



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:36 PM GMT

PDB ID : 1L0L
Title : structure of bovine mitochondrial cytochrome bc1 complex with a bound fungicide famoxadone
Authors : Gao, X.; Wen, X.; Yu, C.A.; Esser, L.; Tsao, S.; Quinn, B.; Zhang, L.; Yu, L.; Xia, D.
Deposited on : 2002-02-11
Resolution : 2.35 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

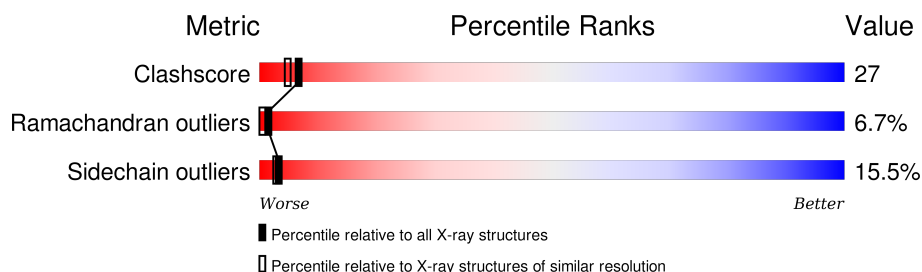
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)

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	
9	I	78	
10	J	62	
11	K	56	

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
14	FES	E	197	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 16795 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.

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.

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	377	Total	C	N	O	S	0	0	0
			2995	2009	470	498	18			

- Molecule 4 is a protein called Cytochrome c1, heme protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	240	Total	C	N	O	S	0	0	0
			1909	1219	328	347	15			

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

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	109	Total	C	N	O	S	0	0	0
			938	592	172	172	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	79	Total	C	N	O	S	0	0	0
			662	431	123	107	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	78	Total	C	N	O	S	0	0	0
			639	384	111	139	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	0	0	0
			495	324	86	85			

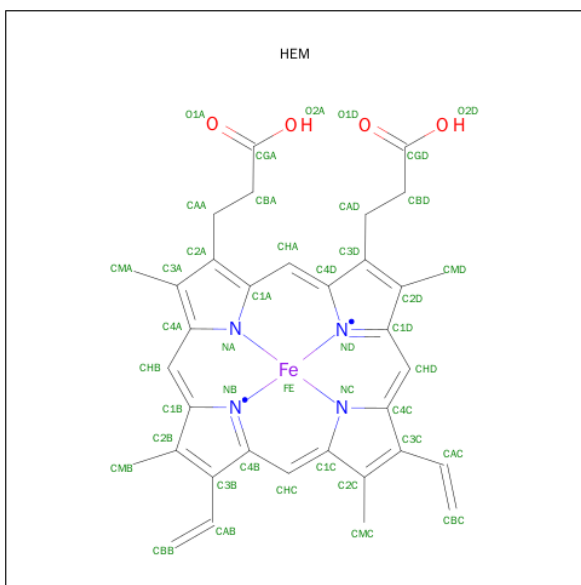
- Molecule 11 is a protein called Ubiquinol-cytochrome C reductase complex 6.4 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	53	Total	C	N	O	S	0	0	0
			441	295	79	66	1			

There is a discrepancy between the modelled and reference sequences:

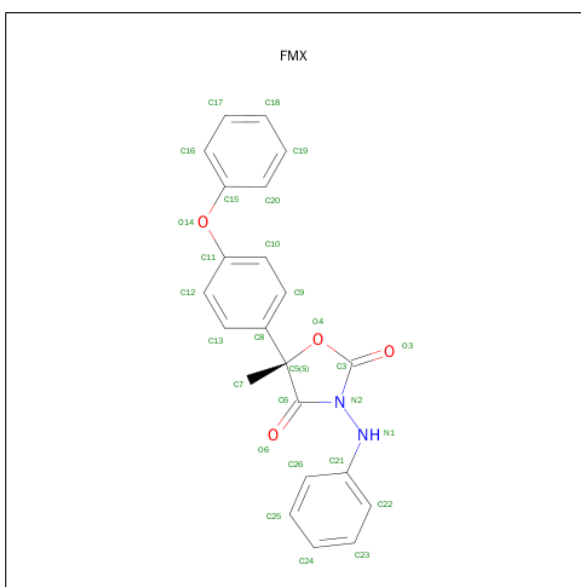
Chain	Residue	Modelled	Actual	Comment	Reference
K	22	GLN	SER	CONFLICT	UNP P07552

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



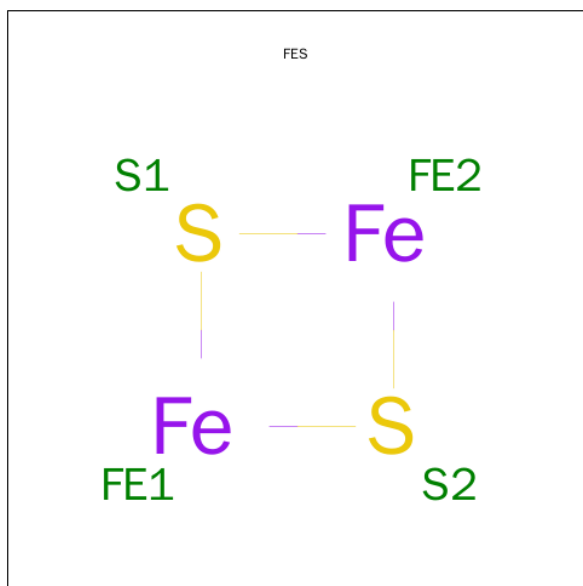
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
12	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
12	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 13 is FAMOXADONE (three-letter code: FMX) (formula: $C_{22}H_{18}N_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	C	1	Total	C	N	O		
			28	22	2	4		

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



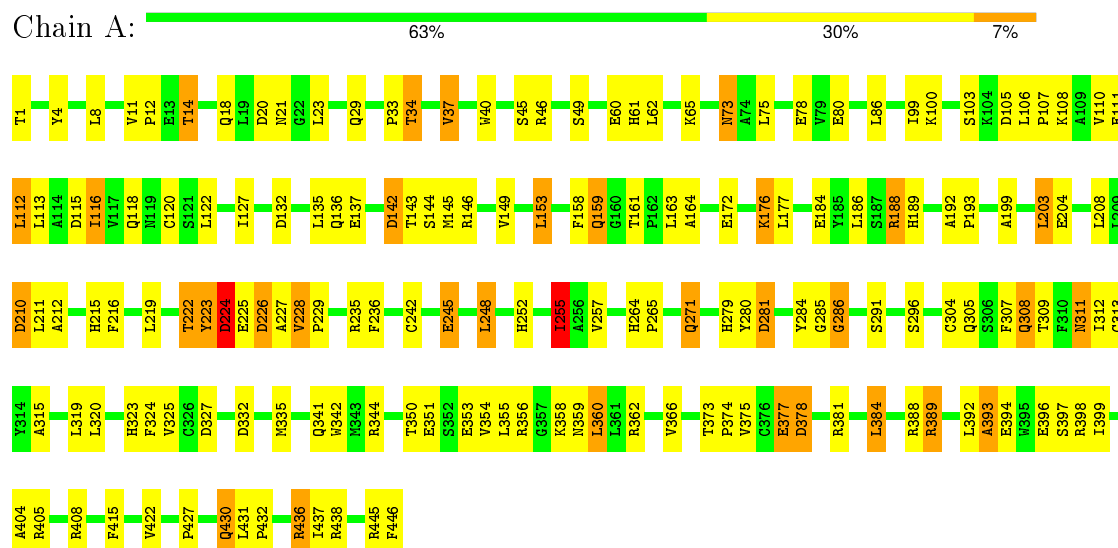
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	E	1	Total	Fe	S	0	0
			4	2	2		

3 Residue-property plots

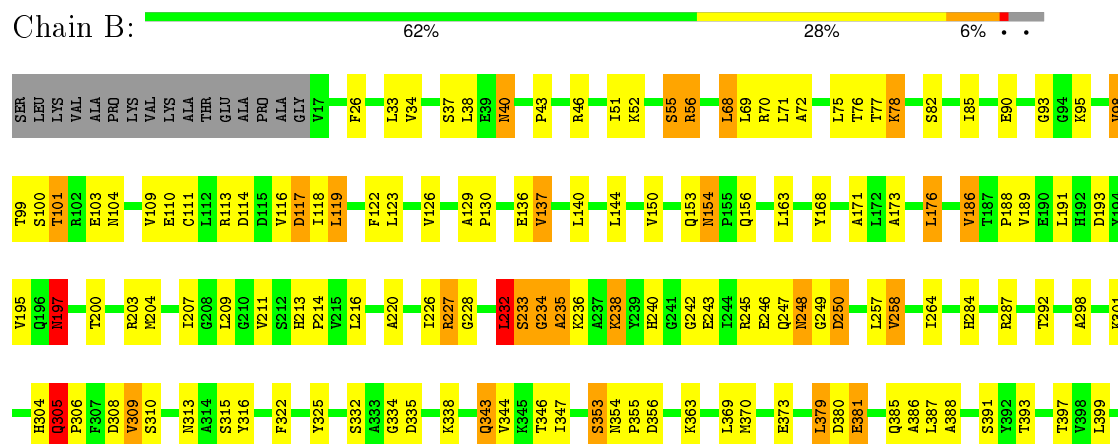
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

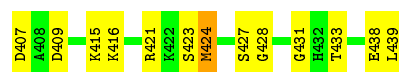
Note EDS was not executed.

• Molecule 1: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN I



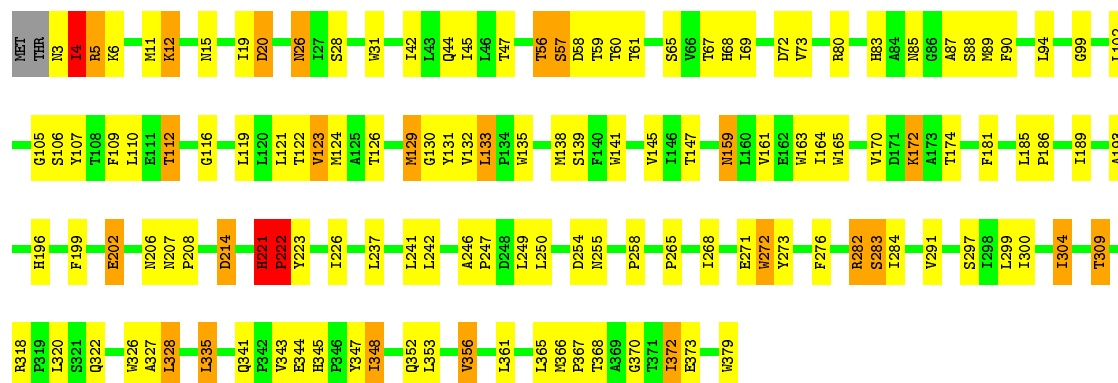
• Molecule 2: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2





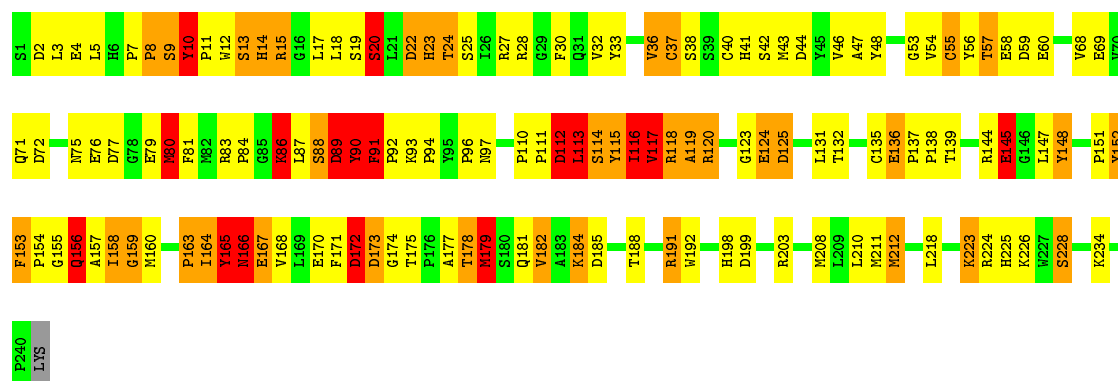
• Molecule 3: Cytochrome B

Chain C: 64% 29% 6% ..



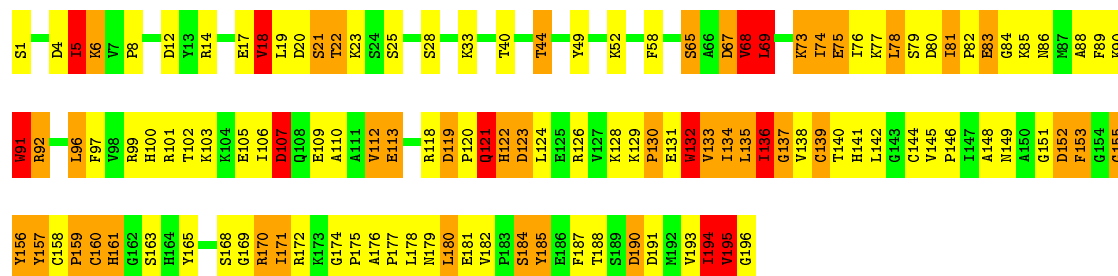
• Molecule 4: Cytochrome c1, heme protein

Chain D: 42% 35% 15% 7%



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

Chain E: 37% 37% 20% 6%



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

Chain F: 66% 26% 5% ..



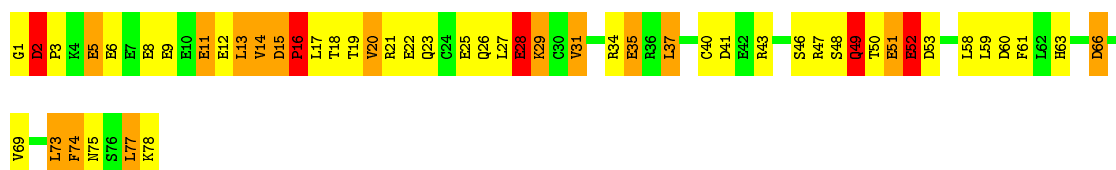
- Molecule 7: Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C

Chain G: 62% 20% 14% . .



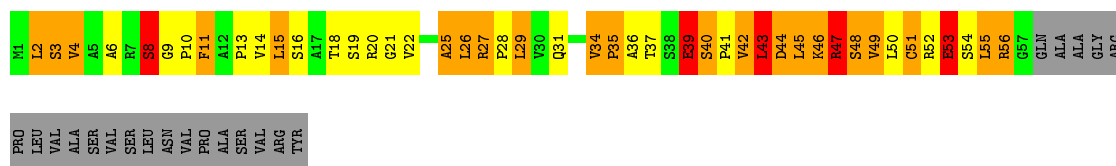
- Molecule 8: Ubiquinol-cytochrome C reductase complex 11 kDa protein

Chain H: 33% 41% 19% 6%



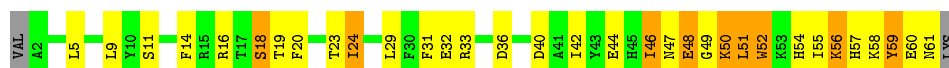
- Molecule 9: UBIQUINOL-CYTOCHROME C REDUCTASE 8 KDA PROTEIN

Chain I: 15% 24% 27% 6% 27%



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

Chain J: 44% 39% 15%



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

Chain K: 57% 23% 13% 5%



4 Data and refinement statistics

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

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.09Å 154.09Å 591.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.35	Depositor
% Data completeness (in resolution range)	96.0 (40.00-2.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.259 , 0.306	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16795	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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, FMX

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	0.86	1/3531 (0.0%)	0.89	13/4792 (0.3%)
2	B	1.11	8/3232 (0.2%)	1.01	19/4386 (0.4%)
3	C	0.84	0/3092	0.88	10/4232 (0.2%)
4	D	0.72	1/1968 (0.1%)	0.96	15/2673 (0.6%)
5	E	0.75	1/1553 (0.1%)	1.04	12/2100 (0.6%)
6	F	1.01	0/958	0.97	7/1284 (0.5%)
7	G	0.91	1/684 (0.1%)	0.86	1/926 (0.1%)
8	H	0.60	0/645	1.01	7/864 (0.8%)
9	I	0.99	2/411 (0.5%)	1.42	8/558 (1.4%)
10	J	0.76	0/508	0.94	1/686 (0.1%)
11	K	0.79	1/457 (0.2%)	0.77	1/625 (0.2%)
All	All	0.89	15/17039 (0.1%)	0.96	94/23126 (0.4%)

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
3	C	0	2

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	438	GLU	CD-OE2	7.77	1.34	1.25
1	A	304	CYS	CB-SG	-7.46	1.69	1.82
2	B	424	MET	SD-CE	-7.18	1.37	1.77
2	B	195	VAL	CB-CG1	7.08	1.67	1.52
5	E	91	TRP	CB-CG	5.82	1.60	1.50

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	42	VAL	O-C-N	10.88	140.12	122.70
3	C	221	HIS	C-N-CD	-10.49	97.52	120.60
9	I	42	VAL	CA-C-N	-9.26	96.84	117.20
2	B	304	HIS	O-C-N	9.08	137.23	122.70
3	C	222	PRO	N-CD-CG	-8.92	89.82	103.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	221	HIS	Mainchain,Peptide

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	3458	0	3356	149	0
2	B	3172	0	3152	121	0
3	C	2995	0	3058	121	0
4	D	1909	0	1857	163	0
5	E	1519	0	1503	172	0
6	F	938	0	932	26	0
7	G	662	0	662	32	0
8	H	639	0	604	50	0
9	I	406	0	437	98	0
10	J	495	0	493	70	0
11	K	441	0	450	26	0
12	C	86	0	60	23	0
12	D	43	0	30	6	0
13	C	28	0	18	0	0
14	E	4	0	0	2	0
All	All	16795	0	16612	902	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 27.

The worst 5 of 902 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)
4:D:40:CYS:SG	12:D:242:HEM:HAC	1.76	1.26
10:J:49:GLY:C	10:J:54:HIS:HE1	1.40	1.23
10:J:51:LEU:O	10:J:55:ILE:HG13	1.43	1.18
3:C:129:MET:CE	3:C:181:PHE:HB2	1.75	1.17
9:I:47:ARG:HG2	9:I:48:SER:H	1.09	1.16

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	444/446 (100%)	408 (92%)	28 (6%)	8 (2%)	11	8
2	B	421/439 (96%)	397 (94%)	17 (4%)	7 (2%)	11	9
3	C	375/379 (99%)	352 (94%)	16 (4%)	7 (2%)	10	7
4	D	238/241 (99%)	164 (69%)	35 (15%)	39 (16%)	0	0
5	E	194/196 (99%)	123 (63%)	35 (18%)	36 (19%)	0	0
6	F	107/110 (97%)	96 (90%)	8 (8%)	3 (3%)	6	3
7	G	77/81 (95%)	64 (83%)	7 (9%)	6 (8%)	1	0
8	H	76/78 (97%)	57 (75%)	7 (9%)	12 (16%)	0	0
9	I	55/78 (70%)	28 (51%)	11 (20%)	16 (29%)	0	0
10	J	58/62 (94%)	46 (79%)	9 (16%)	3 (5%)	2	1
11	K	51/56 (91%)	43 (84%)	4 (8%)	4 (8%)	1	0
All	All	2096/2166 (97%)	1778 (85%)	177 (8%)	141 (7%)	1	0

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	228	VAL
2	B	232	LEU

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Mol	Chain	Res	Type
2	B	234	GLY
2	B	305	GLN
3	C	172	LYS

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%)	317 (86%)	53 (14%)	4	4
2	B	332/343 (97%)	293 (88%)	39 (12%)	7	6
3	C	325/327 (99%)	280 (86%)	45 (14%)	4	4
4	D	205/206 (100%)	161 (78%)	44 (22%)	1	1
5	E	168/168 (100%)	140 (83%)	28 (17%)	3	2
6	F	98/98 (100%)	83 (85%)	15 (15%)	3	3
7	G	69/71 (97%)	58 (84%)	11 (16%)	3	2
8	H	74/74 (100%)	59 (80%)	15 (20%)	1	1
9	I	44/60 (73%)	33 (75%)	11 (25%)	1	0
10	J	50/52 (96%)	42 (84%)	8 (16%)	3	2
11	K	43/46 (94%)	36 (84%)	7 (16%)	3	2
All	All	1778/1815 (98%)	1502 (84%)	276 (16%)	3	3

5 of 276 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	299	LEU
4	D	115	TYR
9	I	27	ARG
3	C	320	LEU
4	D	20	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	313	ASN
3	C	15	ASN
8	H	23	GLN
2	B	342	ASN
2	B	358	GLN

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 ⓘ

5 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	609	3	30,50,50	6.09	17 (56%)	24,82,82	3.73	15 (62%)
12	HEM	C	610	3	30,50,50	5.88	17 (56%)	24,82,82	4.27	12 (50%)
13	FMX	C	611	-	28,31,31	0.81	1 (3%)	35,44,44	1.22	4 (11%)
12	HEM	D	242	4	30,50,50	2.27	8 (26%)	24,82,82	2.77	13 (54%)
14	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	609	3	-	0/10/54/54	0/0/8/8
12	HEM	C	610	3	-	0/10/54/54	0/0/8/8
13	FMX	C	611	-	-	0/14/33/33	0/4/4/4
12	HEM	D	242	4	-	0/10/54/54	0/0/8/8
14	FES	E	197	5	-	0/0/4/4	0/1/1/1

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	C	609	HEM	C3B-C4B	-23.42	1.30	1.51
12	C	610	HEM	C3B-C4B	-19.74	1.34	1.51
12	C	610	HEM	C3D-C4D	-13.66	1.34	1.51
12	C	609	HEM	C3D-C4D	-10.86	1.37	1.51
12	C	609	HEM	C2C-C1C	-9.83	1.33	1.52

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	C	610	HEM	C3C-CAC-CBC	-10.22	108.78	124.46
12	C	610	HEM	C3B-CAB-CBB	-9.18	110.38	124.46
12	C	610	HEM	C1D-CHD-C4C	-8.43	111.72	125.82
12	C	609	HEM	C1D-CHD-C4C	-7.92	112.57	125.82
12	C	609	HEM	C4B-CHC-C1C	-7.62	113.09	125.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	609	HEM	11	0
12	C	610	HEM	12	0
12	D	242	HEM	6	0
14	E	197	FES	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.