



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:31 PM GMT

PDB ID : 4FA7
Title : Structure of Recombinant Cytochrome ba3 Oxidase mutant A204F from *Thermus thermophilus*
Authors : Li, Y.; Chen, Y.; Stout, C.D.
Deposited on : 2012-05-21
Resolution : 2.50 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

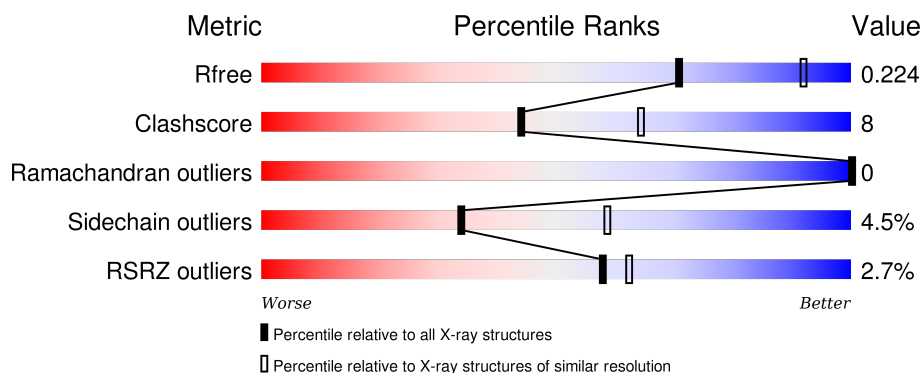
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	568	
2	B	168	
3	C	34	

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
8	OLC	A	605	-	-	-	X
8	OLC	A	606	-	-	-	X
8	OLC	A	608	-	-	-	X
8	OLC	A	609	-	-	-	X
8	OLC	A	610	-	-	-	X
8	OLC	A	612	-	-	-	X
8	OLC	A	613	-	-	-	X
8	OLC	A	614	-	-	-	X
8	OLC	A	615	-	-	-	X
8	OLC	A	616	-	-	-	X
8	OLC	B	202	-	-	-	X
8	OLC	B	203	-	-	-	X
8	OLC	B	204	-	-	-	X
8	OLC	C	101	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6393 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 Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	1	0	0
			4298	2924	684	674	16			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	EXPRESSION TAG	UNP Q5SJ79
A	-4	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-3	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-2	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-1	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	0	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	1	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	204	PHE	ALA	ENGINEERED MUTATION	UNP Q5SJ79

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	166	Total	C	N	O	S	0	0	0
			1289	838	213	234	4			

- Molecule 3 is a protein called Cytochrome c oxidase polypeptide 2A.

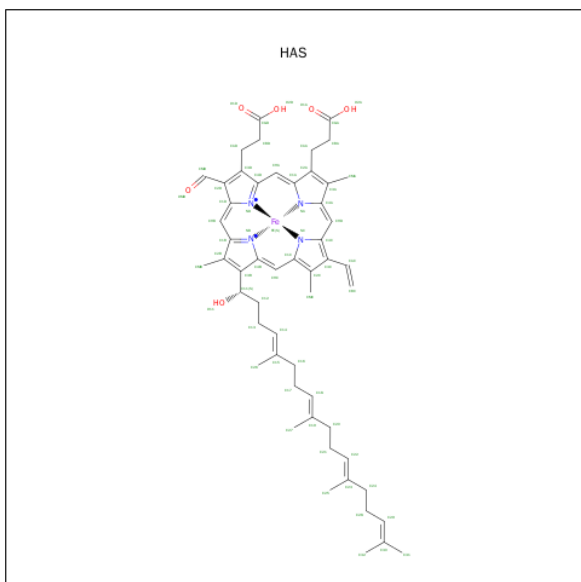
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	31	Total	C	N	O	0	0	0
			241	169	37	35			

- Molecule 4 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cu	0	0
			1	1		

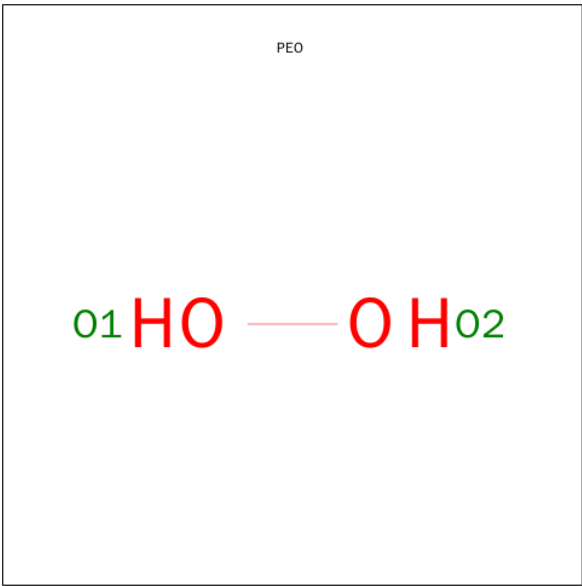
-
- Chemical structure of HEM (Heme) showing a central iron atom coordinated by four nitrogen atoms in a porphyrin-like ring, with various side chains and a central heme group.

- Molecule 6 is HEME-AS (three-letter code: HAS) (formula: $\text{C}_{54}\text{H}_{64}\text{FeN}_4\text{O}_6$).



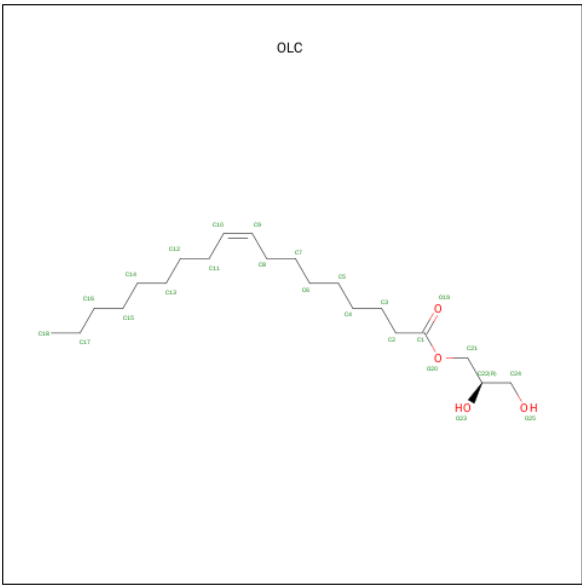
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	Fe	N	O	0	0
			65	54	1	4	6		

- Molecule 7 is HYDROGEN PEROXIDE (three-letter code: PEO) (formula: H₂O₂).



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

- Molecule 8 is (2R)-2,3-DIHYDROXYPROPYL (9Z)-OCTADEC-9-ENOATE (three-letter code: OLC) (formula: C₂₁H₄₀O₄).



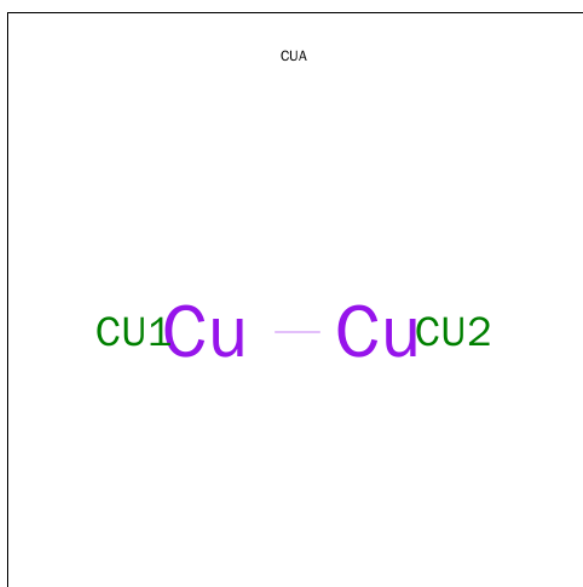
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			25	21	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			25	21	4		
8	A	1	Total	C	O	0	0
			23	19	4		
8	A	1	Total	C	O	0	0
			21	19	2		
8	A	1	Total	C	O	0	0
			18	14	4		
8	A	1	Total	C	O	0	0
			17	13	4		
8	A	1	Total	C	O	0	0
			8	4	4		
8	A	1	Total	C	O	0	0
			15	11	4		
8	A	1	Total	C	O	0	0
			20	16	4		
8	A	1	Total	C	O	0	0
			25	21	4		
8	A	1	Total	C	O	0	0
			21	17	4		
8	A	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	C	1	Total	C	O	0	0
			25	21	4		

- Molecule 9 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total Cu 2 2	0	0

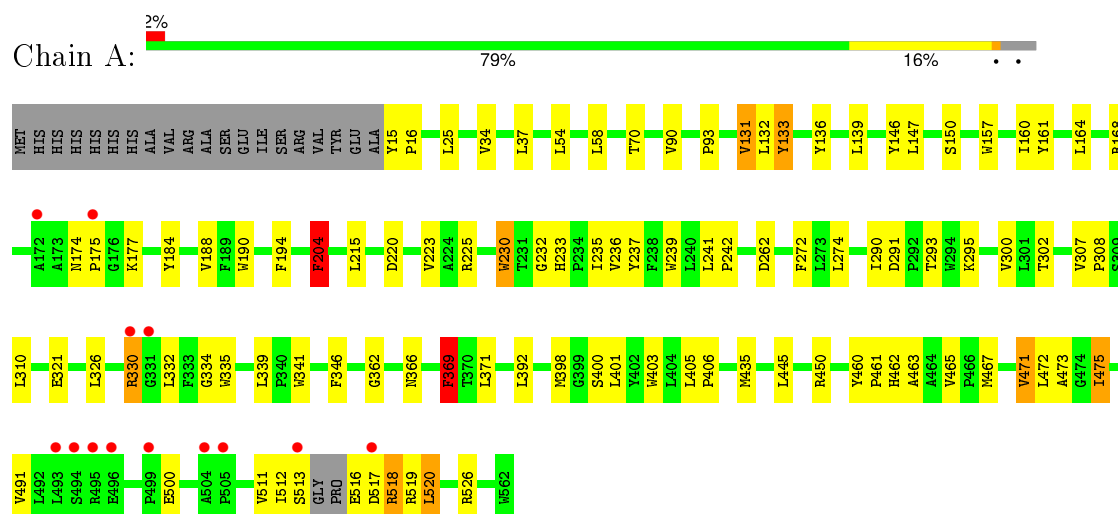
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	69	Total O 69 69	0	0
10	B	38	Total O 38 38	0	0
10	C	2	Total O 2 2	0	0

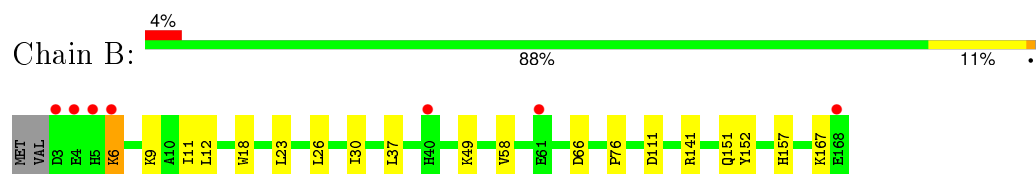
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

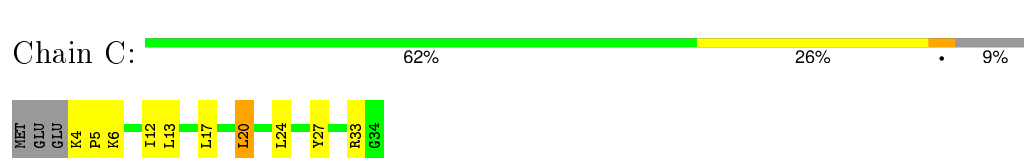
• Molecule 1: Cytochrome c oxidase subunit 1



• Molecule 2: Cytochrome c oxidase subunit 2



• Molecule 3: Cytochrome c oxidase polypeptide 2A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.55Å 98.21Å 94.86Å 90.00° 127.92° 90.00°	Depositor
Resolution (Å)	74.83 – 2.50 19.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (74.83-2.50) 98.6 (19.98-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.169 , 0.220 0.173 , 0.224	Depositor DCC
R_{free} test set	1796 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 35451 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6393	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.33% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OLC, PEO, CUA, HEM, HAS, CU

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	2.41	8/4453 (0.2%)	1.09	9/6115 (0.1%)
2	B	1.09	0/1325	0.88	1/1810 (0.1%)
3	C	1.15	0/247	1.03	2/335 (0.6%)
All	All	2.15	8/6025 (0.1%)	1.05	12/8260 (0.1%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	330	ARG	CZ-NH1	110.97	2.77	1.33
1	A	330	ARG	NE-CZ	72.61	2.27	1.33
1	A	330	ARG	CZ-NH2	-57.27	0.58	1.33
1	A	204	PHE	CB-CG	-7.94	1.37	1.51
1	A	133	TYR	CD1-CE1	-6.90	1.28	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	330	ARG	NE-CZ-NH2	30.65	135.62	120.30
1	A	330	ARG	NE-CZ-NH1	-27.43	106.58	120.30
1	A	330	ARG	CD-NE-CZ	-22.41	92.22	123.60
1	A	25	LEU	CB-CG-CD1	-7.85	97.66	111.00
1	A	131	VAL	CB-CA-C	7.65	125.94	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4298	0	4391	75	0
2	B	1289	0	1264	11	0
3	C	241	0	267	6	0
4	A	1	0	0	0	0
5	A	43	0	30	4	0
6	A	65	0	62	3	0
7	A	2	0	0	0	0
8	A	243	0	353	23	0
8	B	75	0	120	3	0
8	C	25	0	40	2	0
9	B	2	0	0	0	0
10	A	69	0	0	3	0
10	B	38	0	0	4	1
10	C	2	0	0	0	0
All	All	6393	0	6527	103	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 103 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:HIS:NE2	1:A:237:TYR:CE2	1.70	1.56
1:A:233:HIS:NE2	1:A:237:TYR:HE2	0.77	1.25
1:A:233:HIS:CE1	1:A:237:TYR:HE2	1.83	0.96
1:A:233:HIS:CD2	1:A:237:TYR:HE2	1.86	0.92
1:A:168:ARG:HH22	8:A:612:OLC:H6A	1.32	0.92

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:327:HOH:O	10:B:327:HOH:O[2_556]	2.00	0.20

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	542/568 (95%)	518 (96%)	24 (4%)	0	100	100
2	B	164/168 (98%)	161 (98%)	3 (2%)	0	100	100
3	C	29/34 (85%)	29 (100%)	0	0	100	100
All	All	735/770 (96%)	708 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	438/463 (95%)	422 (96%)	16 (4%)	41	68
2	B	134/138 (97%)	126 (94%)	8 (6%)	24	43
3	C	24/27 (89%)	21 (88%)	3 (12%)	6	10
All	All	596/628 (95%)	569 (96%)	27 (4%)	34	59

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	GLU
1	A	526	ARG
3	C	17	LEU
1	A	518	ARG
1	A	215	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	254	GLN
1	A	446	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 1 is monoatomic - leaving 20 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	A	602	1	30,50,50	2.14	8 (26%)	24,82,82	2.71	11 (45%)
6	HAS	A	603	1,7	45,72,72	2.66	11 (24%)	47,109,109	2.09	11 (23%)
7	PEO	A	604	4,6	1,1,1	0.79	0	0,0,0	0.00	-
8	OLC	A	605	-	24,24,24	1.08	1 (4%)	25,25,25	1.07	2 (8%)
8	OLC	A	606	-	24,24,24	0.99	1 (4%)	25,25,25	1.37	3 (12%)
8	OLC	A	607	-	22,22,24	1.02	1 (4%)	23,23,25	1.28	3 (13%)
8	OLC	A	608	-	20,20,24	1.19	1 (5%)	20,20,25	1.13	3 (15%)
8	OLC	A	609	-	17,17,24	1.22	1 (5%)	18,18,25	1.23	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	OLC	A	610	-	16,16,24	1.36	1 (6%)	17,17,25	1.17	3 (17%)
8	OLC	A	611	-	7,7,24	1.73	1 (14%)	6,7,25	0.78	0
8	OLC	A	612	-	14,14,24	1.24	1 (7%)	15,15,25	1.36	2 (13%)
8	OLC	A	613	-	19,19,24	1.16	1 (5%)	19,20,25	1.31	4 (21%)
8	OLC	A	614	-	24,24,24	1.08	1 (4%)	25,25,25	1.27	3 (12%)
8	OLC	A	615	-	20,20,24	1.21	1 (5%)	20,21,25	1.06	2 (10%)
8	OLC	A	616	-	24,24,24	1.02	1 (4%)	25,25,25	1.29	2 (8%)
9	CUA	B	201	2	0,1,1	0.00	-	0,0,0	0.00	-
8	OLC	B	202	-	24,24,24	1.20	1 (4%)	25,25,25	1.07	2 (8%)
8	OLC	B	203	-	24,24,24	1.19	1 (4%)	25,25,25	1.28	3 (12%)
8	OLC	B	204	-	24,24,24	0.99	1 (4%)	25,25,25	1.08	3 (12%)
8	OLC	C	101	-	24,24,24	1.03	1 (4%)	25,25,25	1.16	2 (8%)

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	A	602	1	-	0/10/54/54	0/0/8/8
6	HAS	A	603	1,7	-	0/30/82/82	0/0/8/8
7	PEO	A	604	4,6	-	0/0/0/0	0/0/0/0
8	OLC	A	605	-	-	0/24/24/24	0/0/0/0
8	OLC	A	606	-	-	0/24/24/24	0/0/0/0
8	OLC	A	607	-	-	0/22/22/24	0/0/0/0
8	OLC	A	608	-	-	0/19/19/24	0/0/0/0
8	OLC	A	609	-	-	0/17/17/24	0/0/0/0
8	OLC	A	610	-	-	0/16/16/24	0/0/0/0
8	OLC	A	611	-	-	0/6/6/24	0/0/0/0
8	OLC	A	612	-	-	0/14/14/24	0/0/0/0
8	OLC	A	613	-	-	0/19/19/24	0/0/0/0
8	OLC	A	614	-	-	0/24/24/24	0/0/0/0
8	OLC	A	615	-	-	0/20/20/24	0/0/0/0
8	OLC	A	616	-	-	0/24/24/24	0/0/0/0
9	CUA	B	201	2	-	0/0/0/0	0/0/0/0
8	OLC	B	202	-	-	0/24/24/24	0/0/0/0
8	OLC	B	203	-	-	0/24/24/24	0/0/0/0
8	OLC	B	204	-	-	0/24/24/24	0/0/0/0
8	OLC	C	101	-	-	0/24/24/24	0/0/0/0

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	603	HAS	C2D-C3D	-7.61	1.30	1.40
5	A	602	HEM	C3B-C4B	-6.51	1.46	1.51
5	A	602	HEM	C3D-C4D	-3.16	1.47	1.51
5	A	602	HEM	C2C-C1C	-3.09	1.46	1.52
5	A	602	HEM	C2D-C1D	-2.19	1.44	1.51

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	603	HAS	CAA-CBA-CGA	-6.53	100.78	112.75
5	A	602	HEM	CAA-C2A-C1A	-5.24	121.32	127.01
5	A	602	HEM	C3C-CAC-CBC	-4.54	117.49	124.46
6	A	603	HAS	C3C-C4C-NC	-4.14	103.13	110.94
6	A	603	HAS	C2D-C1D-ND	-3.32	104.92	109.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602	HEM	4	0
6	A	603	HAS	3	0
8	A	605	OLC	1	0
8	A	606	OLC	3	0
8	A	607	OLC	6	0
8	A	611	OLC	4	0
8	A	612	OLC	3	0
8	A	613	OLC	3	0
8	A	614	OLC	9	0
8	A	616	OLC	2	0
8	B	203	OLC	3	0
8	C	101	OLC	2	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	A	546/568 (96%)	-0.60	13 (2%) 62 66	10, 20, 44, 71	2 (0%)
2	B	166/168 (98%)	-0.49	7 (4%) 40 45	12, 22, 44, 87	1 (0%)
3	C	31/34 (91%)	-0.94	0 100 100	15, 20, 37, 43	0
All	All	743/770 (96%)	-0.59	20 (2%) 58 62	10, 21, 44, 87	3 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	6	LYS	6.2
2	B	5	HIS	5.0
2	B	3	ASP	4.9
1	A	499	PRO	4.6
1	A	517	ASP	4.4

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
8	OLC	C	101	25/25	0.66	0.37	76.42	65,68,89,92	0
8	OLC	A	610	17/25	0.67	0.26	15.02	50,57,71,72	0
8	OLC	A	605	25/25	0.78	0.26	10.09	35,45,67,69	0
8	OLC	A	608	21/25	0.79	0.27	9.50	50,54,62,63	0
8	OLC	B	204	25/25	0.61	0.31	7.98	52,64,74,74	0
8	OLC	A	613	20/25	0.80	0.22	6.99	43,50,60,62	0
8	OLC	A	609	18/25	0.82	0.21	5.85	47,60,66,67	0
8	OLC	A	606	25/25	0.82	0.21	5.61	44,53,69,70	0
8	OLC	A	612	15/25	0.75	0.31	5.16	55,64,71,71	0
8	OLC	A	614	25/25	0.89	0.16	3.43	31,42,50,51	0
8	OLC	A	616	25/25	0.84	0.28	3.16	46,52,57,60	0
8	OLC	A	615	21/25	0.75	0.24	2.80	51,58,65,66	0
8	OLC	B	202	25/25	0.71	0.27	2.47	52,57,71,74	0
8	OLC	B	203	25/25	0.71	0.25	2.38	45,60,72,73	0
8	OLC	A	607	23/25	0.91	0.16	1.76	27,41,49,51	0
6	HAS	A	603	65/65	0.98	0.10	0.18	8,14,21,26	0
5	HEM	A	602	43/43	0.98	0.09	-0.20	2,11,16,21	0
7	PEO	A	604	2/2	0.99	0.08	-0.41	7,7,7,14	0
9	CUA	B	201	2/2	0.99	0.04	-3.06	13,13,13,15	0
8	OLC	A	611	8/25	0.89	0.25	-	50,57,62,63	0
4	CU	A	601	1/1	1.00	0.05	-	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.