



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 18, 2018 – 10:13 pm GMT

PDB ID : 1NTM
Title : Crystal Structure of Mitochondrial Cytochrome bc1 Complex at 2.4 Angstrom
Authors : Gao, X.; Wen, X.; Esser, L.; Quinn, B.; Yu, L.; Yu, C.; Xia, D.
Deposited on : 2003-01-30
Resolution : 2.40 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

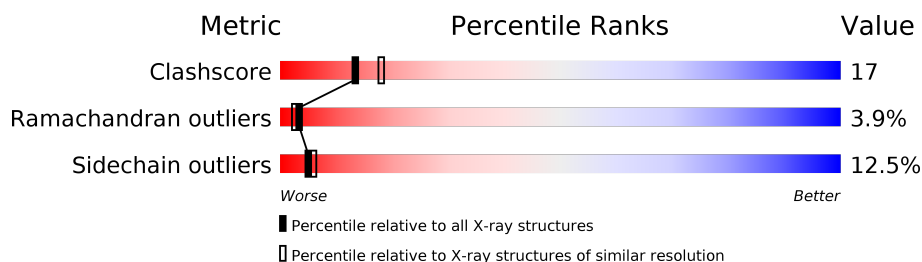
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	122078	3953 (2.40-2.40)
Ramachandran outliers	120005	3894 (2.40-2.40)
Sidechain outliers	119972	3895 (2.40-2.40)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	446	
2	B	439	
3	C	379	
4	D	241	
5	E	196	
6	F	110	
7	G	81	

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Mol	Chain	Length	Quality of chain
8	H	78	<div><div></div><div>58%21%6%14%</div></div>
9	I	57	<div><div></div><div>19%42%35%</div></div>
10	J	62	<div><div></div><div>56%31%10%</div></div>
11	K	56	<div><div></div><div>57%23%11%9%</div></div>

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 17049 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 Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3458	2161	609	668	20			

- Molecule 2 is a protein called Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	0	0	0
			3172	1993	562	610	7			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	378	Total	C	N	O	S	0	0	0
			3003	2013	471	501	18			

- Molecule 4 is a protein called cytochrome c1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	241	Total	C	N	O	S	0	0	0
			1918	1225	330	348	15			

- Molecule 5 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	196	Total	C	N	O	S	0	0	0
			1519	957	263	291	8			

- Molecule 6 is a protein called Ubiquinol-cytochrome C reductase complex 14 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	105	Total	C	N	O	S	0	0	0
			911	576	165	168	2			

- Molecule 7 is a protein called Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	75	Total	C	N	O	S	0	0	0
			628	410	118	99	1			

- Molecule 8 is a protein called Ubiquinol-cytochrome C reductase complex 11 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	67	Total	C	N	O	S	0	0	0
			548	332	99	112	5			

- Molecule 9 is a protein called Ubiquinol-cytochrome C reductase 8 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	57	Total	C	N	O	S	0	0	0
			406	253	77	74	2			

- Molecule 10 is a protein called Ubiquinol-cytochrome C reductase complex 7.2 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	60	Total	C	N	O	S	0	0	0
			478	313	81	84				

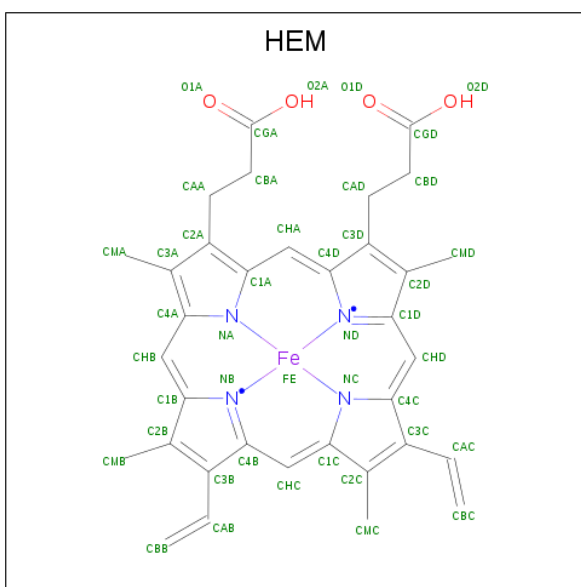
- Molecule 11 is a protein called Ubiquinol-cytochrome C reductase complex 6.4 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	51	Total	C	N	O	S	0	0	0
			421	280	76	64	1			

There is a discrepancy between the modelled and reference sequences:

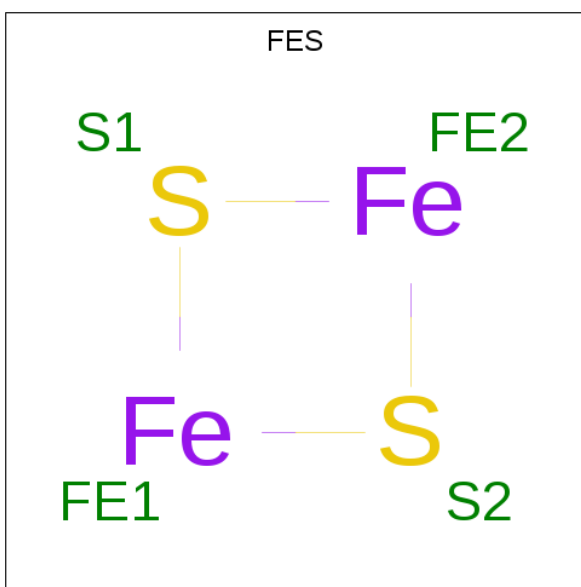
Chain	Residue	Modelled	Actual	Comment	Reference
K	22	GLN	SER	SEE REMARK 999	UNP P07552

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

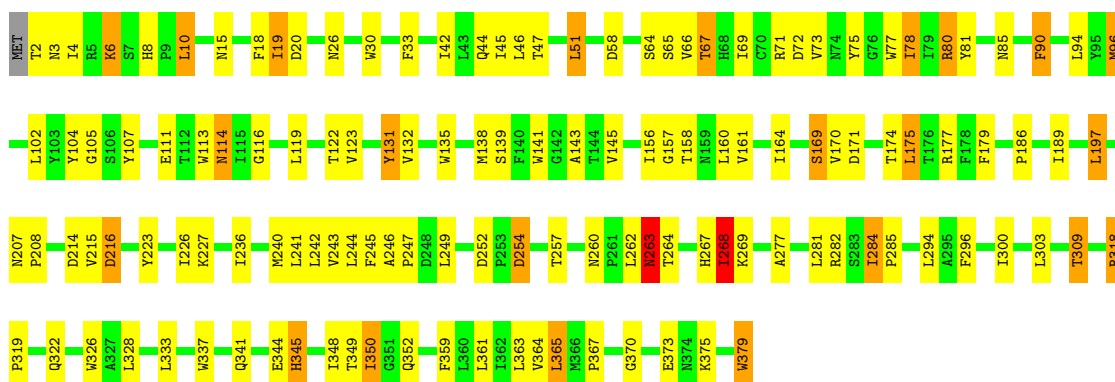
- Molecule 13 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



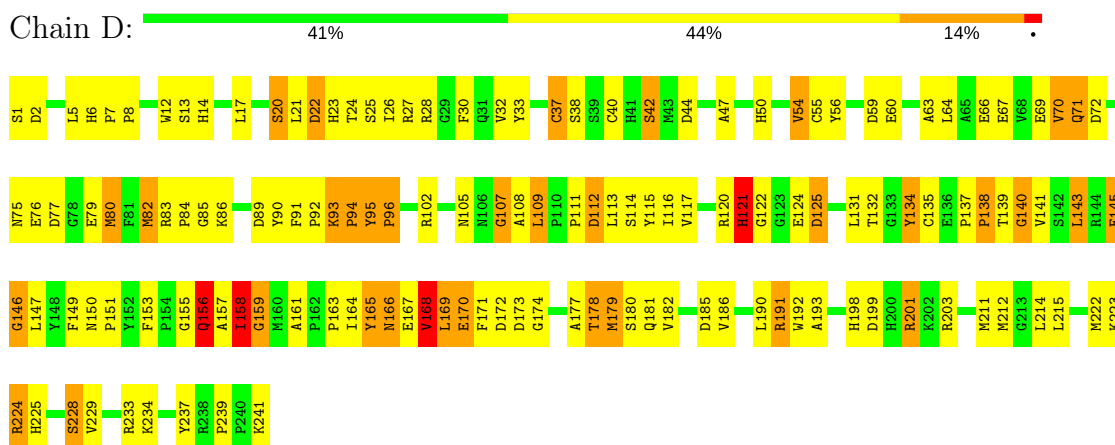
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	E	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 14 is water.

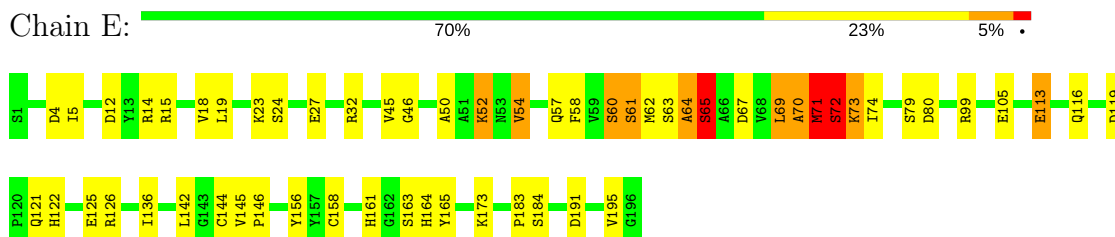
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	99	Total 99	O 99	0	0
14	B	152	Total 152	O 152	0	0
14	C	64	Total 64	O 64	0	0
14	D	43	Total 43	O 43	0	0
14	E	8	Total 8	O 8	0	0
14	F	37	Total 37	O 37	0	0
14	G	23	Total 23	O 23	0	0
14	H	7	Total 7	O 7	0	0
14	I	5	Total 5	O 5	0	0
14	J	6	Total 6	O 6	0	0
14	K	10	Total 10	O 10	0	0



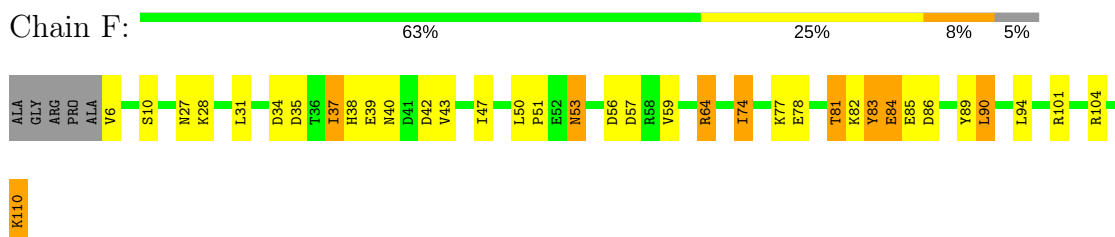
• Molecule 4: cytochrome c1



• Molecule 5: UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, mitochondrial

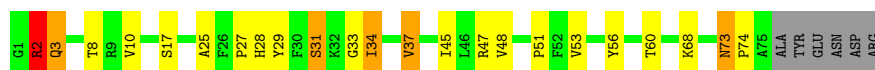


• Molecule 6: Ubiquinol-cytochrome C reductase complex 14 kDa protein



• Molecule 7: Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C

Chain G: 

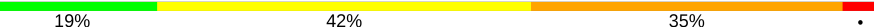


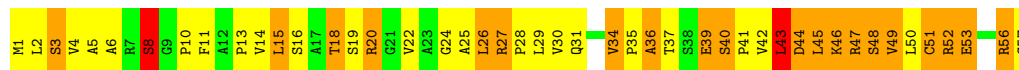
- Molecule 8: Ubiquinol-cytochrome C reductase complex 11 kDa protein

Chain H: 



- Molecule 9: Ubiquinol-cytochrome C reductase 8 kDa protein

Chain I: 



- Molecule 10: Ubiquinol-cytochrome C reductase complex 7.2 kDa protein

Chain J: 



- Molecule 11: Ubiquinol-cytochrome C reductase complex 6.4 kDa protein

Chain K: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.32Å 154.32Å 593.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	85.8 (20.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.237 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17049	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, FES

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	0.68	0/3531	0.91	16/4792 (0.3%)
2	B	0.85	2/3232 (0.1%)	0.93	10/4386 (0.2%)
3	C	0.64	1/3100 (0.0%)	0.84	6/4242 (0.1%)
4	D	0.56	0/1977	0.97	15/2684 (0.6%)
5	E	0.51	0/1553	0.90	10/2100 (0.5%)
6	F	0.79	0/930	0.93	3/1246 (0.2%)
7	G	0.67	0/649	0.78	0/878
8	H	0.47	0/553	0.90	5/741 (0.7%)
9	I	0.87	0/411	1.33	4/558 (0.7%)
10	J	0.59	0/490	0.82	1/665 (0.2%)
11	K	0.53	0/436	0.83	2/598 (0.3%)
All	All	0.68	3/16862 (0.0%)	0.91	72/22890 (0.3%)

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	B	1	0
3	C	1	0
4	D	1	0
7	G	1	0
9	I	2	0
All	All	6	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	424	MET	SD-CE	-6.85	1.39	1.77
2	B	258	VAL	CB-CG1	-6.53	1.39	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	379	TRP	CB-CG	-5.18	1.41	1.50

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	159	GLY	N-CA-C	8.66	134.76	113.10
5	E	71	MET	N-CA-C	8.40	133.67	111.00
6	F	34	ASP	CB-CG-OD2	7.77	125.29	118.30
2	B	114	ASP	CB-CG-OD2	7.47	125.02	118.30
4	D	122	GLY	N-CA-C	-7.27	94.92	113.10

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	305	GLN	CA
3	C	345	HIS	CA
4	D	158	ILE	CA
7	G	2	ARG	CA
9	I	25	ALA	CA

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	3458	0	3356	99	0
2	B	3172	0	3152	114	0
3	C	3003	0	3065	106	0
4	D	1918	0	1870	114	0
5	E	1519	0	1503	37	0
6	F	911	0	904	25	0
7	G	628	0	636	21	0
8	H	548	0	532	11	0
9	I	406	0	437	80	0
10	J	478	0	463	28	0
11	K	421	0	428	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	C	86	0	60	10	0
12	D	43	0	30	3	0
13	E	4	0	0	0	0
14	A	99	0	0	11	0
14	B	152	0	0	13	1
14	C	64	0	0	3	0
14	D	43	0	0	7	0
14	E	8	0	0	2	0
14	F	37	0	0	4	0
14	G	23	0	0	2	0
14	H	7	0	0	0	0
14	I	5	0	0	1	0
14	J	6	0	0	0	0
14	K	10	0	0	1	0
All	All	17049	0	16436	571	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 17.

The worst 5 of 571 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)
14:A:519:HOH:O	7:G:10:VAL:HB	1.40	1.18
1:A:244:ARG:HG2	14:A:519:HOH:O	1.46	1.15
2:B:227:ARG:HG2	14:B:479:HOH:O	1.48	1.14
4:D:169:LEU:HD11	4:D:177:ALA:HB3	1.22	1.12
4:D:169:LEU:HD11	4:D:177:ALA:CB	1.79	1.12

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)
14:B:549:HOH:O	14:B:586:HOH:O[6_565]	1.68	0.52

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	444/446 (100%)	408 (92%)	26 (6%)	10 (2%)	7	7
2	B	421/439 (96%)	386 (92%)	24 (6%)	11 (3%)	6	5
3	C	376/379 (99%)	330 (88%)	41 (11%)	5 (1%)	13	18
4	D	239/241 (99%)	185 (77%)	30 (13%)	24 (10%)	0	0
5	E	194/196 (99%)	175 (90%)	14 (7%)	5 (3%)	6	5
6	F	103/110 (94%)	98 (95%)	3 (3%)	2 (2%)	9	11
7	G	73/81 (90%)	64 (88%)	6 (8%)	3 (4%)	3	2
8	H	65/78 (83%)	53 (82%)	7 (11%)	5 (8%)	1	0
9	I	55/57 (96%)	22 (40%)	19 (34%)	14 (26%)	0	0
10	J	58/62 (94%)	45 (78%)	11 (19%)	2 (3%)	4	3
11	K	49/56 (88%)	41 (84%)	7 (14%)	1 (2%)	8	9
All	All	2077/2145 (97%)	1807 (87%)	188 (9%)	82 (4%)	3	2

5 of 82 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	GLY
1	A	227	ALA
2	B	171	ALA
2	B	305	GLN
2	B	436	ILE

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	370/370 (100%)	331 (90%)	39 (10%)	7	10
2	B	332/343 (97%)	296 (89%)	36 (11%)	7	9
3	C	326/327 (100%)	285 (87%)	41 (13%)	5	6
4	D	206/206 (100%)	171 (83%)	35 (17%)	2	2
5	E	168/168 (100%)	155 (92%)	13 (8%)	14	22
6	F	96/98 (98%)	84 (88%)	12 (12%)	5	6
7	G	66/71 (93%)	56 (85%)	10 (15%)	3	3
8	H	64/74 (86%)	58 (91%)	6 (9%)	9	14
9	I	44/44 (100%)	32 (73%)	12 (27%)	0	0
10	J	46/52 (88%)	39 (85%)	7 (15%)	3	3
11	K	41/46 (89%)	33 (80%)	8 (20%)	1	1
All	All	1759/1799 (98%)	1540 (88%)	219 (12%)	5	6

5 of 219 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	175	LEU
4	D	42	SER
9	I	49	VAL
3	C	197	LEU
3	C	328	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	174	ASN
2	B	362	ASN
7	G	64	GLN
2	B	197	ASN
2	B	305	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are 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
12	HEM	C	381	3	27,50,50	3.02	14 (51%)	17,82,82	1.56	1 (5%)
12	HEM	C	382	3	27,50,50	2.70	15 (55%)	17,82,82	2.03	7 (41%)
12	HEM	D	242	4	27,50,50	2.91	16 (59%)	17,82,82	1.91	6 (35%)
13	FES	E	197	5	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
12	HEM	C	381	3	-	0/6/54/54	0/0/8/8
12	HEM	C	382	3	-	0/6/54/54	0/0/8/8
12	HEM	D	242	4	-	0/6/54/54	0/0/8/8
13	FES	E	197	5	-	0/0/4/4	0/1/1/1

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	C	381	HEM	C3C-C2C	-6.62	1.31	1.40
12	C	381	HEM	C3B-C2B	-6.06	1.32	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	D	242	HEM	C3C-C2C	-5.66	1.32	1.40
12	C	382	HEM	C3B-C2B	-5.15	1.33	1.40
12	D	242	HEM	C3B-C2B	-4.85	1.33	1.40

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	C	382	HEM	CMD-C2D-C1D	-3.58	122.95	128.46
12	D	242	HEM	CAA-CBA-CGA	-2.84	107.80	112.66
12	C	382	HEM	CAA-C2A-C3A	-2.38	122.22	129.00
12	D	242	HEM	CAD-CBD-CGD	-2.34	108.66	112.66
12	D	242	HEM	C4A-C3A-C2A	-2.34	105.37	107.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	381	HEM	5	0
12	C	382	HEM	5	0
12	D	242	HEM	3	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.