRO:HD2	1.96	0.46
1:A:480:ASP:HA	1:A:481:PRO:HD3	1.80	0.46
1:A:231:THR:O	1:A:353:ALA:HA	2.15	0.46
1:B:214:CYS:O	1:B:218:LYS:HG3	2.16	0.46
1:A:249:GLN:HB2	1:A:252:ARG:CG	2.44	0.46
1:A:158:GLU:OE1	1:A:166:HIS:HD2	1.99	0.46
1:A:395:LEU:HD12	1:B:406:LEU:HB2	1.97	0.45
1:B:265:GLY:HA2	1:B:287[B]:ARG:HA	1.97	0.45
1:A:69:LYS:NZ	9:A:1042:HOH:O	2.49	0.45
1:B:474:ALA:HA	9:B:1069:HOH:O	2.16	0.45
1:A:243:PHE:CE1	1:A:298:PRO:CG	3.00	0.45
6:B:800:JI4:N2	6:B:800:JI4:C16	2.80	0.45
1:B:155:VAL:O	1:B:156:GLU:C	2.60	0.44
1:B:71:PRO:HG2	1:B:84:ASP:HB3	1.99	0.44
2:B:500:HEM:CMC	2:B:500:HEM:CBC	2.81	0.44
1:B:189:ARG:O	1:B:192:TRP:HD1	2.00	0.44
1:B:340:ASN:ND2	1:B:340:ASN:H	2.15	0.44
1:A:105:LEU:HA	1:B:465:GLU:HG2	1.99	0.44
1:A:97:THR:HB	1:A:98:PRO:HD2	1.99	0.44
1:A:100:ARG:NH1	1:A:102:LEU:HD22	2.33	0.44
1:A:449:TRP:HA	3:A:600:H4B:N1	2.33	0.44
1:B:457:SER:HA	1:B:462:PHE:CB	2.47	0.44
1:B:102:LEU:O	1:B:103:GLY:C	2.61	0.44
1:A:72:ARG:N	1:B:109[B]:ARG:HH22	2.05	0.43
1:B:345:ILE:O	1:B:346:GLY:C	2.61	0.43
1:A:325:PHE:O	1:A:328:LEU:HB2	2.19	0.43
1:B:256:TYR:CE2	9:B:1102:HOH:O	2.68	0.43
1:B:283:PRO:O	1:B:284:GLY:CA	2.65	0.43
1:A:377:ILE:O	1:A:381:VAL:HG23	2.18	0.43
1:A:372:PRO:HA	1:A:376:ASN:ND2	2.33	0.43
1:B:265:GLY:O	1:B:267:PRO:HD3	2.19	0.43
1:A:105:LEU:HD23	1:A:105:LEU:N	2.34	0.43
1:A:322:LEU:HD13	1:A:324:TRP:CZ2	2.54	0.43
1:A:243:PHE:CE1	1:A:298:PRO:HG2	2.54	0.43
1:A:421:ASP:C	1:A:421:ASP:OD1	2.61	0.43
1:B:172:LEU:HD11	1:B:232:VAL:HG21	2.00	0.42
1:A:451:VAL:HA	1:A:452:PRO:HD3	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:MET:HA	1:B:420:VAL:O	2.19	0.42
1:A:458:LEU:HD21	1:B:401:ALA:HB2	2.01	0.42
2:B:500:HEM:HHC	2:B:500:HEM:CBB	2.42	0.42
1:B:326:ALA:O	1:B:328:LEU:N	2.53	0.42
1:B:226:LEU:HD23	1:B:357:GLY:O	2.20	0.42
1:B:457:SER:HA	1:B:462:PHE:CG	2.55	0.41
1:B:260:ASP:C	1:B:262:SER:H	2.28	0.41
1:A:151:ARG:HD3	1:A:168:ARG:NH2	2.35	0.41
1:B:180:TRP:CE3	1:B:192:TRP:HA	2.54	0.41
1:A:105:LEU:N	1:A:105:LEU:CD2	2.83	0.41
1:B:264:ARG:HH11	1:B:287[B]:ARG:CG	2.32	0.41
1:B:307:LEU:HA	1:B:308:PRO:HD3	1.96	0.41
1:B:315:VAL:HG11	1:B:412:PHE:CD1	2.56	0.41
1:B:196:GLN:HG2	1:B:219:TYR:CE2	2.55	0.41
1:B:249:GLN:HA	1:B:337:ALA:O	2.20	0.41
1:A:267:PRO:HD2	1:A:374:ARG:HA	2.03	0.41
1:A:75:ASN:OD1	1:A:75:ASN:C	2.63	0.40
1:B:224:GLY:O	1:B:417:VAL:HA	2.22	0.40
1:B:273:THR:HA	1:B:291:LEU:HD21	2.03	0.40
1:A:340:ASN:H	1:A:340:ASN:ND2	2.16	0.40
1:B:369:LEU:HB3	1:B:377:ILE:HG12	2.03	0.40
1:B:398:ASP:O	1:B:399:LYS:C	2.63	0.40
1:B:412:PHE:CG	1:B:419:ILE:HD13	2.56	0.40
2:A:500:HEM:HBB2	2:A:500:HEM:CHC	2.49	0.40
1:B:407:ALA:O	1:B:408:VAL:C	2.64	0.40
1:A:240:ARG:HD2	1:A:240:ARG:O	2.20	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	400/444 (90%)	381 (95%)	18 (4%)	1 (0%)	36	42
1	B	402/444 (90%)	372 (92%)	24 (6%)	6 (2%)	8	6
All	All	802/888 (90%)	753 (94%)	42 (5%)	7 (1%)	14	14

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	327	ALA
1	B	103	GLY
1	B	261	GLY
1	B	286	GLY
1	A	108	PRO
1	B	89	GLN
1	B	285	ASN

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	343/377 (91%)	315 (92%)	28 (8%)	10	12
1	B	346/377 (92%)	311 (90%)	35 (10%)	7	7
All	All	689/754 (91%)	626 (91%)	63 (9%)	9	9

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LYS
1	A	92	GLN
1	A	102	LEU
1	A	105	LEU
1	A	107	LEU
1	A	109	ARG
1	A	125	LEU
1	A	143	SER
1	A	146	GLN

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Mol	Chain	Res	Type
1	A	154	GLU
1	A	155	VAL
1	A	168	ARG
1	A	190	ILE
1	A	226	LEU
1	A	236	ARG
1	A	257	ARG
1	A	259	GLN
1	A	260	ASP
1	A	270	VAL
1	A	271	GLU
1	A	293	LEU
1	A	294	LEU
1	A	328	LEU
1	A	340	ASN
1	A	378	LEU
1	A	379	GLU
1	A	390	ARG
1	A	458	LEU
1	B	72	ARG
1	B	82	THR
1	B	90	SER
1	B	92	GLN
1	B	102	LEU
1	B	109[A]	ARG
1	B	109[B]	ARG
1	B	110	LYS
1	B	123	GLU
1	B	124[A]	GLN
1	B	124[B]	GLN
1	B	131	ASP
1	B	138	SER
1	B	139	SER
1	B	173	VAL
1	B	223	ARG
1	B	225	ASN
1	B	252	ARG
1	B	260	ASP
1	B	262	SER
1	B	270	VAL
1	B	278	GLN
1	B	287[A]	ARG

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Mol	Chain	Res	Type
1	B	287[B]	ARG
1	B	311	LEU
1	B	318	GLU
1	B	321	THR
1	B	330	LEU
1	B	340	ASN
1	B	377	ILE
1	B	378	LEU
1	B	393	SER
1	B	414	LEU
1	B	454	ILE
1	B	458	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	166	HIS
1	A	191	GLN
1	A	196	GLN
1	A	278	GLN
1	A	340	ASN
1	A	376	ASN
1	A	413	GLN
1	A	468	ASN
1	B	146	GLN
1	B	196	GLN
1	B	207	GLN
1	B	222	ASN
1	B	235	GLN
1	B	258	GLN
1	B	340	ASN
1	B	376	ASN
1	B	405	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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	$\# Z > 2$
6	JI4	B	800	-	28,29,29	0.72	0	29,38,38	2.07	7 (24%)
7	CAD	B	950	1	0,2,4	-	-	0,1,6	-	-
3	H4B	A	600	-	17,18,18	0.94	0	14,26,26	2.01	6 (42%)
5	GOL	A	880	-	5,5,5	0.39	0	5,5,5	1.22	1 (20%)
5	GOL	B	880	-	5,5,5	0.43	0	5,5,5	1.00	0
2	HEM	A	500	1	50,50,50	1.98	12 (24%)	67,82,82	2.17	22 (32%)
2	HEM	B	500	1	50,50,50	1.81	14 (28%)	67,82,82	1.57	11 (16%)
3	H4B	B	600	-	17,18,18	1.08	2 (11%)	14,26,26	2.65	7 (50%)
4	ACT	A	860	-	3,3,3	0.97	0	3,3,3	0.54	0
6	JI4	A	800	-	28,29,29	1.06	2 (7%)	29,38,38	1.56	6 (20%)
7	CAD	A	950	1	0,2,4	-	-	0,1,6	-	-

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
6	JI4	B	800	-	-	5/13/23/23	0/3/3/3
3	H4B	A	600	-	-	0/8/17/17	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	880	-	-	2/4/4/4	-
5	GOL	B	880	-	-	4/4/4/4	-
2	HEM	A	500	1	-	2/14/54/54	-
2	HEM	B	500	1	-	6/14/54/54	-
3	H4B	B	600	-	-	0/8/17/17	0/2/2/2
6	JI4	A	800	-	-	8/13/23/23	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	HEM	FE-NB	7.14	2.16	1.94
2	B	500	HEM	C3D-C2D	6.76	1.51	1.36
2	A	500	HEM	C3D-C2D	5.94	1.49	1.36
2	B	500	HEM	FE-NA	4.27	2.09	1.95
2	A	500	HEM	CAC-C3C	3.46	1.56	1.47
2	B	500	HEM	CAB-C3B	3.11	1.55	1.47
2	A	500	HEM	FE-ND	3.11	2.04	1.94
2	B	500	HEM	CMA-C3A	3.03	1.57	1.50
2	B	500	HEM	CMD-C2D	2.95	1.56	1.50
2	A	500	HEM	C1B-NB	-2.91	1.35	1.40
2	A	500	HEM	CHD-C1D	-2.69	1.33	1.39
3	B	600	H4B	C4-N3	-2.56	1.34	1.38
2	B	500	HEM	CAC-C3C	2.50	1.54	1.47
2	A	500	HEM	CAB-C3B	2.49	1.54	1.47
2	A	500	HEM	C1D-ND	-2.39	1.34	1.38
2	B	500	HEM	O1D-CGD	2.37	1.29	1.22
2	A	500	HEM	CHD-C4C	-2.37	1.33	1.38
2	A	500	HEM	CMC-C2C	2.36	1.55	1.50
2	B	500	HEM	FE-NB	2.28	2.01	1.94
2	B	500	HEM	CMB-C2B	2.21	1.55	1.50
2	A	500	HEM	C3B-C2B	-2.21	1.32	1.37
2	B	500	HEM	O2A-CGA	-2.20	1.23	1.30
2	B	500	HEM	C2A-C3A	-2.15	1.33	1.38
6	A	800	JI4	C14-C13	2.12	1.41	1.37
2	B	500	HEM	CMC-C2C	2.10	1.55	1.50
2	B	500	HEM	C3C-C4C	-2.09	1.42	1.46
6	A	800	JI4	C51-C41	2.07	1.42	1.39
2	A	500	HEM	CAA-C2A	2.06	1.56	1.51
2	B	500	HEM	C3B-C2B	-2.01	1.33	1.37
3	B	600	H4B	C7-C6	2.00	1.54	1.52

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	HEM	CHD-C4C-NC	7.28	132.38	124.45
3	B	600	H4B	C11-C10-C9	-6.14	104.59	112.11
2	B	500	HEM	CBA-CAA-C2A	-5.29	97.91	112.53
6	B	800	JI4	C61-N11-C21	5.11	121.89	118.07
3	B	600	H4B	C2-N1-C8A	4.83	121.89	113.36
6	B	800	JI4	C1-N1-C3'	4.60	120.76	114.05
2	A	500	HEM	CHD-C4C-C3C	-4.59	117.46	125.21
2	A	500	HEM	CMC-C2C-C1C	4.38	132.44	124.73
2	B	500	HEM	CMD-C2D-C1D	4.29	131.74	125.03
6	B	800	JI4	C31-C21-N11	-4.26	117.87	122.73
2	A	500	HEM	CHB-C1B-NB	4.21	129.58	124.37
3	A	600	H4B	C2-N1-C8A	4.20	120.78	113.36
2	A	500	HEM	C1C-CHC-C4B	-4.18	117.14	126.02
2	A	500	HEM	CBA-CAA-C2A	-4.06	101.32	112.53
2	B	500	HEM	C1D-C2D-C3D	-3.98	102.80	106.98
2	A	500	HEM	C3B-C2B-C1B	3.53	109.06	106.41
6	B	800	JI4	C5'-N1'-C2'	3.52	114.21	105.45
2	A	500	HEM	C4D-ND-C1D	3.50	109.35	105.21
6	B	800	JI4	C71-C21-N11	3.33	120.64	116.57
2	A	500	HEM	CHC-C1C-NC	-3.32	120.84	124.45
6	A	800	JI4	C61-N11-C21	3.30	120.54	118.07
6	A	800	JI4	C5'-N1'-C2'	3.29	113.63	105.45
2	B	500	HEM	CHB-C1B-NB	3.29	128.43	124.37
2	B	500	HEM	C3B-C2B-C1B	3.14	108.77	106.41
2	A	500	HEM	C1B-NB-C4B	3.09	108.86	105.21
2	A	500	HEM	CMC-C2C-C3C	-3.08	120.97	128.43
3	B	600	H4B	C4A-C4-N3	3.04	120.47	112.13
6	A	800	JI4	C4-C11-C12	-2.98	115.53	120.54
2	A	500	HEM	C4C-CHD-C1D	2.95	132.28	126.02
2	A	500	HEM	CBD-CAD-C3D	-2.85	104.64	112.53
2	A	500	HEM	CMA-C3A-C4A	2.83	129.73	125.42
3	A	600	H4B	C4A-C4-N3	2.76	119.70	112.13
3	A	600	H4B	O4-C4-C4A	-2.72	120.69	127.26
2	A	500	HEM	C1A-CHA-C4D	-2.71	119.87	126.25
3	A	600	H4B	C4-C4A-N5	2.67	123.56	116.27
6	B	800	JI4	C14-C13-C12	-2.62	119.77	123.23
2	A	500	HEM	C2B-C1B-NB	-2.59	106.87	109.84
3	A	600	H4B	N3-C2-N1	-2.58	118.60	123.32
2	B	500	HEM	CBC-CAC-C3C	-2.40	115.53	127.53
3	B	600	H4B	C2-N3-C4	-2.30	120.94	125.11
2	A	500	HEM	C4D-C3D-C2D	-2.30	103.54	106.89
2	B	500	HEM	CBD-CAD-C3D	-2.29	106.20	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	800	JI4	N61-C61-N11	2.29	120.27	116.59
6	A	800	JI4	C81-C41-C31	-2.27	117.85	120.92
6	A	800	JI4	F13-C13-C14	2.22	122.11	118.55
2	A	500	HEM	CHA-C1A-NA	2.22	127.89	123.86
2	B	500	HEM	CHA-C4D-ND	2.21	127.10	124.37
2	B	500	HEM	CAD-C3D-C4D	2.21	128.55	124.70
3	B	600	H4B	C4-C4A-N5	2.19	122.23	116.27
2	A	500	HEM	C4C-C3C-C2C	2.17	108.70	106.81
3	B	600	H4B	O4-C4-C4A	-2.17	122.03	127.26
5	A	880	GOL	O3-C3-C2	-2.14	100.77	110.38
3	B	600	H4B	N3-C2-N1	-2.12	119.45	123.32
2	A	500	HEM	C4A-CHB-C1B	2.11	131.21	126.25
2	A	500	HEM	CAD-CBD-CGD	-2.11	108.08	113.67
2	A	500	HEM	CHA-C4D-ND	-2.10	121.77	124.37
2	B	500	HEM	CHD-C4C-NC	2.10	126.74	124.45
2	B	500	HEM	CAD-C3D-C2D	-2.07	123.98	127.87
6	A	800	JI4	C71-C21-N11	2.05	119.08	116.57
3	A	600	H4B	N2-C2-N3	2.04	121.08	116.76

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	880	GOL	C1-C2-C3-O3
5	B	880	GOL	C1-C2-C3-O3
6	A	800	JI4	C2-C1-N1-C3'
6	A	800	JI4	C2'-C3'-N1-C1
6	A	800	JI4	C4'-C3'-N1-C1
6	A	800	JI4	N1-C1-C2-N2
6	B	800	JI4	N2-C3-C4-C11
5	A	880	GOL	O2-C2-C3-O3
6	B	800	JI4	C4-C3-N2-C2
5	B	880	GOL	O2-C2-C3-O3
6	B	800	JI4	C2-C1-N1-C3'
6	A	800	JI4	C1-C2-N2-C3
5	B	880	GOL	O1-C1-C2-O2
6	A	800	JI4	C12-C11-C4-C3
6	A	800	JI4	C16-C11-C4-C3
6	B	800	JI4	C1-C2-N2-C3
2	B	500	HEM	C3D-CAD-CBD-CGD
2	A	500	HEM	CAA-CBA-CGA-O2A
2	B	500	HEM	CAD-CBD-CGD-O2D

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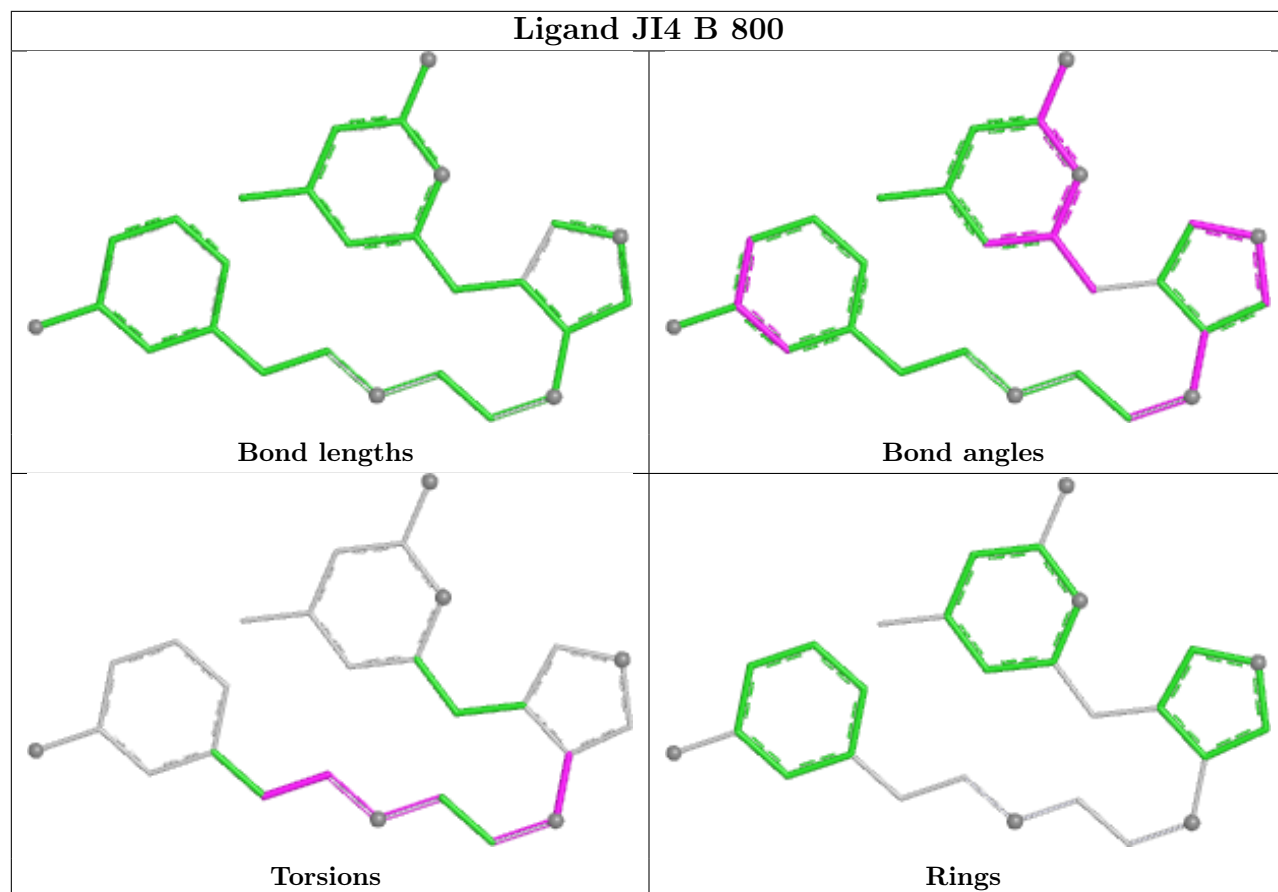
Mol	Chain	Res	Type	Atoms
2	A	500	HEM	CAA-CBA-CGA-O1A
2	B	500	HEM	CAD-CBD-CGD-O1D
6	A	800	JI4	C4-C3-N2-C2
5	B	880	GOL	O1-C1-C2-C3
2	B	500	HEM	C4B-C3B-CAB-CBB
2	B	500	HEM	CAA-CBA-CGA-O2A
6	B	800	JI4	C2'-C3'-N1-C1
2	B	500	HEM	CAA-CBA-CGA-O1A

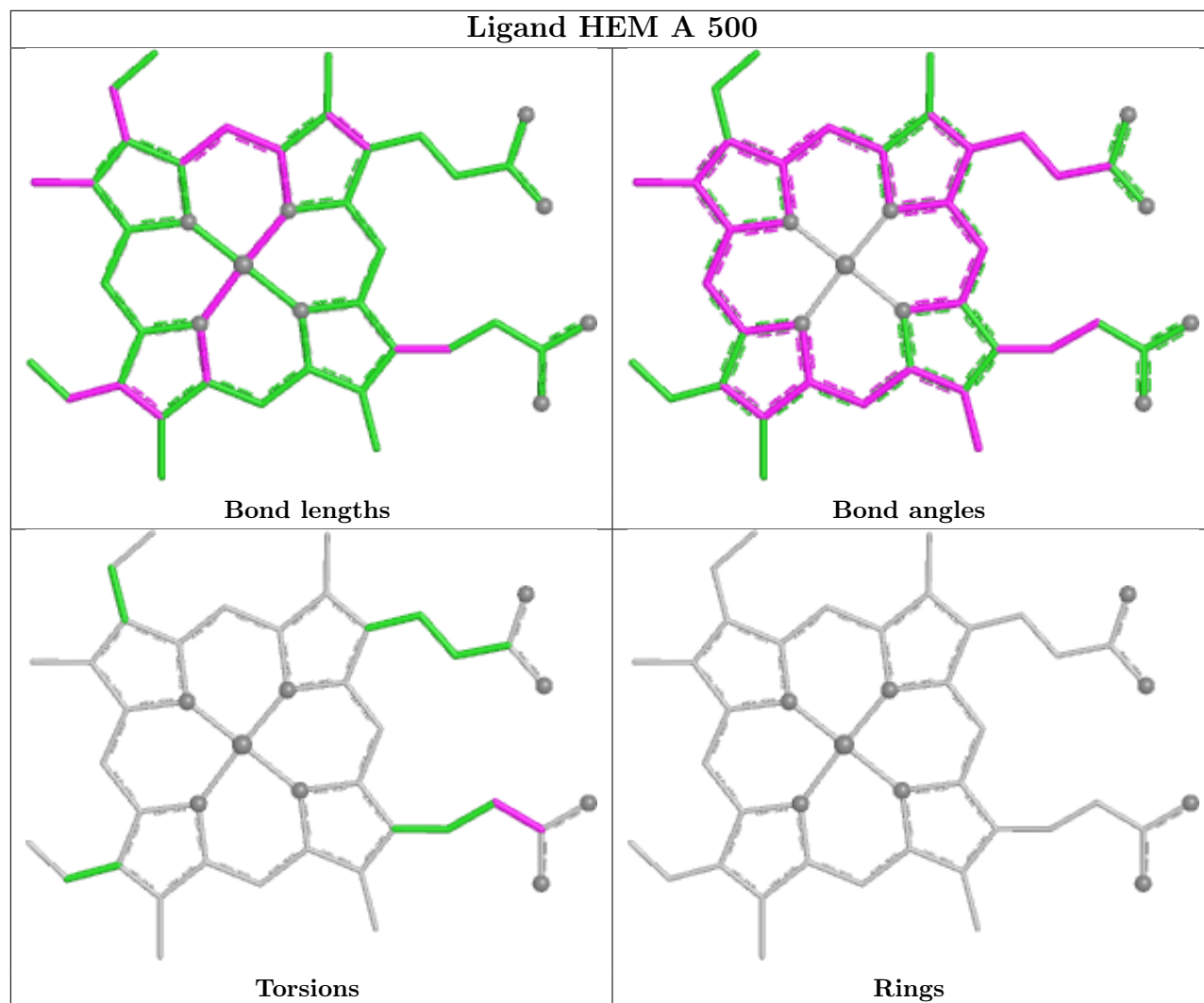
There are no ring outliers.

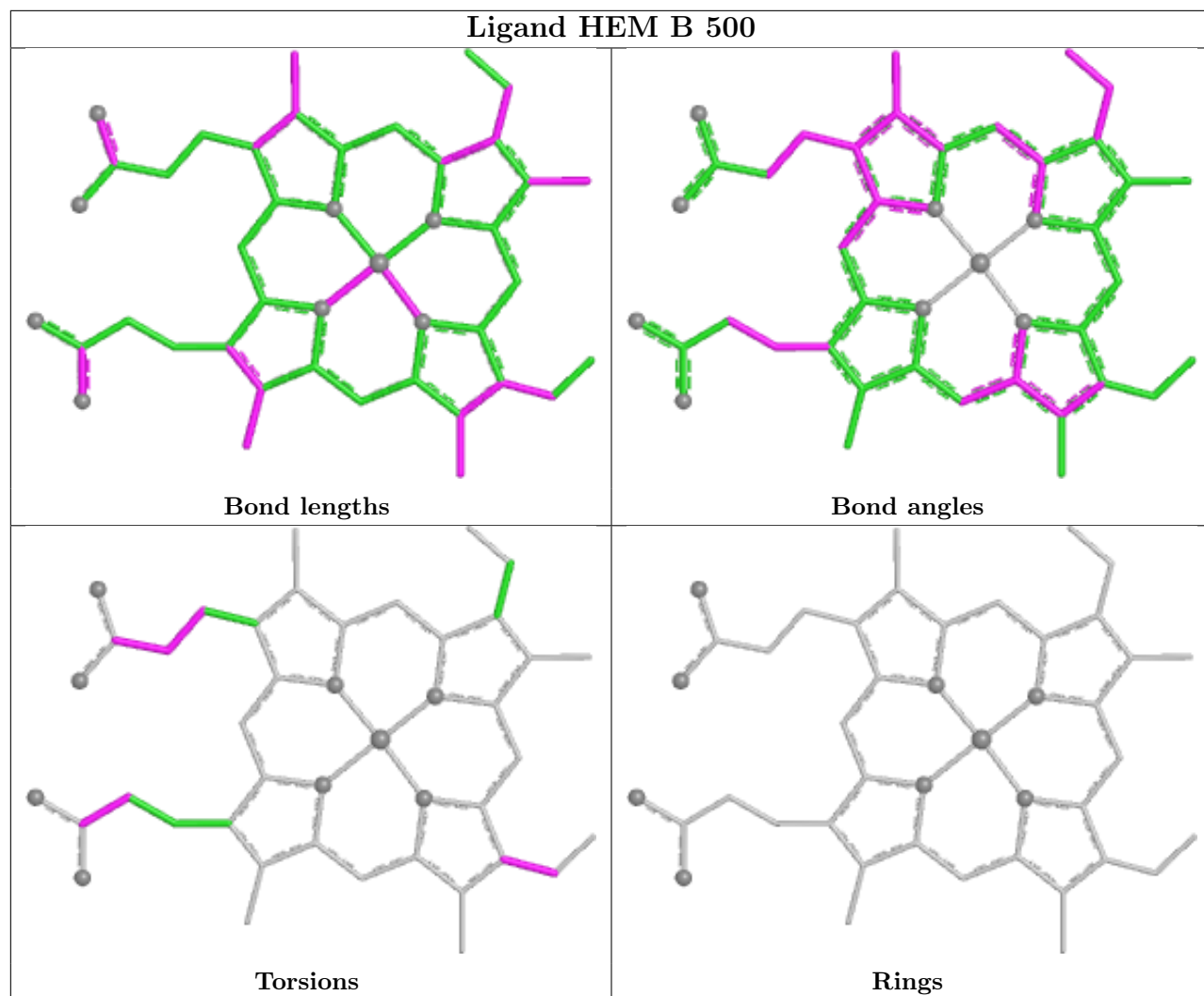
8 monomers are involved in 21 short contacts:

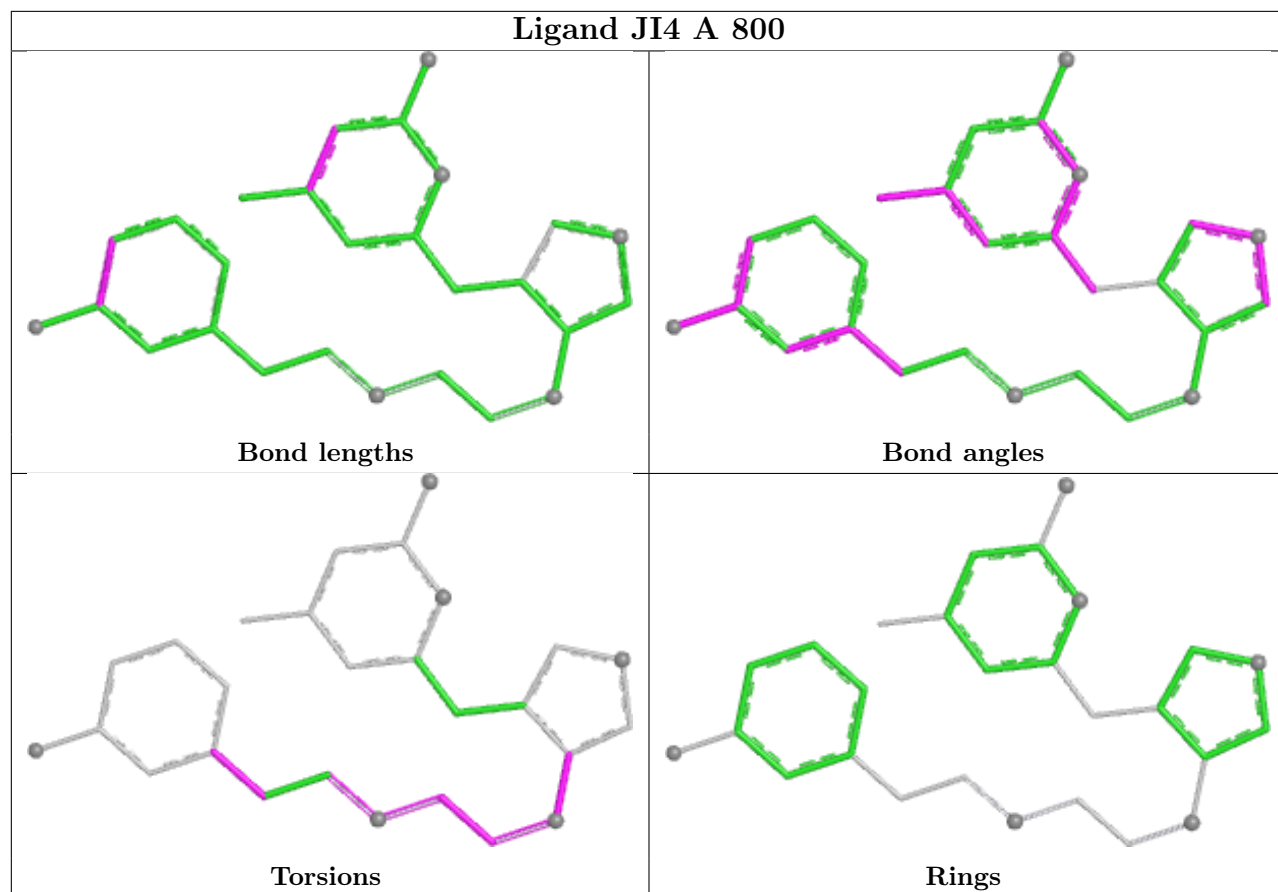
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	800	JI4	4	0
7	B	950	CAD	1	0
3	A	600	H4B	1	0
2	A	500	HEM	6	0
2	B	500	HEM	6	0
3	B	600	H4B	1	0
6	A	800	JI4	1	0
7	A	950	CAD	2	0

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 [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	404/444 (90%)	0.27	3 (0%) 84 82	35, 54, 78, 95	0
1	B	403/444 (90%)	0.38	6 (1%) 72 69	31, 55, 79, 94	3 (0%)
All	All	807/888 (90%)	0.32	9 (1%) 78 76	31, 55, 79, 95	3 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	GLY	3.2
1	B	109[A]	ARG	2.9
1	B	284	GLY	2.7
1	A	122	ALA	2.7
1	B	122	ALA	2.5
1	B	270	VAL	2.4
1	B	281	TRP	2.4
1	A	108	PRO	2.2
1	B	256	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

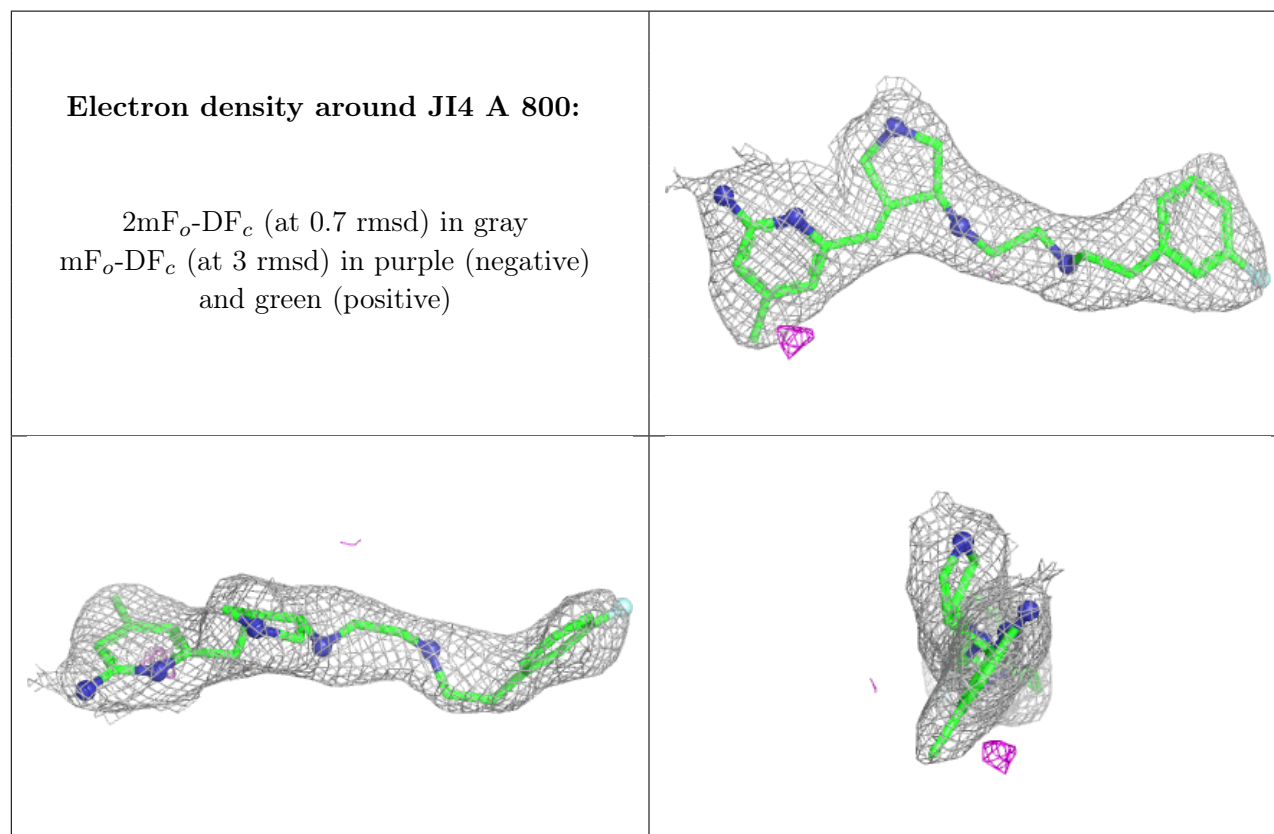
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

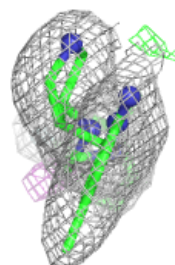
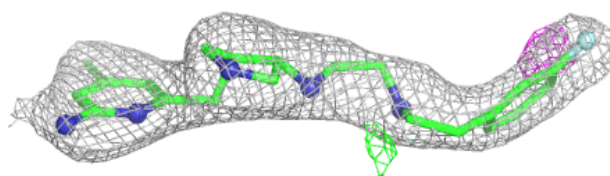
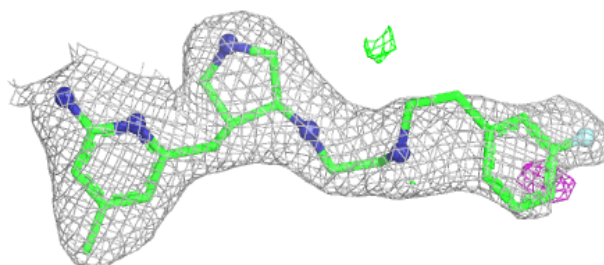
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	ACT	A	860	4/4	0.75	0.17	59,61,62,62	0
6	J14	A	800	27/27	0.89	0.14	33,47,83,85	0
5	GOL	A	880	6/6	0.92	0.12	64,65,67,68	0
6	J14	B	800	27/27	0.92	0.11	40,45,68,69	0
3	H4B	B	600	17/17	0.93	0.08	42,46,50,53	0
5	GOL	B	880	6/6	0.94	0.09	48,51,52,57	0
3	H4B	A	600	17/17	0.95	0.06	36,41,45,51	0
7	CAD	B	950	3/5	0.95	0.12	85,85,86,87	0
2	HEM	B	500	43/43	0.96	0.08	37,43,57,70	0
7	CAD	A	950	3/5	0.97	0.11	71,71,72,75	0
2	HEM	A	500	43/43	0.97	0.08	25,38,55,66	0
8	ZN	A	900	1/1	0.99	0.03	47,47,47,47	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.



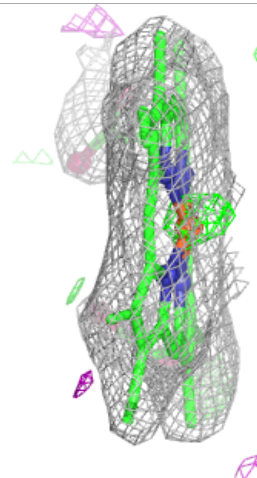
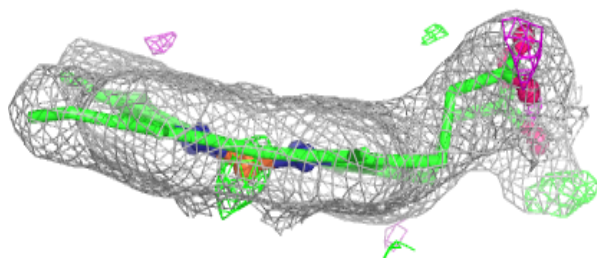
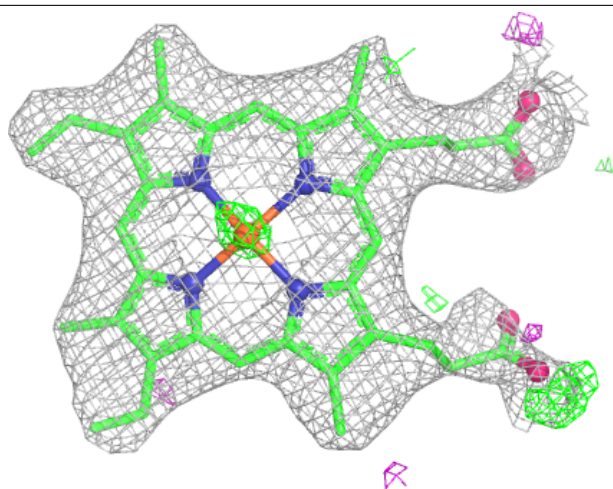
Electron density around JI4 B 800:

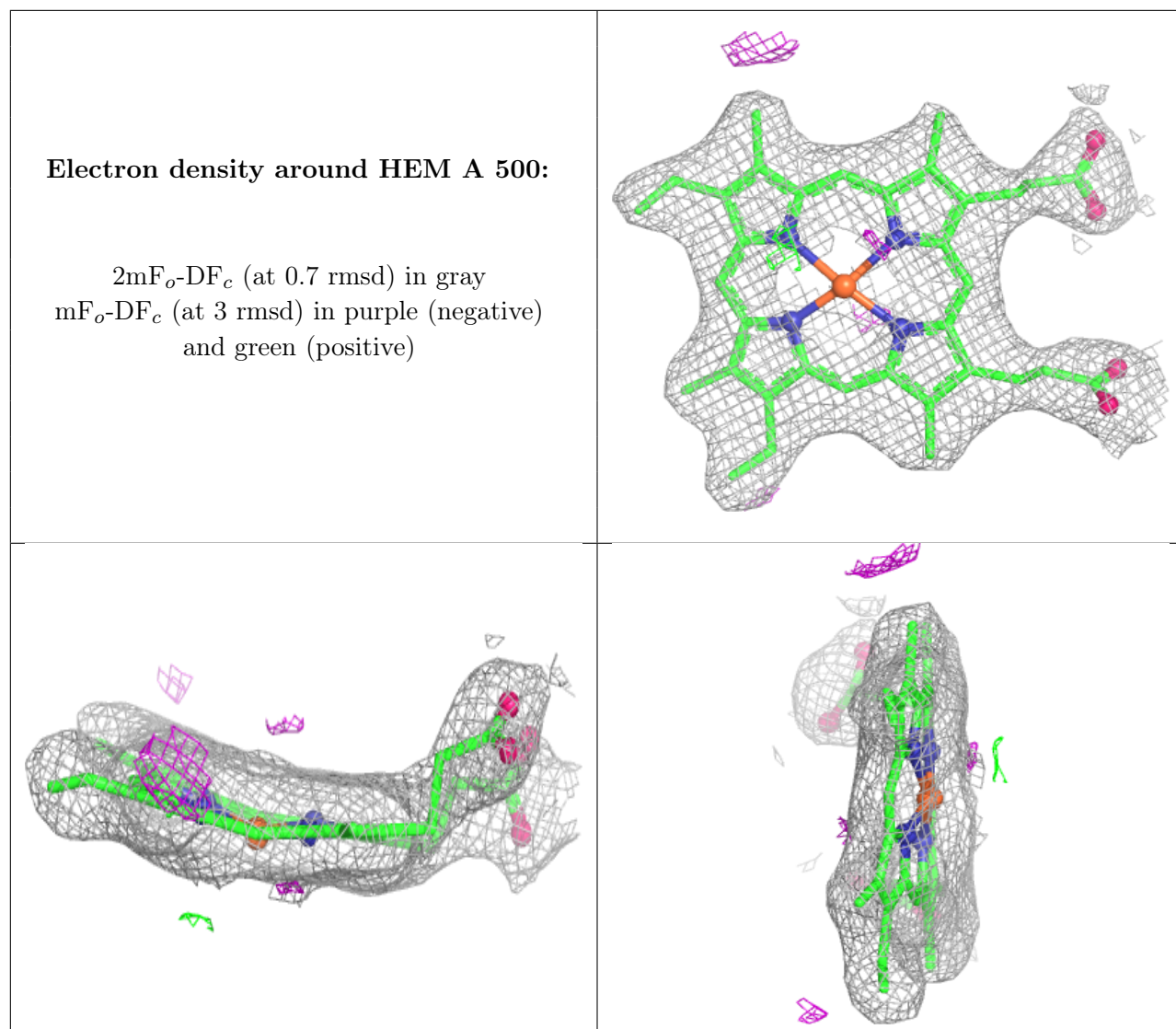
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 500:

$2mF_o-DF_c$ (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.