



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 06:47 AM GMT

PDB ID : 1QLB
Title : respiratory complex II-like fumarate reductase from Wolinella succinogenes
Authors : Lancaster, C.R.D.; Kroeger, A.; Auer, M.; Michel, H.
Deposited on : 1999-08-25
Resolution : 2.33 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

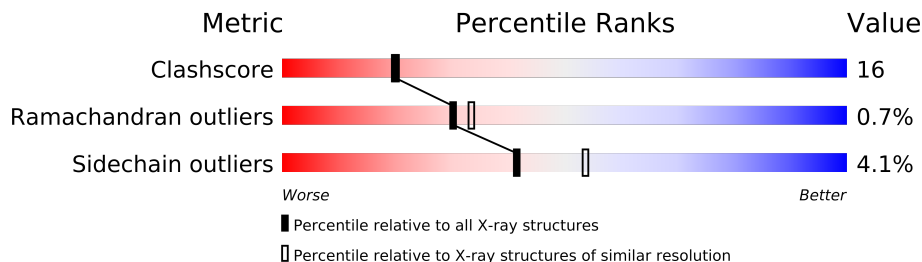
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.33 Å.





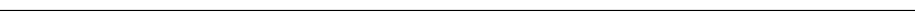
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	656	
1	D	656	
2	B	239	
2	E	239	
3	C	256	
3	F	256	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 19056 atoms, of which 0 are hydrogen and 0 are deuterium.

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 FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	655	Total	C	N	O	S	88	0	0
			5101	3194	913	962	32			
1	D	655	Total	C	N	O	S	88	0	0
			5101	3194	913	962	32			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	ASP	ARG	CONFLICT (SEE REMARK	UNP P17412
A	282	VAL	CYS	CONFLICT (SEE REMARK	UNP P17412
A	283	ASP	GLY	CONFLICT (SEE REMARK	UNP P17412
A	284	GLY	TRP	CONFLICT (SEE REMARK	UNP P17412
A	285	HIS	THR	CONFLICT (SEE REMARK	UNP P17412
A	286	ARG	PRO	CONFLICT (SEE REMARK	UNP P17412
A	287	PHE	ILE	CONFLICT (SEE REMARK	UNP P17412
A	288	MET	HIS	CONFLICT (SEE REMARK	UNP P17412
A	289	PRO	ALA	CONFLICT (SEE REMARK	UNP P17412
D	281	ASP	ARG	CONFLICT (SEE REMARK	UNP P17412
D	282	VAL	CYS	CONFLICT (SEE REMARK	UNP P17412
D	283	ASP	GLY	CONFLICT (SEE REMARK	UNP P17412
D	284	GLY	TRP	CONFLICT (SEE REMARK	UNP P17412
D	285	HIS	THR	CONFLICT (SEE REMARK	UNP P17412
D	286	ARG	PRO	CONFLICT (SEE REMARK	UNP P17412
D	287	PHE	ILE	CONFLICT (SEE REMARK	UNP P17412
D	288	MET	HIS	CONFLICT (SEE REMARK	UNP P17412
D	289	PRO	ALA	CONFLICT (SEE REMARK	UNP P17412

- Molecule 2 is a protein called FUMARATE REDUCTASE IRON-SULFUR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	239	Total	C	N	O	S	0	0	0
			1893	1194	322	354	23			

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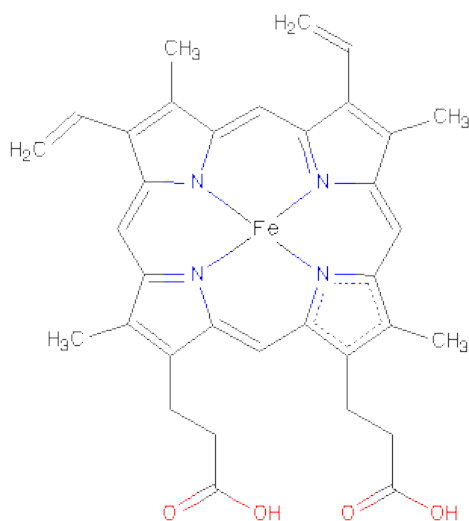
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	239	Total	C	N	O	S	0	0	0
			1893	1194	322	354	23			

- Molecule 3 is a protein called FUMARATE REDUCTASE CYTOCHROME B SUBUNIT.

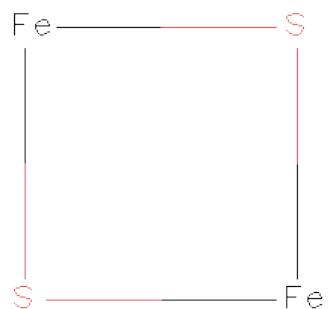
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	254	Total	C	N	O	S	111	0	0
			2080	1388	333	345	14			
3	F	254	Total	C	N	O	S	111	0	0
			2080	1388	333	345	14			

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



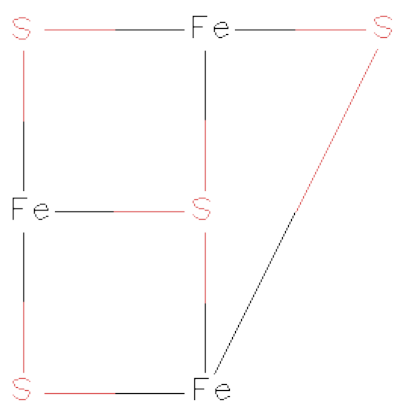
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



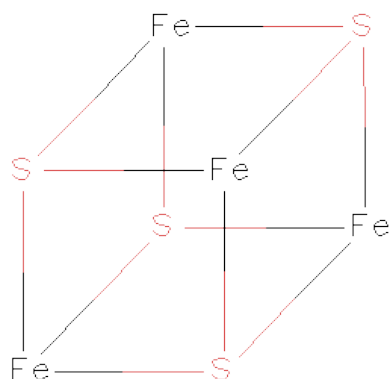
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	Fe	S	0	0
			4	2	2		
5	E	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 6 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



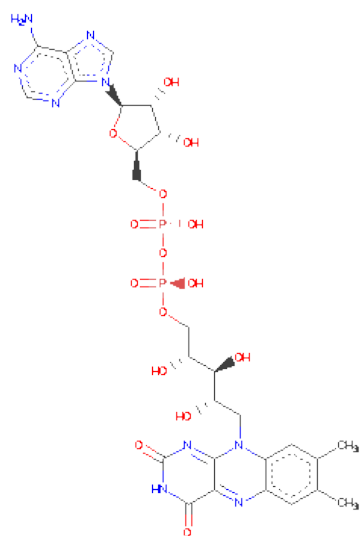
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Fe	S	0	0
			7	3	4		
6	E	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



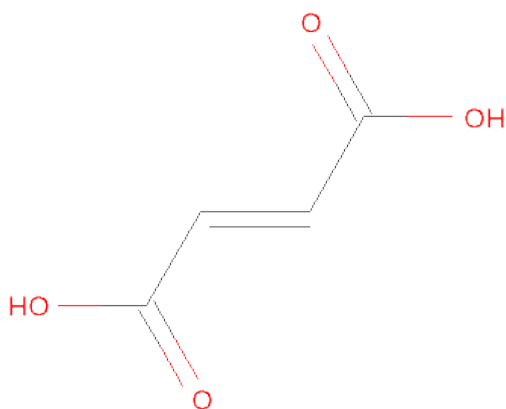
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		
7	E	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 8 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



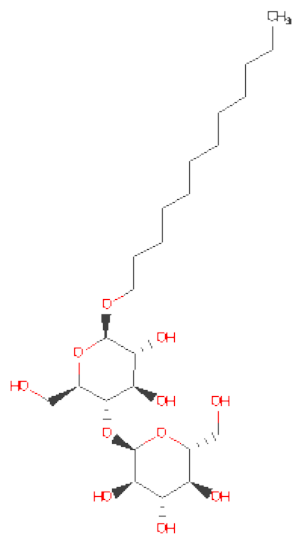
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
8	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 9 is FUMARIC ACID (three-letter code: FUM) (formula: $C_4H_4O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			8	4	4		
9	D	1	Total	C	O	0	0
			8	4	4		

- Molecule 10 is DODECYL-BETA-D-MALTOSIDE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total	C	O	16	0
			35	24	11		
10	F	1	Total	C	O	16	0
			35	24	11		

- Molecule 11 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	1	Total	Ca	0	0
			1	1		
11	D	1	Total	Ca	0	0
			1	1		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	149	Total	O	0	0
			149	149		
12	B	79	Total	O	0	0
			79	79		
12	C	23	Total	O	0	0
			23	23		
12	D	148	Total	O	0	0
			148	148		
12	E	83	Total	O	0	0
			83	83		

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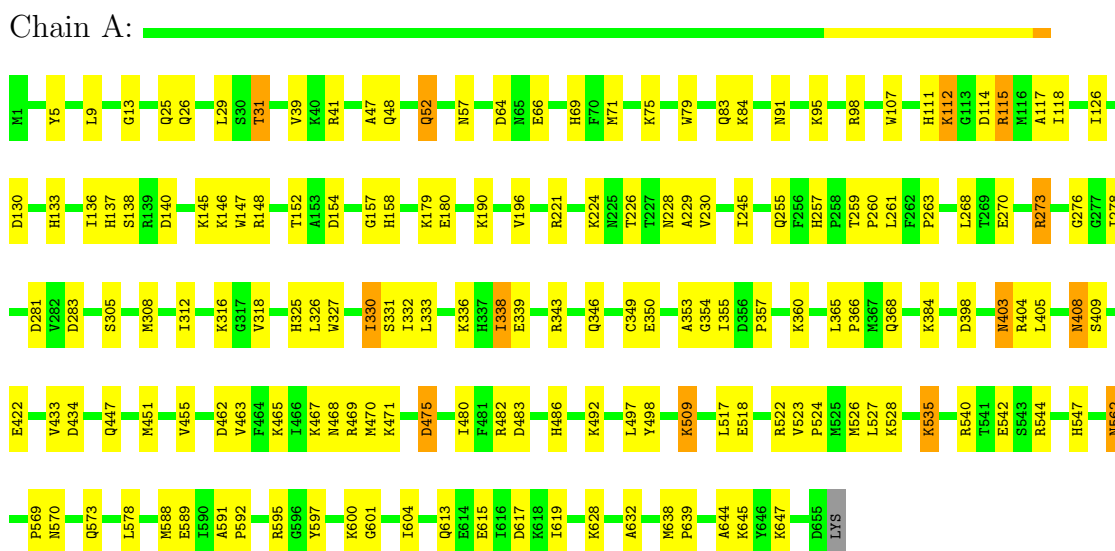
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	F	22	Total	O	0	0
			22	22		

3 Residue-property plots

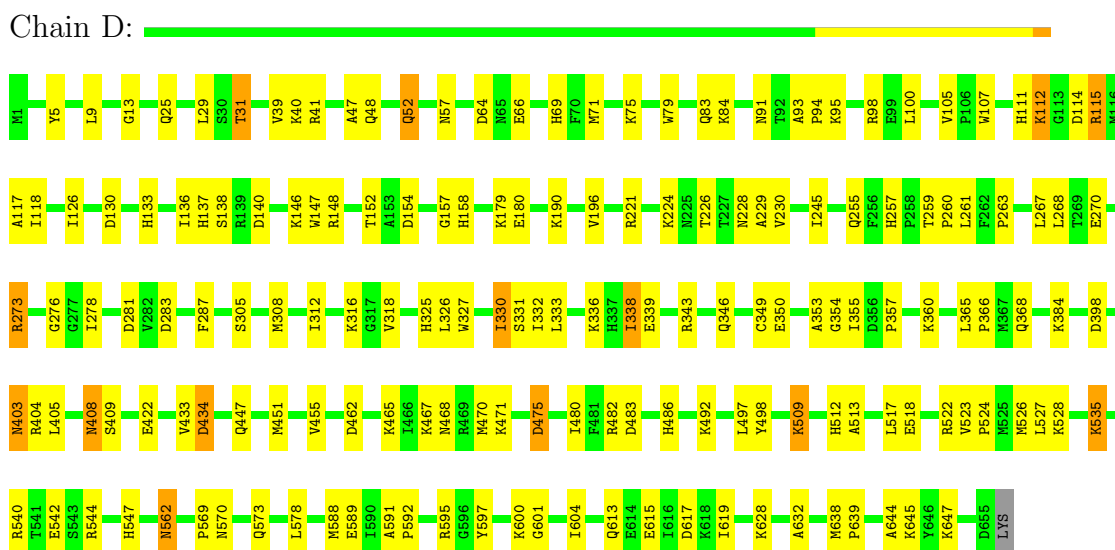
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

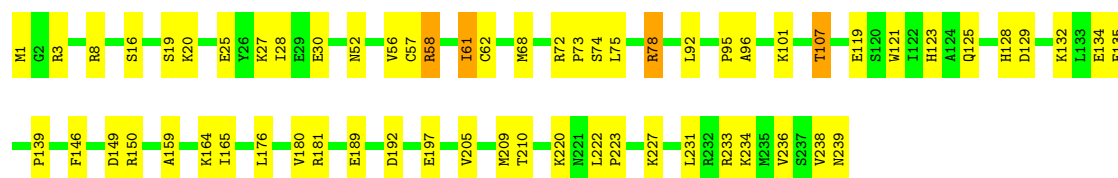


• Molecule 1: FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT



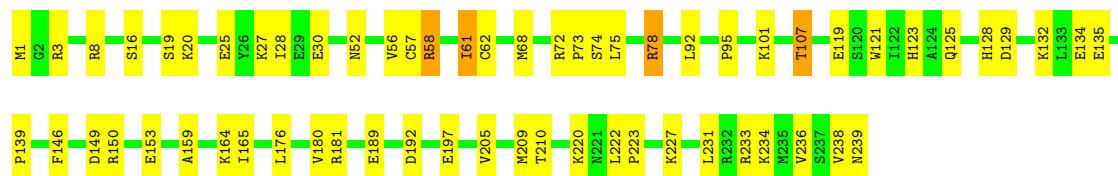
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain B: 



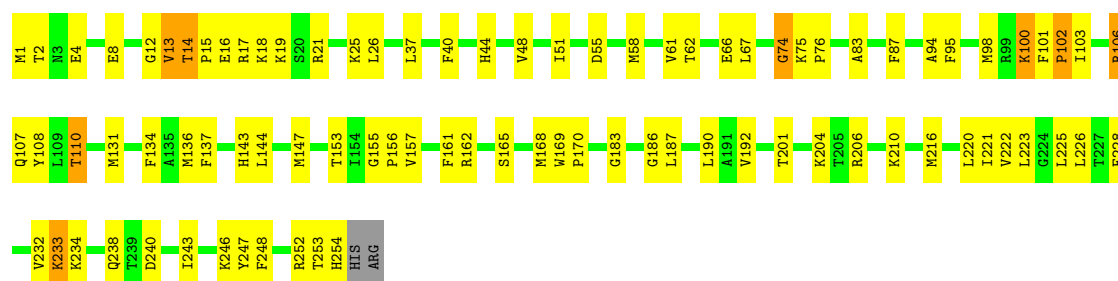
• Molecule 2: FUMARATE REDUCTASE IRON-SULFUR PROTEIN

Chain E: 



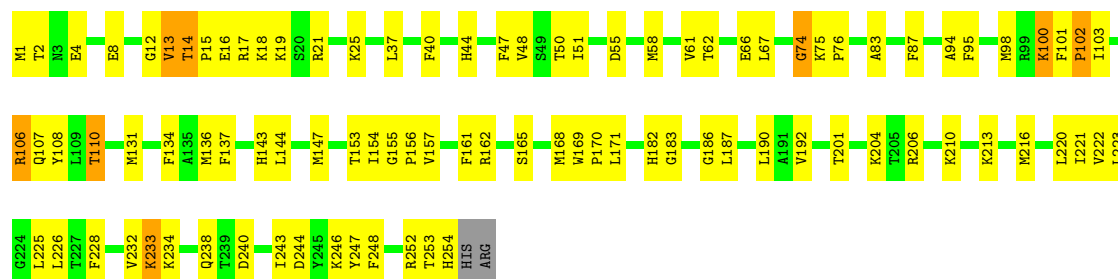
• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain C: 



• Molecule 3: FUMARATE REDUCTASE CYTOCHROME B SUBUNIT

Chain F: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	118.40Å 85.05Å 188.85Å 90.00° 96.46° 90.00°	Depositor
Resolution (Å)	38.87 – 2.33	Depositor
% Data completeness (in resolution range)	95.8 (38.87-2.33)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.213 , 0.223	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	19056	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: SF4, LMT, F3S, FES, HEM, FUM, CA, FAD

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	0.32	0/5197	0.60	0/7006
1	D	0.32	0/5197	0.60	0/7006
2	B	0.35	0/1930	0.59	0/2604
2	E	0.34	0/1930	0.59	0/2604
3	C	0.32	0/2146	0.50	1/2904 (0.0%)
3	F	0.33	0/2146	0.50	1/2904 (0.0%)
All	All	0.33	0/18546	0.58	2/25028 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	102	PRO	N-CA-C	-5.88	96.82	112.10
3	F	102	PRO	N-CA-C	-5.86	96.85	112.10

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5101	0	5079	148	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	5101	0	5079	149	0
2	B	1893	0	1861	61	0
2	E	1893	0	1861	63	0
3	C	2080	0	2101	98	0
3	F	2080	0	2101	103	0
4	C	86	0	60	7	0
4	F	86	0	60	8	0
5	B	4	0	0	0	0
5	E	4	0	0	0	0
6	B	7	0	0	0	0
6	E	7	0	0	0	0
7	B	8	0	0	0	0
7	E	8	0	0	0	0
8	A	53	0	29	1	0
8	D	53	0	29	1	0
9	A	8	0	2	2	0
9	D	8	0	2	1	0
10	C	35	0	46	7	0
10	F	35	0	46	8	0
11	A	1	0	0	0	0
11	D	1	0	0	0	0
12	A	149	0	0	8	0
12	B	79	0	0	2	0
12	C	23	0	0	0	0
12	D	148	0	0	6	0
12	E	83	0	0	3	0
12	F	22	0	0	0	0
All	All	19056	0	18356	576	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

The worst 5 of 576 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:F:253:THR:HG22	3:F:254:HIS:H	1.25	0.99
3:C:253:THR:HG22	3:C:254:HIS:H	1.25	0.98
2:B:239:ASN:ND2	3:C:21:ARG:HH21	1.64	0.96
2:E:239:ASN:ND2	3:F:21:ARG:HH21	1.64	0.95
2:E:239:ASN:HD22	3:F:21:ARG:HH21	1.15	0.91

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	653/656 (100%)	615 (94%)	33 (5%)	5 (1%)	27	30
1	D	653/656 (100%)	615 (94%)	33 (5%)	5 (1%)	27	30
2	B	237/239 (99%)	229 (97%)	8 (3%)	0	100	100
2	E	237/239 (99%)	229 (97%)	8 (3%)	0	100	100
3	C	252/256 (98%)	234 (93%)	15 (6%)	3 (1%)	19	18
3	F	252/256 (98%)	235 (93%)	14 (6%)	3 (1%)	19	18
All	All	2284/2302 (99%)	2157 (94%)	111 (5%)	16 (1%)	30	33

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	ALA
1	A	338	ILE
3	C	67	LEU
1	D	117	ALA
1	D	338	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	534/535 (100%)	511 (96%)	23 (4%)	40	51
1	D	534/535 (100%)	510 (96%)	24 (4%)	38	48
2	B	211/211 (100%)	205 (97%)	6 (3%)	56	71
2	E	211/211 (100%)	205 (97%)	6 (3%)	56	71
3	C	221/223 (99%)	211 (96%)	10 (4%)	38	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	221/223 (99%)	211 (96%)	10 (4%)	38	48
All	All	1932/1938 (100%)	1853 (96%)	79 (4%)	41	54

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	100	LYS
1	D	115	ARG
3	F	58	MET
3	C	106	ARG
1	D	31	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	208	ASN
1	D	133	HIS
3	F	3	ASN
3	C	238	GLN
1	D	48	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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
8	FAD	A	1656	1	58,58,58	2.13	15 (25%)	85,89,89	2.05	16 (18%)
9	FUM	A	1657	-	7,7,7	1.58	2 (28%)	8,8,8	0.76	0
5	FES	B	1240	2	0,4,4	0.00	-	0,4,4	0.00	-
6	F3S	B	1241	2	3,9,9	9.19	1 (33%)	0,15,15	0.00	-
7	SF4	B	1242	2	12,12,12	9.86	10 (83%)	0,24,24	0.00	-
4	HEM	C	1255	3	49,50,50	1.85	15 (30%)	46,82,82	1.44	4 (8%)
4	HEM	C	1256	3	49,50,50	1.82	12 (24%)	46,82,82	1.55	5 (10%)
10	LMT	C	1257	-	36,36,36	1.08	2 (5%)	47,47,47	1.26	4 (8%)
8	FAD	D	1656	1	58,58,58	2.09	12 (20%)	85,89,89	2.03	17 (20%)
9	FUM	D	1657	-	7,7,7	1.58	2 (28%)	8,8,8	0.77	0
5	FES	E	1240	2	0,4,4	0.00	-	0,4,4	0.00	-
6	F3S	E	1241	2	3,9,9	137.64	3 (100%)	0,15,15	0.00	-
7	SF4	E	1242	2	12,12,12	9.94	9 (75%)	0,24,24	0.00	-
4	HEM	F	1255	3	49,50,50	1.86	16 (32%)	46,82,82	1.43	4 (8%)
4	HEM	F	1256	3	49,50,50	1.79	12 (24%)	46,82,82	1.56	5 (10%)
10	LMT	F	1257	-	36,36,36	1.09	2 (5%)	47,47,47	1.26	4 (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
8	FAD	A	1656	1	-	0/34/50/50	0/1/6/6
9	FUM	A	1657	-	-	0/5/5/5	0/0/0/0
5	FES	B	1240	2	-	0/0/4/4	0/0/1/1
6	F3S	B	1241	2	-	0/0/24/24	0/0/3/3
7	SF4	B	1242	2	-	0/0/48/48	0/0/5/5
4	HEM	C	1255	3	-	0/14/114/114	0/0/8/8
4	HEM	C	1256	3	-	0/14/114/114	0/0/8/8
10	LMT	C	1257	-	-	0/21/61/61	0/2/2/2
8	FAD	D	1656	1	-	0/34/50/50	0/1/6/6
9	FUM	D	1657	-	-	0/5/5/5	0/0/0/0
5	FES	E	1240	2	-	0/0/4/4	0/0/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	F3S	E	1241	2	-	0/0/24/24	0/0/3/3
7	SF4	E	1242	2	-	0/0/48/48	0/0/5/5
4	HEM	F	1255	3	-	0/14/114/114	0/0/8/8
4	HEM	F	1256	3	-	0/14/114/114	0/0/8/8
10	LMT	F	1257	-	-	0/21/61/61	0/2/2/2

The worst 5 of 113 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	1241	F3S	S3-FE1	238.30	3.93	2.33
7	B	1242	SF4	S1-FE3	-19.76	2.20	2.33
7	E	1242	SF4	S1-FE3	-18.79	2.20	2.33
7	E	1242	SF4	S4-FE3	-18.76	2.20	2.33
7	B	1242	SF4	S4-FE3	-18.56	2.20	2.33

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	1656	FAD	O4B-C1B-N9A	-7.61	101.36	108.44
8	A	1656	FAD	O4B-C1B-N9A	-7.54	101.43	108.44
8	A	1656	FAD	C2'-C1'-N10	-7.54	102.45	112.45
8	D	1656	FAD	C2'-C1'-N10	-7.46	102.55	112.45
8	A	1656	FAD	C1'-N10-C9A	-6.91	112.15	118.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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.