



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 29, 2016 – 12:56 AM EST

PDB ID : 5KKZ
Title : Rhodobacter sphaeroides bc1 with famoxadone
Authors : Xia, D.; Esser, L.; Zhou, F.; Tang, W.K.; Yu, C.A.
Deposited on : 2016-06-23
Resolution : 2.97 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

<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028320
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

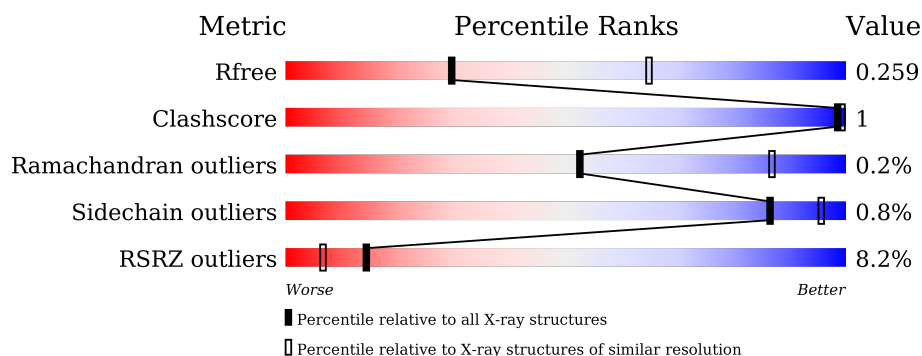
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.97 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}	91344	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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. 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	445	<div> <div>3%</div> <div>92%</div> <div>5%</div> <div>• •</div> </div>
1	E	445	<div> <div>5%</div> <div>92%</div> <div>5%</div> <div>• •</div> </div>
1	K	445	<div> <div>3%</div> <div>91%</div> <div>5%</div> <div>•</div> </div>
1	O	445	<div> <div>7%</div> <div>93%</div> <div>• • •</div> </div>
2	B	272	<div> <div>8%</div> <div>93%</div> <div>6%</div> <div>•</div> </div>
2	F	272	<div> <div>13%</div> <div>92%</div> <div>6%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
2	L	272	 6% 92% 6%
2	P	272	 15% 93% 6%
3	C	187	 14% 96%
3	G	187	 10% 94%
3	M	187	 11% 95%
3	Q	187	 12% 94%

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
4	HEM	A	1001	-	-	-	X
4	HEM	K	1001	-	-	-	X
8	LOP	E	1005	-	-	-	X

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 54985 atoms, of which 27067 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	429	Total	C	H	N	O	S	0	0	0
			6857	2325	3412	548	557	15			
1	E	429	Total	C	H	N	O	S	0	0	0
			6857	2325	3412	548	557	15			
1	K	429	Total	C	H	N	O	S	0	0	0
			6857	2325	3412	548	557	15			
1	O	429	Total	C	H	N	O	S	0	0	0
			6857	2325	3412	548	557	15			

- Molecule 2 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			
2	F	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			
2	L	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			
2	P	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	98	PRO	ALA	variant	UNP Q02760
B	264	GLY	-	expression tag	UNP Q02760
B	265	THR	-	expression tag	UNP Q02760
B	266	GLY	-	expression tag	UNP Q02760
B	267	HIS	-	expression tag	UNP Q02760
B	268	HIS	-	expression tag	UNP Q02760
B	269	HIS	-	expression tag	UNP Q02760
B	270	HIS	-	expression tag	UNP Q02760

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Chain	Residue	Modelled	Actual	Comment	Reference
B	271	HIS	-	expression tag	UNP Q02760
B	272	HIS	-	expression tag	UNP Q02760
F	98	PRO	ALA	variant	UNP Q02760
F	264	GLY	-	expression tag	UNP Q02760
F	265	THR	-	expression tag	UNP Q02760
F	266	GLY	-	expression tag	UNP Q02760
F	267	HIS	-	expression tag	UNP Q02760
F	268	HIS	-	expression tag	UNP Q02760
F	269	HIS	-	expression tag	UNP Q02760
F	270	HIS	-	expression tag	UNP Q02760
F	271	HIS	-	expression tag	UNP Q02760
F	272	HIS	-	expression tag	UNP Q02760
L	98	PRO	ALA	variant	UNP Q02760
L	264	GLY	-	expression tag	UNP Q02760
L	265	THR	-	expression tag	UNP Q02760
L	266	GLY	-	expression tag	UNP Q02760
L	267	HIS	-	expression tag	UNP Q02760
L	268	HIS	-	expression tag	UNP Q02760
L	269	HIS	-	expression tag	UNP Q02760
L	270	HIS	-	expression tag	UNP Q02760
L	271	HIS	-	expression tag	UNP Q02760
L	272	HIS	-	expression tag	UNP Q02760
P	98	PRO	ALA	variant	UNP Q02760
P	264	GLY	-	expression tag	UNP Q02760
P	265	THR	-	expression tag	UNP Q02760
P	266	GLY	-	expression tag	UNP Q02760
P	267	HIS	-	expression tag	UNP Q02760
P	268	HIS	-	expression tag	UNP Q02760
P	269	HIS	-	expression tag	UNP Q02760
P	270	HIS	-	expression tag	UNP Q02760
P	271	HIS	-	expression tag	UNP Q02760
P	272	HIS	-	expression tag	UNP Q02760

- Molecule 3 is a protein called Ubiquinol-cytochrome c reductase iron-sulfur subunit.

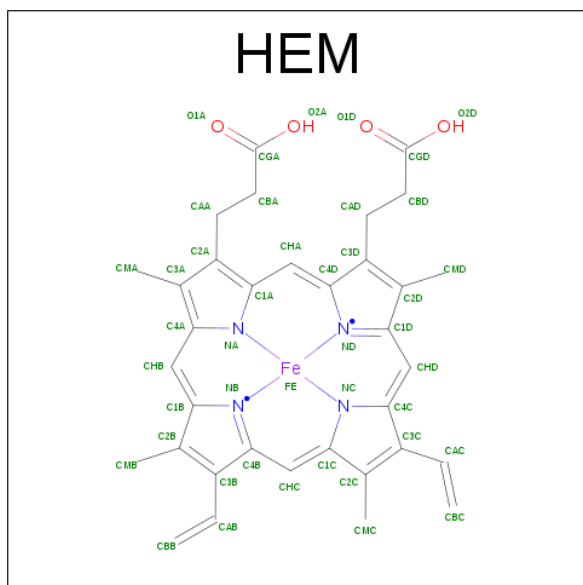
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	179	Total	C	H	N	O	S	0	0	0
			2645	845	1304	237	253	6			
3	G	179	Total	C	H	N	O	S	0	0	0
			2645	845	1304	237	253	6			
3	M	179	Total	C	H	N	O	S	0	0	0
			2645	845	1304	237	253	6			

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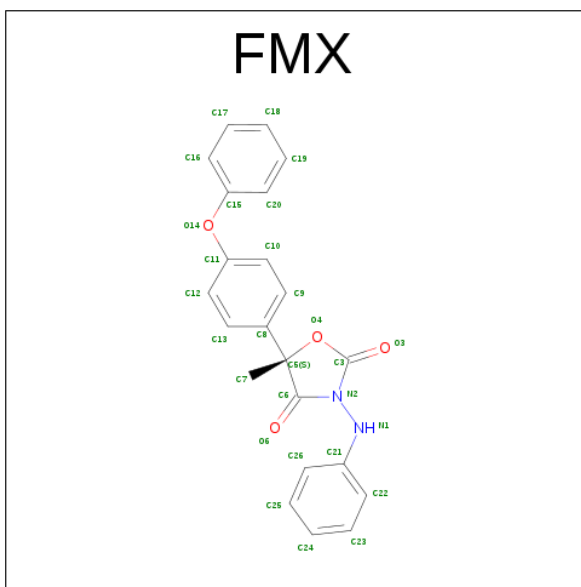
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	Q	179	Total	C	H	N	O	S	0	0	0
			2645	845	1304	237	253	6			

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



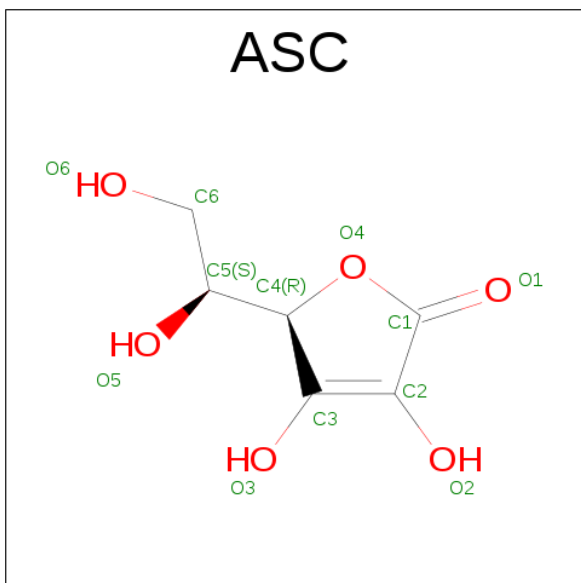
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	E	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	E	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	K	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	K	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	O	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
4	O	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		

- Molecule 5 is FAMOXADONE (three-letter code: FMX) (formula: $C_{22}H_{18}N_2O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			46	22	18	2	4		
5	E	1	Total	C	H	N	O	0	0
			46	22	18	2	4		
5	K	1	Total	C	H	N	O	0	0
			46	22	18	2	4		
5	O	1	Total	C	H	N	O	0	0
			46	22	18	2	4		

- Molecule 6 is ASCORBIC ACID (three-letter code: ASC) (formula: C₆H₈O₆).

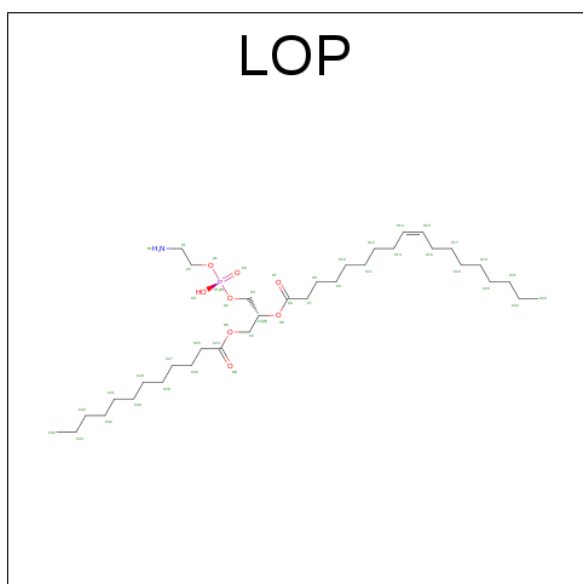


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C H O 19 6 7 6	0	0
6	E	1	Total C H O 19 6 7 6	0	0
6	K	1	Total C H O 19 6 7 6	0	0
6	O	1	Total C H O 19 6 7 6	0	0

- Molecule 7 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

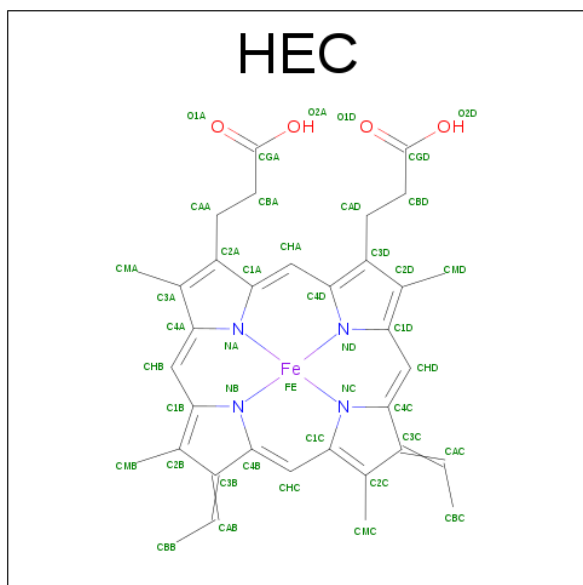
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	P	1	Total Sr 1 1	0	0
7	K	1	Total Sr 1 1	0	0
7	B	1	Total Sr 1 1	0	0
7	A	1	Total Sr 1 1	0	0
7	L	1	Total Sr 1 1	0	0
7	F	1	Total Sr 1 1	0	0

- Molecule 8 is (1R)-2-{[(R)-(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(DODECANOYLOXY)METHYL]ETHYL (9Z)-OCTADEC-9-ENOATE (three-letter code: LOP) (formula: C₃₅H₆₈NO₈P).



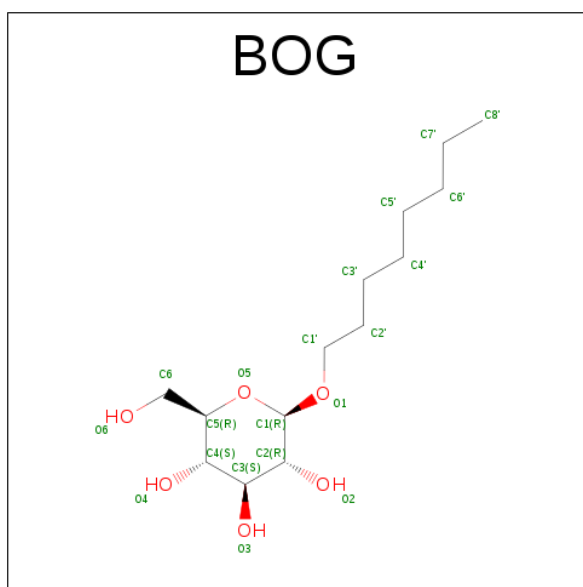
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	P	0	0
			112	35	67	1	8	1		
8	E	1	Total	C	H	N	O	P	0	0
			112	35	67	1	8	1		
8	K	1	Total	C	H	N	O	P	0	0
			112	35	67	1	8	1		
8	O	1	Total	C	H	N	O	P	0	0
			112	35	67	1	8	1		

- Molecule 9 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



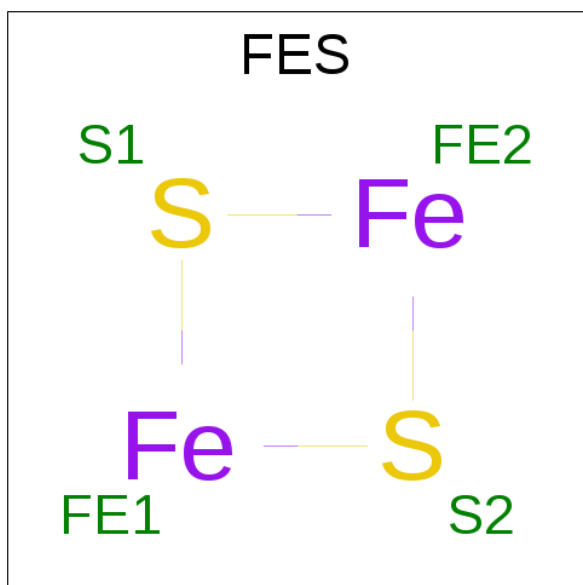
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
9	B	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		
9	F	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		
9	L	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		
9	P	1	Total	C	Fe	H	N	O	0	0
			75	34	1	32	4	4		

- Molecule 10 is B-OCTYLGLUCOSIDE (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	H	O	0	0
			48	14	28	6		
10	F	1	Total	C	H	O	0	0
			47	14	27	6		
10	K	1	Total	C	H	O	0	0
			48	14	28	6		
10	P	1	Total	C	H	O	0	0
			48	14	28	6		

- Molecule 11 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	C	1	Total 4	Fe 2	S 2	0	0
11	G	1	Total 4	Fe 2	S 2	0	0
11	M	1	Total 4	Fe 2	S 2	0	0
11	Q	1	Total 4	Fe 2	S 2	0	0

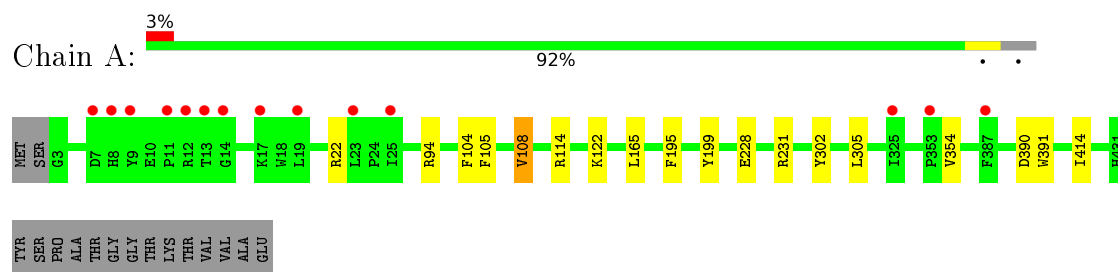
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	1	Total 1	O 1	0	0
12	E	1	Total 1	O 1	0	0
12	K	1	Total 1	O 1	0	0
12	O	1	Total 1	O 1	0	0

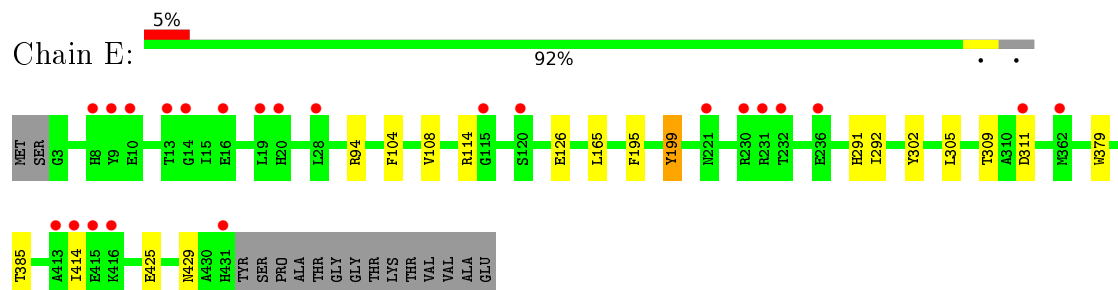
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

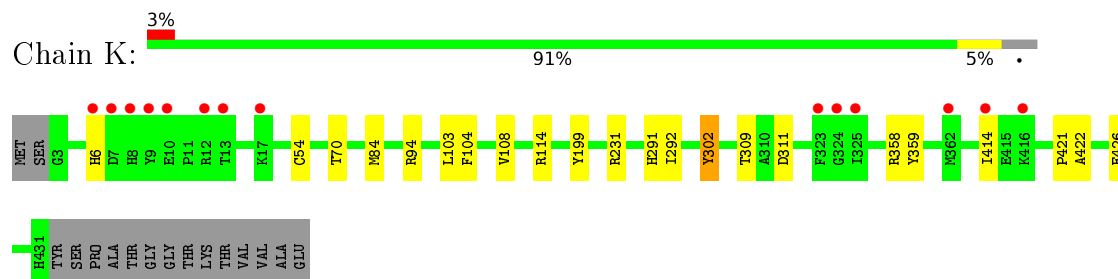
- Molecule 1: Cytochrome b



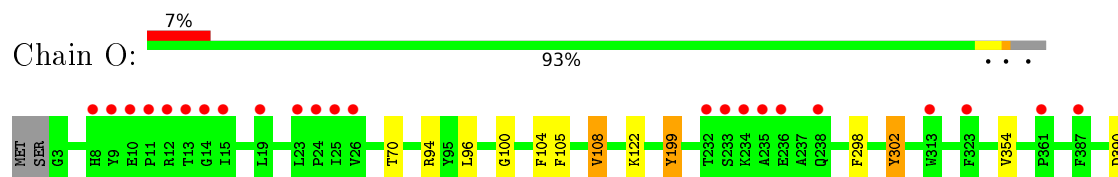
- Molecule 1: Cytochrome b



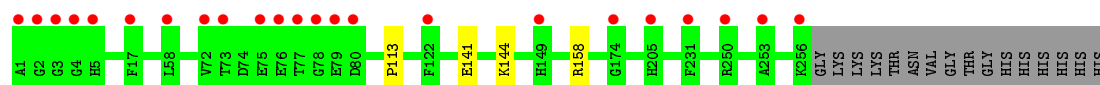
- Molecule 1: Cytochrome b



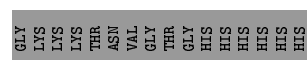
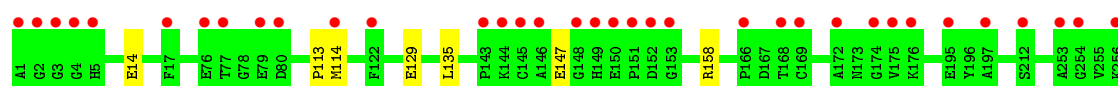
- Molecule 1: Cytochrome b



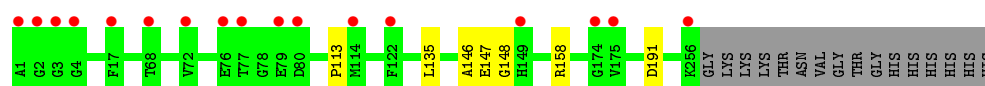
- Molecule 2: Cytochrome c1



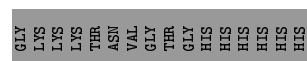
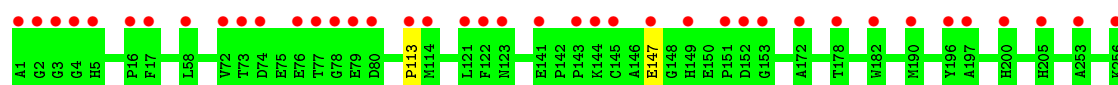
- Molecule 2: Cytochrome c1



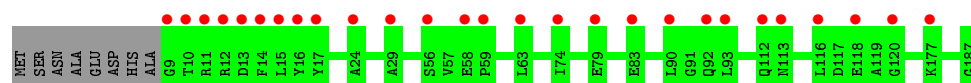
- Molecule 2: Cytochrome c1



- Molecule 2: Cytochrome c1

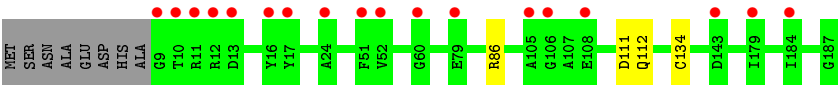


- Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit

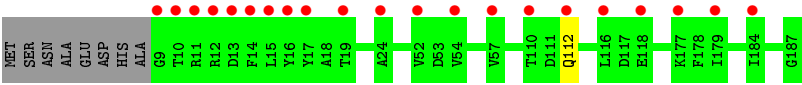
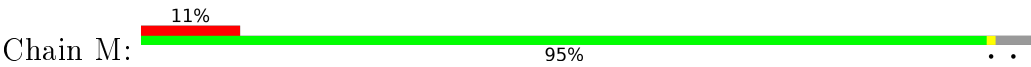


- Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit

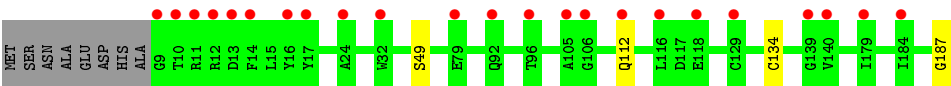
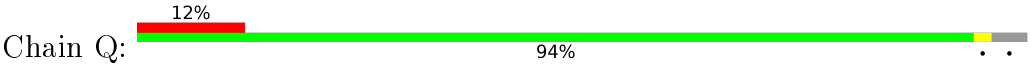




● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	120.77Å 128.28Å 128.28Å 63.92° 88.63° 63.38°	Depositor
Resolution (Å)	29.98 – 2.97 30.58 – 2.95	Depositor EDS
% Data completeness (in resolution range)	96.7 (29.98-2.97) 64.0 (30.58-2.95)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.95Å)	Xtriage
Refinement program	PHENIX (1.11rc1_2513: ???)	Depositor
R, R_{free}	0.215 , 0.258 0.213 , 0.259	Depositor DCC
R_{free} test set	1808 reflections (1.65%)	DCC
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.016 for h,h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	54985	wwPDB-VP
Average B, all atoms (Å ²)	78.0	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 62.96 % 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 1.0410e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: FMX, SR, ASC, LOP, FES, HEC, HEM, BOG

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	0.65	1/3576 (0.0%)	0.72	4/4906 (0.1%)
1	E	0.58	0/3576	0.70	3/4906 (0.1%)
1	K	0.66	1/3576 (0.0%)	0.76	6/4906 (0.1%)
1	O	0.61	1/3576 (0.0%)	0.70	1/4906 (0.0%)
2	B	0.56	0/2010	0.70	1/2733 (0.0%)
2	F	0.51	0/2010	0.65	1/2733 (0.0%)
2	L	0.63	0/2010	0.72	2/2733 (0.1%)
2	P	0.46	0/2010	0.65	0/2733
3	C	0.46	0/1371	0.67	0/1868
3	G	0.49	1/1371 (0.1%)	0.67	0/1868
3	M	0.51	0/1371	0.68	0/1868
3	Q	0.47	1/1371 (0.1%)	0.66	0/1868
All	All	0.57	5/27828 (0.0%)	0.70	18/38028 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Q	134	CYS	CB-SG	-5.81	1.72	1.81
3	G	134	CYS	CB-SG	-5.63	1.72	1.81
1	K	70	THR	C-N	5.35	1.44	1.34
1	O	70	THR	C-N	5.20	1.44	1.34
1	A	228	GLU	CG-CD	5.12	1.59	1.51

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	302	TYR	CB-CG-CD1	-7.13	116.72	121.00
1	K	302	TYR	CB-CG-CD1	-7.02	116.79	121.00
1	A	302	TYR	CB-CG-CD1	-6.77	116.94	121.00
1	K	114	ARG	NE-CZ-NH2	-6.61	117.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	158	ARG	NE-CZ-NH1	6.01	123.31	120.30
2	F	158	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	302	TYR	CB-CG-CD2	5.59	124.35	121.00
1	E	302	TYR	CB-CG-CD2	5.58	124.34	121.00
2	L	158	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	A	231	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	E	114	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	K	231	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	O	302	TYR	CB-CG-CD1	-5.34	117.79	121.00
1	A	231	ARG	NE-CZ-NH1	5.34	122.97	120.30
2	L	191	ASP	CB-CG-OD2	-5.15	113.66	118.30
1	K	302	TYR	CB-CG-CD2	5.13	124.08	121.00
1	K	231	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	K	84	MET	CG-SD-CE	5.00	108.20	100.20

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	3445	3412	3427	7	0
1	E	3445	3412	3427	9	0
1	K	3445	3412	3427	8	0
1	O	3445	3412	3427	6	0
2	B	1953	1839	1848	1	0
2	F	1953	1839	1848	3	0
2	L	1953	1839	1848	2	0
2	P	1953	1839	1848	0	0
3	C	1341	1304	1307	0	0
3	G	1341	1304	1307	2	0
3	M	1341	1304	1307	1	0
3	Q	1341	1304	1307	2	0
4	A	86	60	60	3	0
4	E	86	60	60	1	0
4	K	86	60	60	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	O	86	60	60	3	0
5	A	28	18	18	0	0
5	E	28	18	18	0	0
5	K	28	18	18	0	0
5	O	28	18	18	0	0
6	A	12	7	7	0	0
6	E	12	7	7	1	0
6	K	12	7	7	2	0
6	O	12	7	7	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	F	1	0	0	0	0
7	K	1	0	0	0	0
7	L	1	0	0	0	0
7	P	1	0	0	0	0
8	A	45	67	67	0	0
8	E	45	67	67	0	0
8	K	45	67	67	1	0
8	O	45	67	67	0	0
9	B	43	32	30	1	0
9	F	43	32	30	3	0
9	L	43	32	30	2	0
9	P	43	32	30	2	0
10	B	20	28	28	0	0
10	F	20	27	28	0	0
10	K	20	28	28	0	0
10	P	20	28	28	0	0
11	C	4	0	0	0	0
11	G	4	0	0	0	0
11	M	4	0	0	0	0
11	Q	4	0	0	0	0
12	A	1	0	0	0	0
12	E	1	0	0	0	0
12	K	1	0	0	0	0
12	O	1	0	0	0	0
All	All	27918	27067	27168	51	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 1.

All (51) 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:K:291:HIS:ND1	6:K:1004:ASC:O1	2.18	0.77
9:P:1001:HEC:HMC1	9:P:1001:HEC:HBC3	1.81	0.63
1:A:122:LYS:NZ	1:A:354:VAL:O	2.26	0.61
3:Q:49:SER:OG	3:Q:187:GLY:O	2.21	0.59
9:L:1001:HEC:HMB1	9:L:1001:HEC:HBB3	1.89	0.55
9:P:1001:HEC:HMB1	9:P:1001:HEC:HBB3	1.89	0.55
1:E:291:HIS:ND1	6:E:1004:ASC:O1	2.40	0.54
4:A:1001:HEM:HHO	4:A:1001:HEM:HBC2	1.88	0.54
4:O:1001:HEM:HHC	4:O:1001:HEM:HBB2	1.90	0.54
1:E:309:THR:OG1	1:E:311:ASP:OD1	2.22	0.53
1:O:122:LYS:NZ	1:O:354:VAL:O	2.34	0.53
1:A:114:ARG:NH1	4:A:1002:HEM:O2A	2.38	0.53
4:K:1001:HEM:HBB2	4:K:1001:HEM:HHC	1.90	0.53
9:F:1001:HEC:HMC1	9:F:1001:HEC:HBC3	1.92	0.52
1:K:309:THR:OG1	1:K:311:ASP:OD1	2.24	0.49
4:K:1001:HEM:HHO	4:K:1001:HEM:HBC2	1.95	0.48
1:K:358:ARG:NH2	8:K:1006:LOP:O1	2.47	0.47
1:O:390:ASP:OD1	1:O:391:TRP:N	2.46	0.47
4:A:1001:HEM:HBB2	4:A:1001:HEM:HHC	1.98	0.46
9:F:1001:HEC:HMB1	9:F:1001:HEC:HBB3	1.98	0.46
1:A:390:ASP:OD1	1:A:391:TRP:N	2.49	0.46
1:A:22:ARG:NE	1:E:126:GLU:OE1	2.47	0.46
1:E:379:TRP:NE1	2:F:114:MET:O	2.48	0.45
4:K:1001:HEM:HHA	4:K:1001:HEM:HBD2	1.98	0.44
1:E:425:GLU:O	1:E:429:ASN:ND2	2.42	0.44
3:Q:112:GLN:N	3:Q:112:GLN:OE1	2.50	0.43
1:A:105:PHE:HA	1:A:108:VAL:HG22	2.00	0.43
2:F:14:GLU:OE2	2:F:129:GLU:OE2	2.36	0.43
4:O:1001:HEM:HHA	4:O:1001:HEM:HBD2	1.98	0.43
1:K:422:ALA:N	1:K:426:GLU:OE1	2.46	0.43
1:E:165:LEU:HD22	1:E:305:LEU:HD11	2.01	0.42
1:E:292:ILE:HG13	1:E:292:ILE:O	2.19	0.42
2:L:135:LEU:HD21	9:L:1001:HEC:HMB2	2.01	0.42
1:O:298:PHE:CE2	1:O:302:TYR:HB2	2.55	0.42
1:A:195:PHE:HE2	1:E:195:PHE:HE2	1.66	0.42
9:B:1001:HEC:HBB3	9:B:1001:HEC:HMB1	2.02	0.42
1:O:199:TYR:CZ	4:O:1001:HEM:HBC1	2.55	0.41
1:O:96:LEU:O	1:O:100:GLY:N	2.48	0.41
3:G:112:GLN:N	3:G:112:GLN:OE1	2.50	0.41
1:K:302:TYR:HH	6:K:1004:ASC:HO6	1.68	0.41
3:G:86:ARG:HG2	3:G:111:ASP:HB3	2.02	0.41
3:M:112:GLN:OE1	3:M:112:GLN:N	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:LEU:HD22	1:A:305:LEU:HD11	2.03	0.41
1:K:292:ILE:HG13	1:K:292:ILE:O	2.21	0.41
1:E:199:TYR:CE2	4:E:1001:HEM:HBC1	2.55	0.41
2:B:141:GLU:OE2	2:B:144:LYS:NZ	2.49	0.41
2:F:135:LEU:HD21	9:F:1001:HEC:HMB2	2.03	0.40
2:L:146:ALA:O	2:L:148:GLY:N	2.54	0.40
1:K:54:CYS:SG	1:K:103:LEU:HG	2.61	0.40
1:K:359:TYR:CZ	1:K:421:PRO:HD3	2.56	0.40
1:O:105:PHE:HA	1:O:108:VAL:HG22	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	427/445 (96%)	422 (99%)	5 (1%)	0	100	100
1	E	427/445 (96%)	422 (99%)	5 (1%)	0	100	100
1	K	427/445 (96%)	422 (99%)	5 (1%)	0	100	100
1	O	427/445 (96%)	422 (99%)	5 (1%)	0	100	100
2	B	254/272 (93%)	244 (96%)	9 (4%)	1 (0%)	39	79
2	F	254/272 (93%)	244 (96%)	8 (3%)	2 (1%)	24	65
2	L	254/272 (93%)	244 (96%)	8 (3%)	2 (1%)	24	65
2	P	254/272 (93%)	244 (96%)	8 (3%)	2 (1%)	24	65
3	C	177/187 (95%)	168 (95%)	9 (5%)	0	100	100
3	G	177/187 (95%)	169 (96%)	8 (4%)	0	100	100
3	M	177/187 (95%)	170 (96%)	7 (4%)	0	100	100
3	Q	177/187 (95%)	169 (96%)	8 (4%)	0	100	100
All	All	3432/3616 (95%)	3340 (97%)	85 (2%)	7 (0%)	52	87

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	113	PRO
2	B	113	PRO
2	L	113	PRO
2	P	147	GLU
2	F	147	GLU
2	L	147	GLU
2	P	113	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	354/366 (97%)	349 (99%)	5 (1%)	74	92
1	E	354/366 (97%)	348 (98%)	6 (2%)	68	90
1	K	354/366 (97%)	348 (98%)	6 (2%)	68	90
1	O	354/366 (97%)	349 (99%)	5 (1%)	74	92
2	B	203/216 (94%)	203 (100%)	0	100	100
2	F	203/216 (94%)	203 (100%)	0	100	100
2	L	203/216 (94%)	203 (100%)	0	100	100
2	P	203/216 (94%)	203 (100%)	0	100	100
3	C	138/144 (96%)	138 (100%)	0	100	100
3	G	138/144 (96%)	138 (100%)	0	100	100
3	M	138/144 (96%)	138 (100%)	0	100	100
3	Q	138/144 (96%)	138 (100%)	0	100	100
All	All	2780/2904 (96%)	2758 (99%)	22 (1%)	86	95

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	ARG
1	A	104	PHE

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Mol	Chain	Res	Type
1	A	108	VAL
1	A	199	TYR
1	A	414	ILE
1	E	94	ARG
1	E	104	PHE
1	E	108	VAL
1	E	199	TYR
1	E	385	THR
1	E	414	ILE
1	K	6	HIS
1	K	94	ARG
1	K	104	PHE
1	K	108	VAL
1	K	199	TYR
1	K	414	ILE
1	O	94	ARG
1	O	104	PHE
1	O	108	VAL
1	O	199	TYR
1	O	414	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	316	GLN
2	L	111	HIS
1	O	316	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 ⓘ

Of 38 ligands modelled in this entry, 6 are monoatomic - leaving 32 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$
4	HEM	A	1001	1	24,50,50	2.51	8 (33%)	16,82,82	1.38	2 (12%)
4	HEM	A	1002	1	24,50,50	2.20	5 (20%)	16,82,82	2.02	4 (25%)
5	FMX	A	1003	-	29,31,31	0.91	1 (3%)	37,44,44	1.98	10 (27%)
6	ASC	A	1004	-	12,12,12	0.94	0	16,17,17	3.00	5 (31%)
8	LOP	A	1006	-	43,44,44	0.97	1 (2%)	44,49,49	1.46	6 (13%)
9	HEC	B	1001	2	24,50,50	2.14	6 (25%)	19,82,82	2.80	6 (31%)
10	BOG	B	1003	-	20,20,20	1.01	1 (5%)	25,25,25	1.36	3 (12%)
11	FES	C	1001	3	0,4,4	0.00	-	0,4,4	0.00	-
4	HEM	E	1001	1	24,50,50	2.06	6 (25%)	16,82,82	1.85	4 (25%)
4	HEM	E	1002	1	24,50,50	2.01	6 (25%)	16,82,82	2.02	4 (25%)
5	FMX	E	1003	-	29,31,31	0.79	2 (6%)	37,44,44	1.28	4 (10%)
6	ASC	E	1004	-	12,12,12	0.93	0	16,17,17	2.83	8 (50%)
8	LOP	E	1005	-	43,44,44	1.04	2 (4%)	44,49,49	1.33	8 (18%)
9	HEC	F	1001	2	24,50,50	2.17	3 (12%)	19,82,82	2.92	6 (31%)
10	BOG	F	1003	-	20,20,20	1.07	2 (10%)	25,25,25	1.26	3 (12%)
11	FES	G	1001	3	0,4,4	0.00	-	0,4,4	0.00	-
4	HEM	K	1001	1	24,50,50	2.42	9 (37%)	16,82,82	1.88	4 (25%)
4	HEM	K	1002	1	24,50,50	1.97	6 (25%)	16,82,82	1.87	5 (31%)
5	FMX	K	1003	-	29,31,31	0.80	1 (3%)	37,44,44	1.59	8 (21%)
6	ASC	K	1004	-	12,12,12	0.99	1 (8%)	16,17,17	2.76	8 (50%)
8	LOP	K	1006	-	43,44,44	1.10	2 (4%)	44,49,49	1.11	6 (13%)
10	BOG	K	1007	-	20,20,20	1.11	2 (10%)	25,25,25	1.04	1 (4%)
9	HEC	L	1001	2	24,50,50	2.22	4 (16%)	19,82,82	2.99	6 (31%)
11	FES	M	1001	3	0,4,4	0.00	-	0,4,4	0.00	-
4	HEM	O	1001	1	24,50,50	2.27	11 (45%)	16,82,82	1.97	6 (37%)
4	HEM	O	1002	1	24,50,50	1.97	6 (25%)	16,82,82	2.12	5 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FMX	O	1003	-	29,31,31	1.05	3 (10%)	37,44,44	1.74	6 (16%)
6	ASC	O	1004	-	12,12,12	1.07	0	16,17,17	3.09	6 (37%)
8	LOP	O	1005	-	43,44,44	1.10	2 (4%)	44,49,49	1.18	6 (13%)
9	HEC	P	1001	2	24,50,50	2.31	6 (25%)	19,82,82	2.37	5 (26%)
10	BOG	P	1003	-	20,20,20	1.00	1 (5%)	25,25,25	1.09	1 (4%)
11	FES	Q	1001	3	0,4,4	0.00	-	0,4,4	0.00	-

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
4	HEM	A	1001	1	-	0/6/54/54	0/0/8/8
4	HEM	A	1002	1	-	0/6/54/54	0/0/8/8
5	FMX	A	1003	-	-	0/14/33/33	0/4/4/4
6	ASC	A	1004	-	-	0/6/22/22	0/1/1/1
8	LOP	A	1006	-	-	0/48/48/48	0/0/0/0
9	HEC	B	1001	2	-	0/6/54/54	0/0/8/8
10	BOG	B	1003	-	-	0/11/31/31	0/1/1/1
11	FES	C	1001	3	-	0/0/4/4	0/1/1/1
4	HEM	E	1001	1	-	0/6/54/54	0/0/8/8
4	HEM	E	1002	1	-	0/6/54/54	0/0/8/8
5	FMX	E	1003	-	-	0/14/33/33	0/4/4/4
6	ASC	E	1004	-	-	0/6/22/22	0/1/1/1
8	LOP	E	1005	-	-	0/48/48/48	0/0/0/0
9	HEC	F	1001	2	-	0/6/54/54	0/0/8/8
10	BOG	F	1003	-	-	0/11/31/31	0/1/1/1
11	FES	G	1001	3	-	0/0/4/4	0/1/1/1
4	HEM	K	1001	1	-	0/6/54/54	0/0/8/8
4	HEM	K	1002	1	-	0/6/54/54	0/0/8/8
5	FMX	K	1003	-	-	0/14/33/33	0/4/4/4
6	ASC	K	1004	-	-	0/6/22/22	0/1/1/1
8	LOP	K	1006	-	-	0/48/48/48	0/0/0/0
10	BOG	K	1007	-	-	0/11/31/31	0/1/1/1
9	HEC	L	1001	2	-	0/6/54/54	0/0/8/8
11	FES	M	1001	3	-	0/0/4/4	0/1/1/1
4	HEM	O	1001	1	-	0/6/54/54	0/0/8/8
4	HEM	O	1002	1	-	0/6/54/54	0/0/8/8
5	FMX	O	1003	-	-	0/14/33/33	0/4/4/4
6	ASC	O	1004	-	-	0/6/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	LOP	O	1005	-	-	0/48/48/48	0/0/0/0
9	HEC	P	1001	2	-	0/6/54/54	0/0/8/8
10	BOG	P	1003	-	-	0/11/31/31	0/1/1/1
11	FES	Q	1001	3	-	0/0/4/4	0/1/1/1

All (97) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1001	HEM	C3B-C2B	-7.41	1.31	1.40
9	L	1001	HEC	C3B-C2B	-6.93	1.33	1.40
4	A	1002	HEM	C3C-C2C	-6.77	1.31	1.40
9	F	1001	HEC	C3B-C2B	-6.46	1.34	1.40
9	P	1001	HEC	C3B-C2B	-6.21	1.34	1.40
4	O	1001	HEM	C3B-C2B	-5.77	1.33	1.40
9	P	1001	HEC	C3C-C2C	-5.66	1.34	1.40
4	K	1001	HEM	C3B-C2B	-5.66	1.33	1.40
9	B	1001	HEC	C3B-C2B	-5.45	1.35	1.40
4	O	1002	HEM	C3C-C2C	-5.39	1.33	1.40
4	A	1001	HEM	C3C-C2C	-5.28	1.33	1.40
9	B	1001	HEC	C3C-C2C	-5.22	1.35	1.40
4	E	1001	HEM	C3C-C2C	-4.98	1.34	1.40
4	E	1002	HEM	C3C-C2C	-4.83	1.34	1.40
4	K	1001	HEM	C3C-C2C	-4.64	1.34	1.40
9	F	1001	HEC	C3C-C2C	-4.43	1.36	1.40
9	L	1001	HEC	C3C-C2C	-4.41	1.36	1.40
4	E	1001	HEM	C3B-C2B	-4.33	1.34	1.40
4	A	1002	HEM	C3B-C2B	-3.97	1.35	1.40
4	O	1002	HEM	C3B-C2B	-3.52	1.35	1.40
4	O	1001	HEM	C3C-C2C	-3.30	1.36	1.40
4	K	1002	HEM	C3B-C2B	-3.24	1.36	1.40
4	K	1002	HEM	C3C-C2C	-3.24	1.36	1.40
4	E	1002	HEM	C3B-C2B	-2.58	1.37	1.40
5	O	1003	FMX	O6-C6	-2.37	1.18	1.22
5	E	1003	FMX	O6-C6	-2.15	1.18	1.22
5	O	1003	FMX	C5-C6	-2.14	1.51	1.54
5	A	1003	FMX	C21-N1	2.02	1.44	1.41
10	F	1003	BOG	O3-C3	2.06	1.47	1.43
9	B	1001	HEC	CMC-C2C	2.08	1.56	1.51
9	P	1001	HEC	CMC-C2C	2.09	1.56	1.51
4	O	1001	HEM	C1C-NC	2.13	1.39	1.36
9	P	1001	HEC	CAA-C2A	2.14	1.55	1.52
4	A	1001	HEM	CAD-C3D	2.14	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	1004	ASC	O4-C1	2.14	1.39	1.35
4	K	1002	HEM	C1B-NB	2.17	1.39	1.36
4	A	1001	HEM	CMA-C3A	2.18	1.56	1.51
4	E	1001	HEM	C3B-CAB	2.19	1.52	1.47
4	O	1001	HEM	C3B-CAB	2.20	1.52	1.47
4	O	1002	HEM	CMA-C3A	2.20	1.56	1.51
4	O	1001	HEM	CMA-C3A	2.20	1.56	1.51
8	E	1005	LOP	C25-C24	2.21	1.57	1.50
4	O	1001	HEM	CMB-C2B	2.23	1.56	1.51
9	P	1001	HEC	CAD-C3D	2.25	1.55	1.52
9	B	1001	HEC	CMB-C2B	2.26	1.56	1.51
4	O	1002	HEM	CMB-C2B	2.27	1.56	1.51
4	K	1001	HEM	CMB-C2B	2.28	1.56	1.51
9	B	1001	HEC	CAA-C2A	2.31	1.55	1.52
4	E	1002	HEM	CMB-C2B	2.32	1.56	1.51
4	K	1001	HEM	CMC-C2C	2.32	1.56	1.51
4	E	1001	HEM	CMA-C3A	2.34	1.56	1.51
5	E	1003	FMX	C21-N1	2.35	1.45	1.41
4	O	1001	HEM	CMD-C2D	2.40	1.56	1.51
9	L	1001	HEC	CAA-C2A	2.48	1.55	1.52
8	O	1005	LOP	C25-C24	2.51	1.57	1.50
4	E	1002	HEM	CMC-C2C	2.52	1.57	1.51
10	K	1007	BOG	O3-C3	2.57	1.49	1.43
8	A	1006	LOP	C7-C6	2.63	1.58	1.50
4	O	1001	HEM	CAD-C3D	2.66	1.55	1.52
4	A	1001	HEM	C3B-CAB	2.67	1.53	1.47
4	E	1001	HEM	CMB-C2B	2.71	1.57	1.51
4	O	1001	HEM	C4D-ND	2.73	1.40	1.36
4	A	1001	HEM	CMC-C2C	2.73	1.57	1.51
8	K	1006	LOP	C7-C6	2.73	1.58	1.50
4	K	1001	HEM	C1C-NC	2.73	1.40	1.36
5	O	1003	FMX	C21-N1	2.81	1.45	1.41
8	O	1005	LOP	C7-C6	2.85	1.58	1.50
4	A	1002	HEM	C3C-CAC	2.87	1.53	1.47
4	A	1002	HEM	CAA-C2A	2.89	1.56	1.52
4	K	1001	HEM	C3B-CAB	2.92	1.54	1.47
8	E	1005	LOP	C7-C6	2.93	1.59	1.50
5	K	1003	FMX	C21-N1	2.95	1.46	1.41
4	K	1001	HEM	C4D-ND	2.95	1.40	1.36
4	K	1002	HEM	CMB-C2B	2.98	1.58	1.51
10	K	1007	BOG	O5-C1	3.02	1.49	1.41
4	K	1001	HEM	CAD-C3D	3.12	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	K	1006	LOP	C25-C24	3.15	1.59	1.50
4	A	1001	HEM	C1C-NC	3.20	1.41	1.36
4	O	1001	HEM	CMC-C2C	3.22	1.58	1.51
10	F	1003	BOG	O5-C1	3.24	1.50	1.41
10	B	1003	BOG	O5-C1	3.24	1.50	1.41
10	P	1003	BOG	O5-C1	3.34	1.50	1.41
4	A	1001	HEM	C3C-CAC	3.38	1.54	1.47
4	O	1002	HEM	C3B-CAB	3.42	1.55	1.47
4	O	1001	HEM	C3C-CAC	3.57	1.55	1.47
4	E	1001	HEM	C3C-CAC	3.57	1.55	1.47
4	O	1002	HEM	C3C-CAC	3.61	1.55	1.47
4	A	1002	HEM	C3B-CAB	3.71	1.55	1.47
4	K	1001	HEM	C3C-CAC	4.01	1.56	1.47
4	K	1002	HEM	C3B-CAB	4.05	1.56	1.47
4	E	1002	HEM	C3C-CAC	4.08	1.56	1.47
4	E	1002	HEM	C3B-CAB	4.13	1.56	1.47
4	K	1002	HEM	C3C-CAC	4.35	1.56	1.47
9	P	1001	HEC	C3D-C2D	4.43	1.50	1.37
9	L	1001	HEC	C3D-C2D	4.52	1.51	1.37
9	B	1001	HEC	C3D-C2D	4.53	1.51	1.37
9	F	1001	HEC	C3D-C2D	4.73	1.51	1.37

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	O	1004	ASC	C4-O4-C1	-8.43	101.06	109.29
9	B	1001	HEC	CBB-CAB-C3B	-6.78	112.51	127.34
9	F	1001	HEC	CBB-CAB-C3B	-6.52	113.09	127.34
9	F	1001	HEC	CBC-CAC-C3C	-6.34	113.48	127.34
9	L	1001	HEC	CBC-CAC-C3C	-6.29	113.59	127.34
9	P	1001	HEC	CBB-CAB-C3B	-6.13	113.94	127.34
6	A	1004	ASC	C4-O4-C1	-6.05	103.38	109.29
9	B	1001	HEC	CAA-CBA-CGA	-5.95	101.21	112.78
6	A	1004	ASC	O5-C5-C4	-5.94	100.15	110.33
9	L	1001	HEC	CBB-CAB-C3B	-5.85	114.55	127.34
6	A	1004	ASC	O4-C4-C3	-5.71	99.61	104.13
5	O	1003	FMX	O6-C6-C5	-5.63	121.78	126.00
5	A	1003	FMX	O4-C3-N2	-5.55	104.80	108.70
6	O	1004	ASC	O5-C5-C4	-5.44	101.01	110.33
9	L	1001	HEC	CBD-CAD-C3D	-5.41	102.99	112.49
4	K	1001	HEM	CBA-CAA-C2A	-5.18	103.39	112.49
9	P	1001	HEC	CBC-CAC-C3C	-5.00	116.41	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1004	ASC	C4-O4-C1	-4.94	104.47	109.29
6	K	1004	ASC	C4-O4-C1	-4.90	104.50	109.29
9	B	1001	HEC	CBC-CAC-C3C	-4.69	117.08	127.34
6	A	1004	ASC	O4-C1-C2	-4.53	106.06	109.94
9	F	1001	HEC	CAA-CBA-CGA	-4.44	104.15	112.78
9	L	1001	HEC	CMC-C2C-C1C	-4.41	120.82	128.31
4	O	1001	HEM	CBA-CAA-C2A	-4.40	104.75	112.49
9	P	1001	HEC	CAA-CBA-CGA	-4.37	104.28	112.78
6	E	1004	ASC	C5-C4-C3	-4.32	107.94	114.17
6	E	1004	ASC	O4-C1-C2	-4.10	106.43	109.94
6	K	1004	ASC	C6-C5-C4	-4.07	105.08	111.95
5	K	1003	FMX	O4-C3-N2	-3.90	105.95	108.70
6	K	1004	ASC	O5-C5-C4	-3.87	103.69	110.33
5	E	1003	FMX	O4-C3-N2	-3.77	106.05	108.70
4	E	1002	HEM	CMD-C2D-C1D	-3.76	121.91	128.31
9	F	1001	HEC	CMC-C2C-C1C	-3.74	121.94	128.31
6	E	1004	ASC	O6-C6-C5	-3.73	102.80	111.07
4	A	1001	HEM	CBA-CAA-C2A	-3.68	106.02	112.49
9	B	1001	HEC	CMC-C2C-C1C	-3.67	122.06	128.31
9	F	1001	HEC	CBD-CAD-C3D	-3.60	106.16	112.49
6	E	1004	ASC	O5-C5-C4	-3.56	104.22	110.33
9	L	1001	HEC	CAA-CBA-CGA	-3.54	105.89	112.78
6	O	1004	ASC	O4-C1-C2	-3.52	106.92	109.94
4	E	1001	HEM	CBA-CAA-C2A	-3.36	106.59	112.49
6	O	1004	ASC	O4-C4-C3	-3.32	101.50	104.13
5	A	1003	FMX	C13-C8-C5	-3.26	115.97	120.53
5	K	1003	FMX	C13-C8-C5	-3.22	116.02	120.53
4	E	1001	HEM	CBD-CAD-C3D	-3.21	106.84	112.47
6	K	1004	ASC	O1-C1-C2	-3.18	125.42	129.30
8	O	1005	LOP	O6-C24-O8	-3.16	115.22	123.51
4	A	1002	HEM	CAA-CBA-CGA	-3.14	106.67	112.78
4	K	1001	HEM	CMD-C2D-C1D	-3.09	123.05	128.31
4	O	1002	HEM	CBA-CAA-C2A	-3.08	107.07	112.49
4	O	1001	HEM	CMD-C2D-C1D	-2.96	123.28	128.31
4	O	1002	HEM	CMD-C2D-C1D	-2.95	123.29	128.31
9	B	1001	HEC	CBD-CAD-C3D	-2.95	107.31	112.49
5	K	1003	FMX	O4-C5-C8	-2.76	103.74	108.49
6	K	1004	ASC	C5-C4-C3	-2.66	110.33	114.17
6	K	1004	ASC	O4-C1-C2	-2.65	107.67	109.94
8	K	1006	LOP	O6-C24-O8	-2.62	116.65	123.51
4	K	1002	HEM	CMD-C2D-C1D	-2.61	123.86	128.31
10	F	1003	BOG	C6-C5-C4	-2.59	106.49	112.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1003	FMX	O4-C5-C8	-2.53	104.15	108.49
5	O	1003	FMX	C13-C8-C5	-2.51	117.01	120.53
4	A	1001	HEM	CMD-C2D-C1D	-2.45	124.15	128.31
4	K	1002	HEM	CAD-CBD-CGD	-2.39	108.13	112.78
4	A	1002	HEM	CAD-CBD-CGD	-2.38	108.14	112.78
9	P	1001	HEC	CMC-C2C-C1C	-2.34	124.33	128.31
5	A	1003	FMX	C9-C10-C11	-2.29	116.88	119.74
4	O	1002	HEM	CAD-CBD-CGD	-2.22	108.45	112.78
4	K	1002	HEM	CBD-CAD-C3D	-2.19	108.63	112.47
4	O	1001	HEM	CAD-C3D-C2D	-2.18	122.79	129.00
8	O	1005	LOP	O5-C6-O7	-2.18	117.75	123.67
8	A	1006	LOP	O6-C24-O8	-2.15	117.86	123.51
8	E	1005	LOP	O6-C24-O8	-2.13	117.93	123.51
6	E	1004	ASC	C6-C5-C4	-2.10	108.40	111.95
8	A	1006	LOP	O5-C6-O7	-2.09	117.99	123.67
8	E	1005	LOP	O8-C24-C25	-2.04	115.96	123.76
8	O	1005	LOP	C5-O6-C24	2.02	123.01	117.00
8	K	1006	LOP	O5-C4-C3	2.05	115.55	108.36
4	K	1001	HEM	CMB-C2B-C3B	2.05	129.10	125.09
8	E	1005	LOP	O5-C4-C3	2.05	115.57	108.36
10	B	1003	BOG	C4-C3-C2	2.06	114.58	110.79
10	B	1003	BOG	C3-C4-C5	2.08	113.93	110.23
5	O	1003	FMX	C9-C8-C5	2.10	123.47	120.53
8	K	1006	LOP	O5-C6-C7	2.15	116.05	111.53
5	A	1003	FMX	O6-C6-N2	2.17	128.44	125.61
5	A	1003	FMX	C21-N1-N2	2.21	120.54	116.14
10	F	1003	BOG	O5-C5-C4	2.26	113.98	109.67
4	O	1001	HEM	CMC-C2C-C3C	2.30	129.59	125.09
5	K	1003	FMX	O6-C6-N2	2.32	128.63	125.61
5	A	1003	FMX	O4-C5-C7	2.33	111.12	107.25
4	E	1001	HEM	CMC-C2C-C3C	2.35	129.69	125.09
8	E	1005	LOP	C5-O6-C24	2.40	124.14	117.00
10	K	1007	BOG	C3-C4-C5	2.43	114.56	110.23
4	O	1001	HEM	CMB-C2B-C3B	2.46	129.90	125.09
5	E	1003	FMX	C5-O4-C3	2.49	111.87	109.18
9	P	1001	HEC	CMC-C2C-C3C	2.50	128.56	125.67
8	O	1005	LOP	O6-C5-C4	2.51	115.47	108.70
8	K	1006	LOP	O6-C24-C25	2.52	119.61	111.85
4	E	1002	HEM	CMD-C2D-C3D	2.53	130.53	125.24
8	K	1006	LOP	C5-C4-C3	2.55	118.02	112.08
5	E	1003	FMX	C21-N1-N2	2.60	121.31	116.14
6	O	1004	ASC	O5-C5-C6	2.67	115.56	109.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	1003	FMX	O4-C5-C7	2.68	111.71	107.25
5	A	1003	FMX	C5-O4-C3	2.70	112.10	109.18
8	E	1005	LOP	C5-C4-C3	2.74	118.48	112.08
8	E	1005	LOP	O5-C6-C7	2.76	117.35	111.53
8	A	1006	LOP	C5-C4-C3	2.80	118.61	112.08
8	O	1005	LOP	C5-C4-C3	2.82	118.66	112.08
4	K	1001	HEM	CBD-CAD-C3D	2.86	117.48	112.47
8	K	1006	LOP	C5-O6-C24	2.99	125.91	117.00
10	P	1003	BOG	O1-C1-C2	3.06	111.77	108.00
5	K	1003	FMX	O4-C3-O3	3.07	125.73	122.53
8	O	1005	LOP	O6-C24-C25	3.18	121.64	111.85
4	O	1001	HEM	CBD-CAD-C3D	3.20	118.08	112.47
5	K	1003	FMX	C5-O4-C3	3.20	112.64	109.18
10	F	1003	BOG	O1-C1-C2	3.22	111.97	108.00
4	K	1002	HEM	CMB-C2B-C3B	3.26	131.47	125.09
8	E	1005	LOP	O6-C24-C25	3.28	121.95	111.85
5	O	1003	FMX	C21-N1-N2	3.29	122.68	116.14
5	A	1003	FMX	C9-C8-C5	3.32	125.19	120.53
4	K	1002	HEM	CMC-C2C-C3C	3.41	131.76	125.09
6	K	1004	ASC	O4-C4-C5	3.59	115.82	109.69
6	A	1004	ASC	O4-C1-O1	3.61	125.36	121.27
9	B	1001	HEC	CMC-C2C-C3C	3.61	129.85	125.67
4	E	1002	HEM	CMC-C2C-C3C	3.61	132.15	125.09
5	E	1003	FMX	O4-C3-O3	3.65	126.33	122.53
9	F	1001	HEC	CMC-C2C-C3C	3.66	129.91	125.67
4	E	1002	HEM	CMB-C2B-C3B	3.72	132.36	125.09
6	E	1004	ASC	O4-C1-O1	3.73	125.50	121.27
4	O	1002	HEM	CMC-C2C-C3C	3.81	132.53	125.09
9	L	1001	HEC	CMC-C2C-C3C	3.81	130.08	125.67
6	O	1004	ASC	O4-C1-O1	3.85	125.64	121.27
4	A	1002	HEM	CMB-C2B-C3B	3.85	132.62	125.09
8	E	1005	LOP	O6-C5-C4	3.90	119.23	108.70
8	A	1006	LOP	O5-C6-C7	3.91	119.77	111.53
10	B	1003	BOG	O1-C1-C2	3.91	112.82	108.00
5	O	1003	FMX	O6-C6-N2	3.98	130.81	125.61
5	K	1003	FMX	C9-C8-C5	4.03	126.18	120.53
4	O	1002	HEM	CMB-C2B-C3B	4.11	133.12	125.09
6	E	1004	ASC	O4-C4-C5	4.24	116.92	109.69
8	A	1006	LOP	O6-C5-C4	4.25	120.18	108.70
4	A	1002	HEM	CMC-C2C-C3C	4.28	133.45	125.09
5	O	1003	FMX	O4-C3-O3	4.41	127.13	122.53
8	A	1006	LOP	O6-C24-C25	4.42	125.44	111.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1001	HEM	CMB-C2B-C3B	4.47	133.84	125.09
6	K	1004	ASC	O4-C1-O1	4.84	126.76	121.27
5	A	1003	FMX	O4-C3-O3	6.45	129.24	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	HEM	2	0
4	A	1002	HEM	1	0
9	B	1001	HEC	1	0
4	E	1001	HEM	1	0
6	E	1004	ASC	1	0
9	F	1001	HEC	3	0
4	K	1001	HEM	3	0
6	K	1004	ASC	2	0
8	K	1006	LOP	1	0
9	L	1001	HEC	2	0
4	O	1001	HEM	3	0
9	P	1001	HEC	2	0

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(Å²)	Q<0.9
1	A	429/445 (96%)	0.20	14 (3%)	50	29	50, 60, 93, 184	0
1	E	429/445 (96%)	0.23	23 (5%)	29	15	34, 62, 102, 156	0
1	K	429/445 (96%)	-0.02	14 (3%)	50	29	20, 50, 89, 150	0
1	O	429/445 (96%)	0.18	30 (6%)	19	9	27, 62, 96, 168	0
2	B	256/272 (94%)	0.29	23 (8%)	12	6	48, 68, 113, 174	0
2	F	256/272 (94%)	0.58	35 (13%)	4	2	45, 77, 132, 164	0
2	L	256/272 (94%)	0.27	17 (6%)	22	10	36, 61, 113, 145	0
2	P	256/272 (94%)	0.65	40 (15%)	3	1	42, 82, 124, 169	0
3	C	179/187 (95%)	0.94	27 (15%)	3	1	61, 97, 150, 212	0
3	G	179/187 (95%)	0.47	18 (10%)	9	5	46, 86, 131, 168	0
3	M	179/187 (95%)	0.66	21 (11%)	6	3	41, 84, 126, 154	0
3	Q	179/187 (95%)	0.65	23 (12%)	5	2	54, 95, 139, 167	0
All	All	3456/3616 (95%)	0.35	285 (8%)	14	7	20, 68, 120, 212	0

All (285) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	9	GLY	10.7
3	C	10	THR	10.6
3	C	9	GLY	8.5
2	P	3	GLY	8.4
2	F	2	GLY	8.3
2	L	4	GLY	7.7
3	G	9	GLY	7.5
2	F	1	ALA	7.3
3	C	13	ASP	7.2
3	M	10	THR	7.1
2	L	2	GLY	7.0

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Mol	Chain	Res	Type	RSRZ
2	P	2	GLY	7.0
2	L	3	GLY	6.9
3	Q	116	LEU	6.6
3	M	13	ASP	6.5
2	F	256	LYS	6.4
3	G	12	ARG	6.4
3	G	13	ASP	6.3
2	P	149	HIS	6.2
1	K	8	HIS	6.2
2	F	175	VAL	6.1
2	L	175	VAL	6.0
3	Q	9	GLY	6.0
3	C	16	TYR	5.9
3	C	116	LEU	5.8
3	Q	10	THR	5.8
3	M	12	ARG	5.7
3	M	16	TYR	5.5
3	C	17	TYR	5.5
2	P	256	LYS	5.4
3	G	10	THR	5.3
2	B	4	GLY	5.3
2	F	174	GLY	5.3
3	G	16	TYR	5.3
1	O	15	ILE	5.2
3	M	52	VAL	5.1
2	L	256	LYS	5.0
1	A	8	HIS	5.0
2	L	17	PHE	5.0
1	E	8	HIS	5.0
2	B	2	GLY	5.0
3	C	12	ARG	5.0
3	C	92	GLN	4.9
3	M	17	TYR	4.9
2	B	256	LYS	4.9
2	B	3	GLY	4.9
2	L	1	ALA	4.9
3	C	15	LEU	4.9
1	E	416	LYS	4.6
2	L	77	THR	4.6
3	G	179	ILE	4.6
3	C	120	GLY	4.6
3	Q	12	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	13	THR	4.5
1	O	13	THR	4.4
1	A	7	ASP	4.4
2	P	151	PRO	4.3
2	B	1	ALA	4.3
2	F	149	HIS	4.3
2	P	152	ASP	4.3
1	E	414	ILE	4.2
1	E	232	THR	4.2
3	C	14	PHE	4.2
2	F	76	GLU	4.1
2	P	1	ALA	4.1
2	F	80	ASP	4.1
1	E	236	GLU	4.0
2	P	144	LYS	4.0
2	P	122	PHE	4.0
1	O	416	LYS	4.0
3	Q	13	ASP	4.0
1	E	9	TYR	4.0
2	F	3	GLY	4.0
1	E	14	GLY	3.9
2	P	172	ALA	3.9
2	F	143	PRO	3.9
1	O	232	THR	3.9
2	L	76	GLU	3.9
3	C	83	GLU	3.9
2	F	146	ALA	3.9
3	C	79	GLU	3.8
2	P	5	HIS	3.8
1	O	234	LYS	3.8
3	Q	79	GLU	3.8
2	B	77	THR	3.8
3	M	118	GLU	3.7
2	P	143	PRO	3.7
3	C	11	ARG	3.7
2	P	73	THR	3.7
1	K	7	ASP	3.7
2	P	197	ALA	3.7
3	G	52	VAL	3.6
2	F	153	GLY	3.6
1	O	233	SER	3.6
2	F	144	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
3	C	118	GLU	3.5
2	B	58	LEU	3.5
1	O	413	ALA	3.5
2	B	73	THR	3.5
3	Q	96	THR	3.5
2	B	76	GLU	3.5
3	M	184	ILE	3.4
1	K	13	THR	3.4
2	L	79	GLU	3.4
1	O	414	ILE	3.4
2	F	253	ALA	3.4
3	C	58	GLU	3.4
1	E	413	ALA	3.4
1	K	414	ILE	3.4
2	B	79	GLU	3.4
3	M	14	PHE	3.3
2	F	122	PHE	3.3
2	P	79	GLU	3.3
1	A	14	GLY	3.3
2	B	72	VAL	3.3
1	O	12	ARG	3.3
3	G	108	GLU	3.3
1	K	12	ARG	3.3
1	K	9	TYR	3.3
3	G	17	TYR	3.2
3	G	105	ALA	3.2
3	Q	179	ILE	3.2
2	P	182	TRP	3.2
2	F	4	GLY	3.2
2	B	80	ASP	3.2
2	P	80	ASP	3.2
1	E	431	HIS	3.2
1	A	19	LEU	3.2
2	F	166	PRO	3.2
2	B	122	PHE	3.2
3	Q	11	ARG	3.1
1	O	236	GLU	3.1
1	A	12	ARG	3.1
1	O	235	ALA	3.1
2	P	141	GLU	3.1
2	P	77	THR	3.1
3	Q	16	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	24	ALA	3.0
2	F	145	CYS	3.0
2	P	114	MET	3.0
1	K	416	LYS	3.0
1	E	19	LEU	3.0
3	G	143	ASP	3.0
2	F	197	ALA	3.0
2	B	253	ALA	3.0
3	M	11	ARG	3.0
2	B	17	PHE	3.0
2	F	168	THR	3.0
3	M	19	THR	3.0
2	F	151	PRO	2.9
1	O	25	ILE	2.9
2	F	5	HIS	2.9
2	L	72	VAL	2.9
3	C	177	LYS	2.9
2	P	78	GLY	2.9
1	O	313	TRP	2.9
1	O	23	LEU	2.9
2	P	190	MET	2.9
1	O	361	PRO	2.8
1	O	9	TYR	2.8
1	K	325	ILE	2.8
1	K	324	GLY	2.8
3	Q	14	PHE	2.8
2	F	77	THR	2.8
3	M	57	VAL	2.8
1	E	311	ASP	2.8
1	O	8	HIS	2.7
2	L	114	MET	2.7
3	M	15	LEU	2.7
3	Q	92	GLN	2.7
1	E	415	GLU	2.7
3	M	54	VAL	2.7
2	P	200	HIS	2.7
2	P	178	THR	2.7
1	E	28	LEU	2.7
1	O	19	LEU	2.7
3	C	93	LEU	2.7
2	P	205	HIS	2.7
1	A	9	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
3	Q	184	ILE	2.7
1	O	430	ALA	2.7
3	G	79	GLU	2.7
3	G	106	GLY	2.6
2	F	17	PHE	2.6
2	F	79	GLU	2.6
2	B	5	HIS	2.6
3	M	24	ALA	2.6
3	C	112	GLN	2.6
1	A	353	PRO	2.6
1	K	10	GLU	2.6
1	A	23	LEU	2.6
2	B	149	HIS	2.6
1	E	10	GLU	2.6
1	E	230	ARG	2.6
2	F	148	GLY	2.5
3	C	74	ILE	2.5
3	Q	106	GLY	2.5
3	M	110	THR	2.5
1	E	231	ARG	2.5
2	F	172	ALA	2.5
1	A	387	PHE	2.5
3	Q	105	ALA	2.5
1	O	431	HIS	2.5
1	O	429	ASN	2.5
2	P	253	ALA	2.5
1	A	25	ILE	2.5
2	L	80	ASP	2.5
1	K	6	HIS	2.5
2	F	150	GLU	2.5
2	P	72	VAL	2.5
2	P	121	LEU	2.5
2	F	176	LYS	2.4
2	B	174	GLY	2.4
2	P	4	GLY	2.4
2	F	195	GLU	2.4
2	P	58	LEU	2.4
3	M	116	LEU	2.4
3	Q	112	GLN	2.4
1	O	387	PHE	2.4
2	L	122	PHE	2.4
1	E	115	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	O	14	GLY	2.4
1	O	238	GLN	2.4
1	O	10	GLU	2.4
2	F	152	ASP	2.4
3	C	113	ASN	2.4
3	G	60	GLY	2.4
3	C	59	PRO	2.4
3	G	11	ARG	2.4
2	B	250	ARG	2.3
1	A	325	ILE	2.3
2	B	78	GLY	2.3
2	P	17	PHE	2.3
1	E	13	THR	2.3
3	C	90	LEU	2.3
1	K	362	MET	2.3
2	L	149	HIS	2.3
1	O	415	GLU	2.3
3	C	29	ALA	2.3
2	P	145	CYS	2.3
3	M	177	LYS	2.3
2	P	74	ASP	2.3
1	A	17	LYS	2.3
2	P	16	PRO	2.2
2	P	113	PRO	2.2
3	Q	140	VAL	2.2
1	A	11	PRO	2.2
3	M	179	ILE	2.2
2	P	196	TYR	2.2
2	P	147	GLU	2.2
2	F	212	SER	2.2
2	L	68	THR	2.2
1	E	221	ASN	2.2
2	B	231	PHE	2.2
2	P	153	GLY	2.2
3	Q	32	TRP	2.2
3	G	24	ALA	2.2
1	K	17	LYS	2.2
3	Q	24	ALA	2.1
1	E	120	SER	2.1
2	L	174	GLY	2.1
1	E	16	GLU	2.1
3	G	51	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	F	169	CYS	2.1
2	F	114	MET	2.1
3	C	56	SER	2.1
3	Q	139	GLY	2.1
3	Q	17	TYR	2.1
2	F	254	GLY	2.1
1	O	24	PRO	2.1
2	B	75	GLU	2.1
3	Q	118	GLU	2.1
1	O	11	PRO	2.1
1	O	26	VAL	2.1
2	P	76	GLU	2.1
3	M	112	GLN	2.0
1	K	323	PHE	2.0
1	E	20	HIS	2.0
3	C	63	LEU	2.0
3	Q	129	CYS	2.0
2	B	205	HIS	2.0
3	G	184	ILE	2.0
1	E	362	MET	2.0
1	O	323	PHE	2.0
2	P	123	ASN	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	HEM	K	1001	43/43	0.96	0.27	2.07	40,49,65,71	0
4	HEM	A	1001	43/43	0.95	0.31	2.03	51,52,62,62	0
8	LOP	E	1005	45/45	0.82	0.30	2.02	71,92,108,113	0
8	LOP	O	1005	45/45	0.84	0.27	1.78	51,84,107,118	0
10	BOG	B	1003	20/20	0.85	0.34	1.68	50,63,70,73	0
11	FES	C	1001	4/4	0.99	0.24	1.63	82,82,83,87	0
8	LOP	A	1006	45/45	0.88	0.28	1.62	56,76,90,94	0
4	HEM	A	1002	43/43	0.96	0.28	1.53	54,58,70,70	0
10	BOG	F	1003	20/20	0.88	0.32	1.50	48,65,80,81	0
4	HEM	O	1002	43/43	0.96	0.29	1.45	46,56,70,73	0
10	BOG	K	1007	20/20	0.90	0.30	1.41	39,60,75,75	0
4	HEM	E	1002	43/43	0.95	0.33	1.41	53,64,77,77	0
4	HEM	O	1001	43/43	0.97	0.24	1.40	33,50,66,72	0
4	HEM	E	1001	43/43	0.96	0.27	1.35	46,52,69,82	0
8	LOP	K	1006	45/45	0.90	0.23	1.24	49,71,92,103	0
11	FES	Q	1001	4/4	0.98	0.24	1.06	67,70,72,73	0
6	ASC	O	1004	12/12	0.91	0.22	0.91	25,43,59,63	0
4	HEM	K	1002	43/43	0.97	0.23	0.78	30,49,74,78	0
11	FES	G	1001	4/4	0.99	0.23	0.74	59,63,65,65	0
5	FMX	K	1003	28/28	0.95	0.20	0.70	47,58,69,78	0
10	BOG	P	1003	20/20	0.80	0.31	0.69	50,67,85,90	0
6	ASC	E	1004	12/12	0.95	0.18	0.23	52,56,71,76	0
9	HEC	B	1001	43/43	0.96	0.20	0.21	53,57,69,70	0
9	HEC	L	1001	43/43	0.96	0.19	0.21	34,52,66,72	0
5	FMX	O	1003	28/28	0.96	0.20	0.13	52,64,75,81	0
9	HEC	P	1001	43/43	0.95	0.21	0.05	63,71,89,95	0
9	HEC	F	1001	43/43	0.96	0.20	0.04	61,69,82,90	0
5	FMX	E	1003	28/28	0.95	0.20	-0.07	53,67,77,79	0
6	ASC	K	1004	12/12	0.94	0.18	-0.15	39,48,57,60	0
5	FMX	A	1003	28/28	0.95	0.19	-0.47	52,62,72,77	0
6	ASC	A	1004	12/12	0.96	0.16	-0.70	35,46,56,62	0
11	FES	M	1001	4/4	0.97	0.17	-0.85	64,65,65,65	0
7	SR	P	1002	1/1	0.97	0.06	-2.45	109,109,109,109	0
7	SR	B	1002	1/1	0.94	0.07	-2.78	96,96,96,96	0
7	SR	F	1002	1/1	0.95	0.04	-2.81	111,111,111,111	0
7	SR	K	1005	1/1	0.92	0.04	-3.12	110,110,110,110	0
7	SR	L	1002	1/1	0.99	0.07	-3.51	88,88,88,88	0
7	SR	A	1005	1/1	0.85	0.06	-3.58	148,148,148,148	0

6.5 Other polymers ⓘ

There are no such residues in this entry.