



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:28 AM GMT

PDB ID : 2X5U
Title : 80 microsecond laue diffraction snapshot from crystals of a photosynthetic reaction centre without illumination.
Authors : Wohri, A.B.; Katona, G.; Johansson, L.C.; Fritz, E.; Malmerberg, E.; Andersson, M.; Vincent, J.; Eklund, M.; Cammarata, M.; Wulff, M.; Davidsson, J.; Groenhof, G.; Neutze, R.
Deposited on : 2010-02-10
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

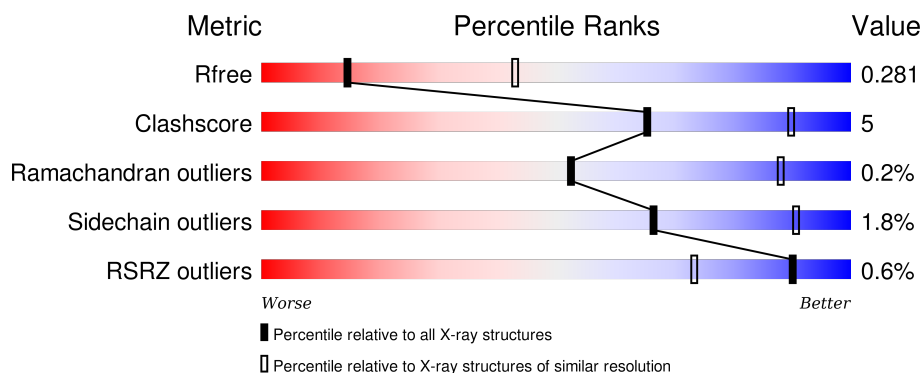
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	C	336	<div> <div>89%</div> <div>10%</div> </div>
2	H	258	<div> <div>2%</div> <div>85%</div> <div>8%</div> <div>6%</div> </div>
3	L	274	<div> <div>84%</div> <div>15%</div> </div>
4	M	324	<div> <div>90%</div> <div>10%</div> </div>

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
6	BCB	M	1324	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 9853 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 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	332	Total	C	N	O	S	4	0	0
			2602	1640	466	478	18			

- Molecule 2 is a protein called REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	243	Total	C	N	O	S	26	0	0
			1906	1218	327	359	2			

- Molecule 3 is a protein called REACTION CENTER PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	273	Total	C	N	O	S	10	2	0
			2180	1465	350	358	7			

- Molecule 4 is a protein called REACTION CENTER PROTEIN M CHAIN.

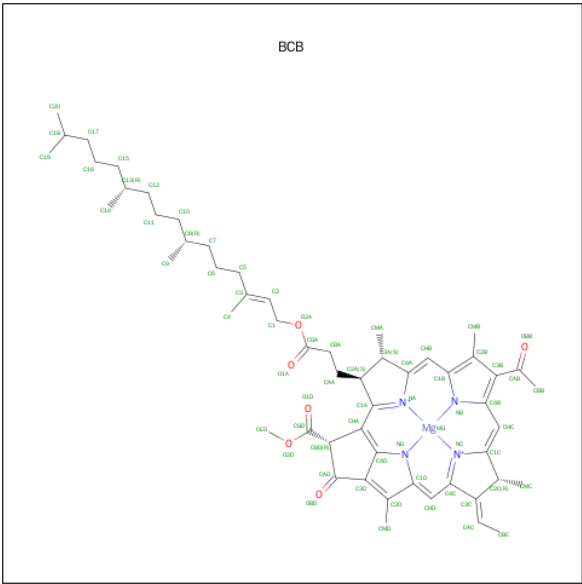
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	323	Total	C	N	O	S	7	0	0
			2555	1702	419	423	11			

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



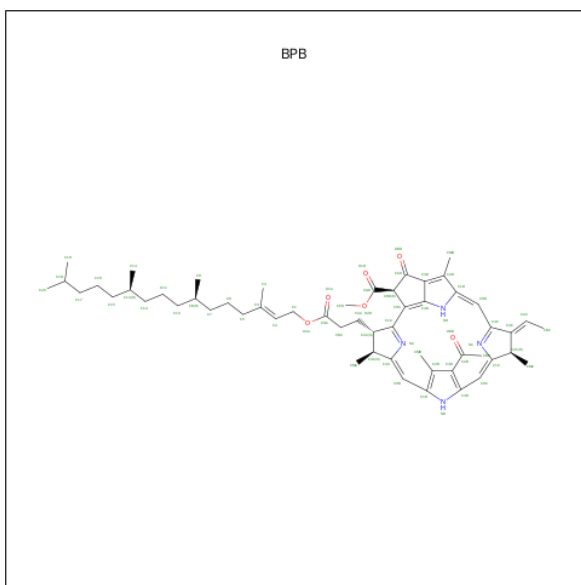
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is BACTERIOCHLOROPHYLL B (three-letter code: BCB) (formula: $C_{55}H_{72}MgN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	M	1	Total 65	C 54	Mg 1	N 4	O 6	0	0
6	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

- Molecule 7 is BACTERIOPHEOPHYTIN B (three-letter code: BPB) (formula: $C_{55}H_{74}N_4O_6$).

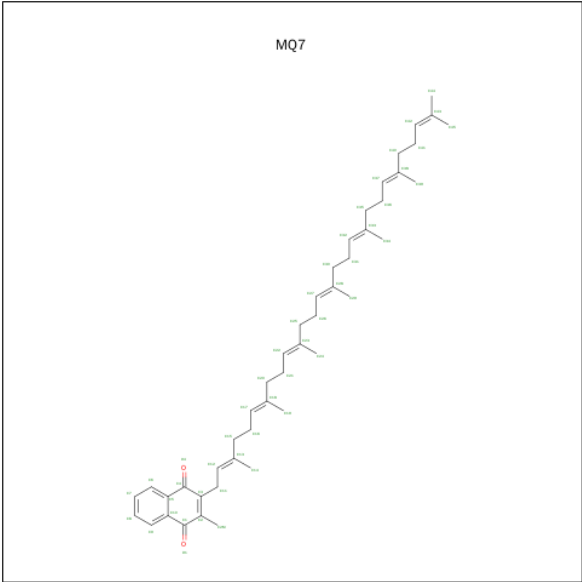


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			65	55	4	6		
7	M	1	Total	C	N	O	0	0
			61	51	4	6		

- Molecule 8 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	M	1	Total	Fe	0	0
			1	1		

- Molecule 9 is MENAQUINONE-7 (three-letter code: MQ7) (formula: $C_{46}H_{64}O_2$).

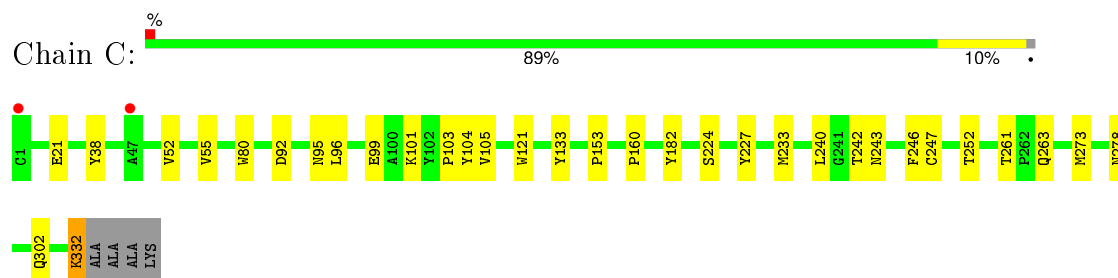


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	M	1	Total	C	O	0	0
			48	46	2		

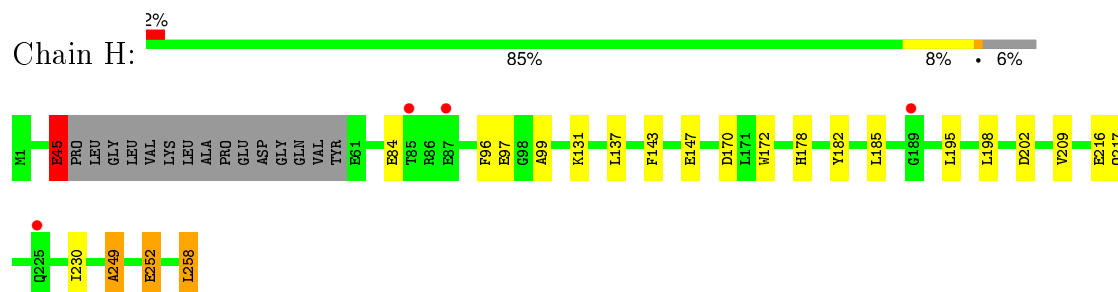
3 Residue-property plots [i](#)

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.

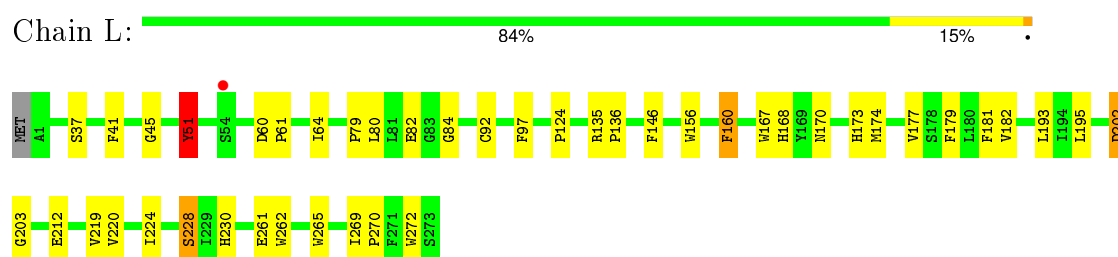
- Molecule 1: PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT



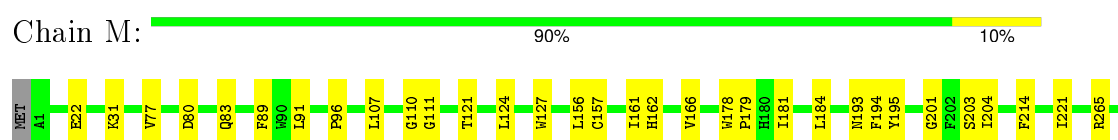
- Molecule 2: REACTION CENTER PROTEIN H CHAIN



- Molecule 3: REACTION CENTER PROTEIN L CHAIN



- Molecule 4: REACTION CENTER PROTEIN M CHAIN



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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	85.69Å 143.47Å 178.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 – 3.00 46.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.3 (48.78-3.00) 91.3 (46.79-3.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.48 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.250 , 0.284 0.246 , 0.281	Depositor DCC
R_{free} test set	2077 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.604	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	2 of 40854 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	9853	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BPB, BCB, FE2, MQ7, HEM, FME

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	C	0.96	1/2669 (0.0%)	0.51	1/3637 (0.0%)
2	H	1.57	7/1939 (0.4%)	0.90	8/2646 (0.3%)
3	L	0.96	2/2274 (0.1%)	0.94	5/3104 (0.2%)
4	M	0.58	2/2659 (0.1%)	0.53	2/3637 (0.1%)
All	All	1.04	12/9541 (0.1%)	0.73	16/13024 (0.1%)

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
2	H	0	2
3	L	0	1
All	All	0	3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	332	LYS	CB-CG	46.30	2.77	1.52
2	H	45	GLU	CG-CD	42.59	2.15	1.51
3	L	51	TYR	CB-CG	36.83	2.06	1.51
2	H	216	GLU	CB-CG	31.28	2.11	1.52
2	H	147	GLU	CG-CD	-28.21	1.09	1.51

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	202	ASP	CB-CG-OD2	25.69	141.42	118.30
2	H	97	GLU	CA-CB-CG	-24.93	58.55	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	202	ASP	CB-CG-OD1	-23.45	97.20	118.30
3	L	51	TYR	CB-CG-CD2	-21.24	108.26	121.00
3	L	51	TYR	CB-CG-CD1	16.07	130.64	121.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	252	GLU	Sidechain
2	H	45	GLU	Sidechain
3	L	51	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	C	2602	0	2579	18	0
2	H	1906	0	1903	8	0
3	L	2180	0	2109	33	0
4	M	2555	0	2452	19	0
5	C	172	0	120	3	0
6	L	132	0	144	18	0
6	M	131	0	140	11	0
7	L	65	0	74	9	0
7	M	61	0	63	5	0
8	M	1	0	0	0	0
9	M	48	0	64	0	0
All	All	9853	0	9648	97	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 5.

The worst 5 of 97 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)
7:M:1326:BPB:HHC	7:M:1326:BPB:HBBB	1.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:1324:BCB:HBB2	6:M:1324:BCB:HHC	1.63	0.79
3:L:181:PHE:HB3	7:M:1326:BPB:HBBA	1.72	0.72
7:L:1276:BPB:HHC	7:L:1276:BPB:CBB	2.21	0.71
6:M:1325:BCB:HAA1	6:M:1325:BCB:HBD	1.74	0.69

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	C	330/336 (98%)	312 (94%)	18 (6%)	0	100	100
2	H	239/258 (93%)	223 (93%)	15 (6%)	1 (0%)	39	80
3	L	273/274 (100%)	261 (96%)	12 (4%)	0	100	100
4	M	321/324 (99%)	308 (96%)	12 (4%)	1 (0%)	46	84
All	All	1163/1192 (98%)	1104 (95%)	57 (5%)	2 (0%)	52	88

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	249	ALA
4	M	193	ASN

5.3.2 Protein sidechains [i](#)

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	C	281/282 (100%)	277 (99%)	4 (1%)	74	93
2	H	200/212 (94%)	196 (98%)	4 (2%)	63	89
3	L	220/219 (100%)	216 (98%)	4 (2%)	66	91
4	M	249/250 (100%)	244 (98%)	5 (2%)	63	89
All	All	950/963 (99%)	933 (98%)	17 (2%)	66	91

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	258	LEU
3	L	51	TYR
4	M	194	PHE
2	H	198	LEU
4	M	203	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	302	GLN
2	H	8	GLN
2	H	178	HIS
4	M	108	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FME	H	1	2	8,9,10	0.65	0	6,9,11	3.75	4 (66%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FME	H	1	2	-	1/6/9/11	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	FME	CA-N-CN	-7.35	111.51	122.82
2	H	1	FME	O1-CN-N	-3.58	119.61	124.76
2	H	1	FME	O-C-CA	-2.00	120.15	125.44
2	H	1	FME	CE-SD-CG	3.61	112.69	100.37

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	1	FME	O1-CN-N-CA

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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
5	HEM	C	1333	1	30,50,50	2.27	9 (30%)	24,82,82	2.41	11 (45%)
5	HEM	C	1334	1	30,50,50	2.18	10 (33%)	24,82,82	2.35	11 (45%)
5	HEM	C	1335	1	30,50,50	2.17	9 (30%)	24,82,82	2.38	11 (45%)
5	HEM	C	1336	1	30,50,50	2.19	10 (33%)	24,82,82	2.20	7 (29%)
6	BCB	L	1274	3	56,74,74	2.48	13 (23%)	57,115,115	2.10	20 (35%)
6	BCB	L	1275	3	56,74,74	2.50	13 (23%)	57,115,115	2.19	15 (26%)
7	BPB	L	1276	-	63,70,70	2.96	16 (25%)	63,101,101	2.33	16 (25%)
6	BCB	M	1324	4	55,73,74	2.48	12 (21%)	55,113,115	2.27	17 (30%)
6	BCB	M	1325	4	56,74,74	2.50	12 (21%)	57,115,115	2.23	17 (29%)
7	BPB	M	1326	-	59,66,70	3.01	16 (27%)	58,96,101	2.33	17 (29%)
9	MQ7	M	1328	-	49,49,49	1.34	2 (4%)	62,63,63	1.26	6 (9%)

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
5	HEM	C	1333	1	-	0/10/54/54	0/0/8/8
5	HEM	C	1334	1	-	0/10/54/54	0/0/8/8
5	HEM	C	1335	1	-	0/10/54/54	0/0/8/8
5	HEM	C	1336	1	-	0/10/54/54	0/0/8/8
6	BCB	L	1274	3	-	1/37/137/137	0/0/9/9
6	BCB	L	1275	3	-	1/37/137/137	0/0/9/9
7	BPB	L	1276	-	-	0/46/105/105	0/1/6/6
6	BCB	M	1324	4	-	1/36/136/137	0/0/9/9
6	BCB	M	1325	4	-	1/37/137/137	0/0/9/9
7	BPB	M	1326	-	-	1/42/101/105	0/1/6/6
9	MQ7	M	1328	-	-	0/41/61/61	0/2/2/2

The worst 5 of 122 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1333	HEM	C3B-C4B	-7.24	1.45	1.51
5	C	1336	HEM	C3B-C4B	-7.05	1.45	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1335	HEM	C3B-C4B	-6.95	1.45	1.51
5	C	1334	HEM	C3B-C4B	-6.86	1.45	1.51
5	C	1333	HEM	C3D-C4D	-5.21	1.44	1.51

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	1276	BPB	CBC-CAC-C3C	-7.29	110.24	127.07
7	M	1326	BPB	CBC-CAC-C3C	-7.11	110.66	127.07
7	L	1276	BPB	C4D-C3D-C2D	-6.78	99.07	106.74
7	M	1326	BPB	C4D-C3D-C2D	-6.27	99.64	106.74
7	M	1326	BPB	C2C-C3C-C4C	-5.84	101.90	107.24

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	1275	BCB	CBC-CAC-C3C-C2C
6	M	1324	BCB	CBC-CAC-C3C-C2C
6	M	1325	BCB	CBC-CAC-C3C-C2C
6	L	1274	BCB	CBC-CAC-C3C-C2C
7	M	1326	BPB	CBC-CAC-C3C-C2C

There are no ring outliers.

9 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1333	HEM	1	0
5	C	1334	HEM	1	0
5	C	1335	HEM	1	0
6	L	1274	BCB	12	0
6	L	1275	BCB	6	0
7	L	1276	BPB	9	0
6	M	1324	BCB	6	0
6	M	1325	BCB	5	0
7	M	1326	BPB	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	C	332/336 (98%)	-0.37	2 (0%)	90 73	13, 25, 38, 44	1 (0%)
2	H	242/258 (93%)	-0.07	4 (1%)	73 45	24, 34, 58, 62	8 (3%)
3	L	273/274 (99%)	-0.46	1 (0%)	93 80	10, 22, 43, 53	2 (0%)
4	M	323/324 (99%)	-0.56	0	100 100	10, 19, 33, 36	2 (0%)
All	All	1170/1192 (98%)	-0.38	7 (0%)	90 73	10, 25, 45, 62	13 (1%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	85	THR	3.3
1	C	1	CYS	2.8
2	H	87	GLU	2.7
3	L	54	SER	2.6
1	C	47	ALA	2.3

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	FME	H	1	10/11	0.71	0.35	-	56,56,58,58	0

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
6	BCB	M	1324	65/66	0.92	0.21	2.13	10,13,43,44	0
7	BPB	L	1276	65/65	0.93	0.22	1.84	22,26,27,28	0
9	MQ7	M	1328	48/48	0.91	0.21	1.18	27,30,40,41	0
7	BPB	M	1326	61/65	0.91	0.22	1.05	18,22,44,45	0
6	BCB	L	1274	66/66	0.96	0.19	1.00	8,11,21,22	0
6	BCB	L	1275	66/66	0.94	0.20	0.98	16,18,30,31	0
6	BCB	M	1325	66/66	0.95	0.17	0.54	8,11,16,18	0
5	HEM	C	1334	43/43	0.96	0.17	-0.10	19,22,23,24	0
5	HEM	C	1336	43/43	0.96	0.14	-0.16	16,18,21,22	0
5	HEM	C	1333	43/43	0.95	0.16	-0.50	21,26,28,28	0
5	HEM	C	1335	43/43	0.98	0.13	-1.22	13,13,16,16	0
8	FE2	M	1327	1/1	0.99	0.10	-3.35	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.