



# wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 02:18 PM GMT

PDB ID : 1D4C  
Title : CRYSTAL STRUCTURE OF THE UNCOMPLEXED FORM OF THE FLAVOCYTOCHROME C FUMARATE REDUCTASE OF SHEWANELLA PUTREFACIENS STRAIN MR-1  
Authors : Leys, D.; Tsapin, A.S.; Meyer, T.E.; Cusanovich, M.A.; Van Beeumen, J.J.  
Deposited on : 1999-10-03  
Resolution : 2.90 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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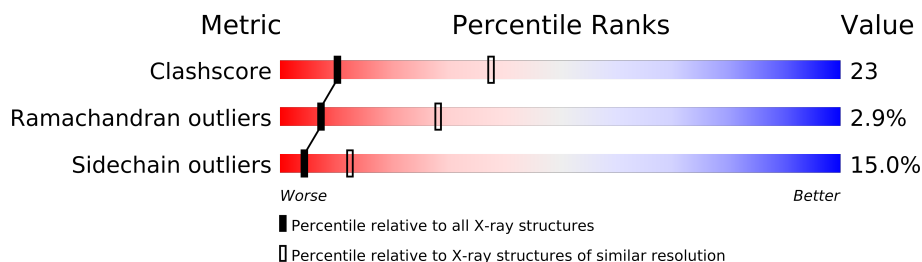
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.90 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	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)

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  $\geq 3$ , 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	572	
1	B	572	
1	C	572	
1	D	572	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 17470 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 FLAVOCYTOCHROME C FUMARATE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	570	Total	C	N	O	S	0	0	0
			4124	2562	736	807	19			
1	B	566	Total	C	N	O	S	0	0	0
			4093	2542	731	801	19			
1	C	568	Total	C	N	O	S	0	0	0
			4099	2546	733	801	19			
1	D	570	Total	C	N	O	S	0	0	0
			4113	2553	734	807	19			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



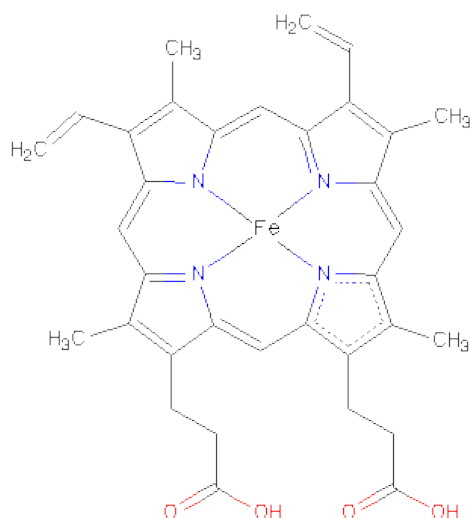
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



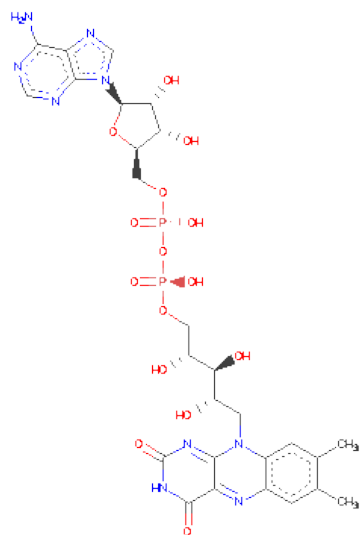
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
3	A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
3	A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
3	A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
3	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
3	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
3	B	1	Total	C	Fe	N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

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

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	48	Total 48	O 48	0	0
5	B	29	Total 29	O 29	0	0
5	C	30	Total 30	O 30	0	0
5	D	19	Total 19	O 19	0	0

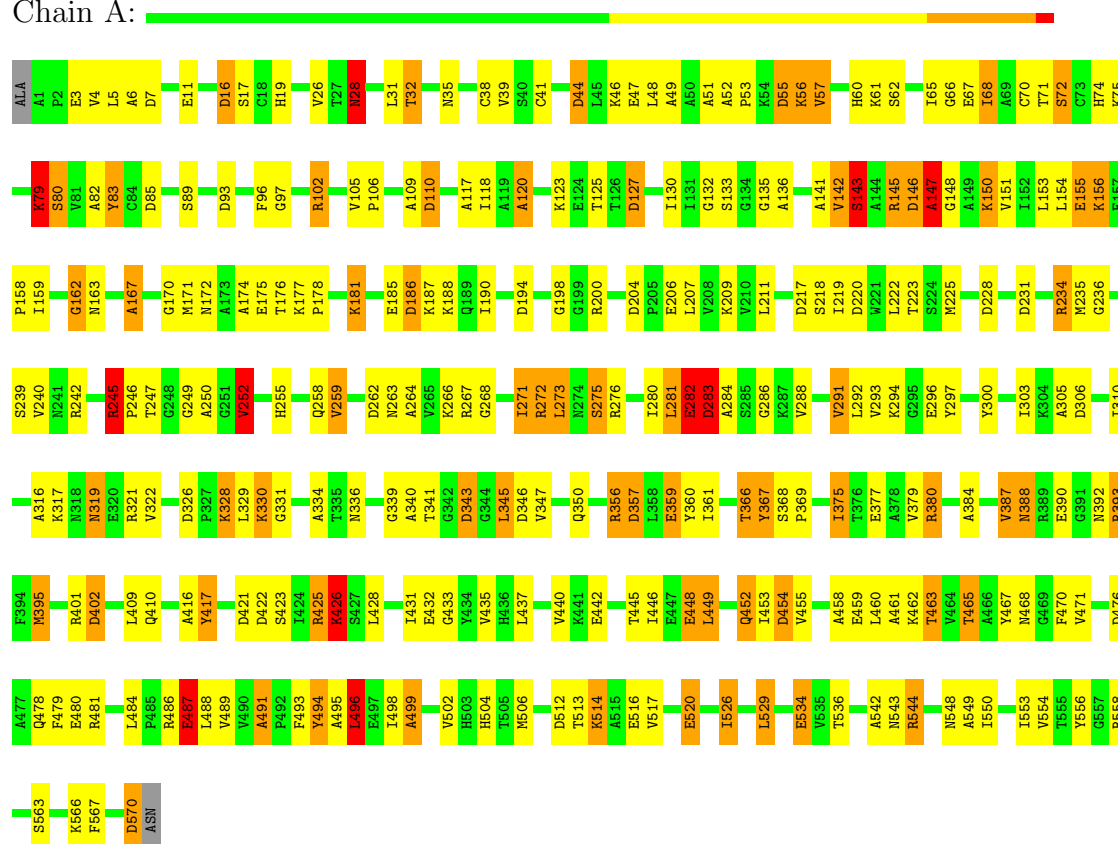
### 3 Residue-property plots

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.

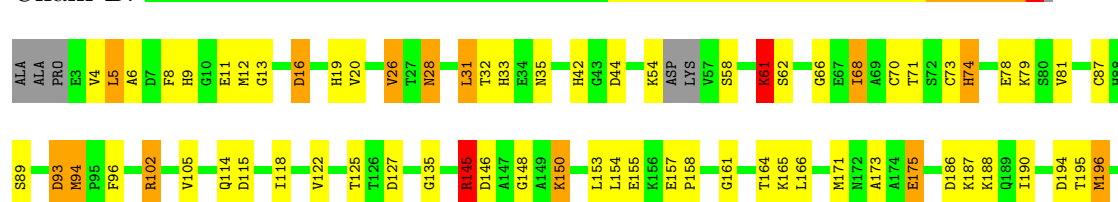
#### • Molecule 1: FLAVOCYTOCHROME C FUMARATE REDUCTASE

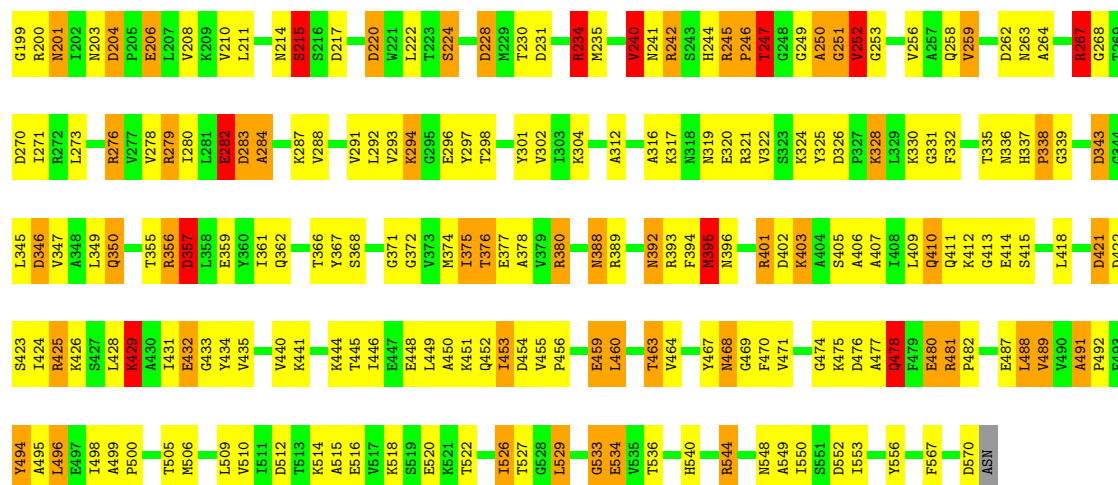
Chain A:



#### • Molecule 1: FLAVOCYTOCHROME C FUMARATE REDUCTASE

Chain B:







S563	D476	S405	K328	N241
D570	A477	A406	L329	R242
ASN	Q478	L409	K330	S243
	F479	Q410	G331	H244
	E480	Q411		R245
	R481		N336	P246
	P482	S415		T247
	D483		A340	G248
	L484	L418		G249
	P485	V419	L345	A250
	R486	F420	D346	G251
	E487	D421	V347	V252
	L488	D422	A348	
	V489	S423	L349	
	V490	I424	Q350	Q258
	A491	R425		V259
	P492	K426	T355	L260
	F493	S427	R356	D262
	Y494	L428	D357	
	A495	K429	L358	R267
	L496	A430	E359	G268
	E497	I431	Y360	T269
	I498	E432	I361	D270
	A499	G433		
	P500	Y434	H364	L273
	A501		P365	
	V502	I439	T366	V277
		V440	Y367	V278
	M506	K441	S368	R279
			P369	I280
	V510	K444	A370	L281
		T445	G371	E282
	K514	I446	G372	D283
	A515	E447		A284
	E516	E448	I375	
	K517	L449	T376	V288
	K518	A450	E377	
	S519	K451	A378	V291
	E520	Q452	V379	L292
		I453	R380	V293
	P525	D454	G381	
	I526	V455	N382	Y297
		P456	G383	
	L529	A457	A384	Y300
		A458	I385	
	H540	E459		I303
	N543	L460	N388	
	R544	A461	R389	A307
	L545	K462		
	G546	T463	N392	I310
	G547	V464	R393	
	N548		F394	A316
	A549	Y467	M395	
		N468	N396	N319
	D552	G469		E320
	I553	F470	T400	R321
	V554	V471	R401	V322
			D402	
			K403	D326
			A404	P327

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.69Å 216.36Å 112.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90	Depositor
% Data completeness (in resolution range)	93.7 (15.00-2.90)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.210 , 0.300	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17470	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	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, SO4, 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	0.76	0/4192	2.22	144/5683 (2.5%)
1	B	0.74	7/4159 (0.2%)	1.97	112/5637 (2.0%)
1	C	0.71	3/4166 (0.1%)	2.04	126/5649 (2.2%)
1	D	0.64	1/4179 (0.0%)	1.94	98/5665 (1.7%)
All	All	0.72	11/16696 (0.1%)	2.05	480/22634 (2.1%)

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
1	A	0	3
1	B	0	2
1	C	0	3
1	D	0	2
All	All	0	10

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	480	GLU	CD-OE1	9.81	1.36	1.25
1	C	459	GLU	CD-OE1	9.29	1.35	1.25
1	C	459	GLU	CD-OE2	8.55	1.35	1.25
1	B	476	ASP	CG-OD1	8.47	1.44	1.25
1	B	459	GLU	CD-OE2	7.25	1.33	1.25

The worst 5 of 480 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	245	ARG	CD-NE-CZ	29.02	164.23	123.60
1	A	267	ARG	CD-NE-CZ	24.00	157.20	123.60
1	A	102	ARG	NE-CZ-NH2	23.33	131.97	120.30
1	D	401	ARG	CD-NE-CZ	21.85	154.19	123.60
1	D	242	ARG	NE-CZ-NH1	20.69	130.65	120.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	146	ASP	Mainchain
1	A	491	ALA	Mainchain,Peptide
1	B	491	ALA	Mainchain,Peptide
1	C	477	ALA	Mainchain
1	C	491	ALA	Mainchain

## 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	4124	0	4013	181	1
1	B	4093	0	3976	179	0
1	C	4099	0	3977	192	2
1	D	4113	0	3987	210	1
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	172	0	120	15	0
3	B	172	0	120	17	0
3	C	172	0	120	13	0
3	D	172	0	120	19	0
4	A	53	0	31	9	0
4	B	53	0	31	8	0
4	C	53	0	31	12	0
4	D	53	0	30	9	0
5	A	48	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	29	0	0	3	0
5	C	30	0	0	2	0
5	D	19	0	0	2	0
All	All	17470	0	16556	789	2

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 23.

The worst 5 of 789 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:70:CYS:SG	3:D:602:HEM:HAB	1.27	1.72
1:D:18:CYS:SG	3:D:603:HEM:HAC	1.21	1.71
1:D:41:CYS:SG	3:D:604:HEM:HAC	1.13	1.70
1:B:87:CYS:SG	3:B:601:HEM:HAC	1.33	1.68
4:B:700:FAD:C2'	4:B:700:FAD:C1'	1.77	1.62

All (2) 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	Distance(Å)	Clash(Å)
1:A:125:THR:OG1	1:C:247:THR:OG1[4.555]	2.12	0.08
1:C:125:THR:OG1	1:D:247:THR:OG1[4.456]	2.15	0.05

## 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	568/572 (99%)	504 (89%)	51 (9%)	13 (2%)	10	36
1	B	562/572 (98%)	495 (88%)	52 (9%)	15 (3%)	8	30
1	C	566/572 (99%)	482 (85%)	64 (11%)	20 (4%)	6	23
1	D	566/572 (99%)	488 (86%)	61 (11%)	17 (3%)	7	27
All	All	2262/2288 (99%)	1969 (87%)	228 (10%)	65 (3%)	7	28

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	VAL
1	A	142	VAL
1	A	147	ALA
1	A	454	ASP
1	B	250	ALA

### 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	409/429 (95%)	350 (86%)	59 (14%)	5	13
1	B	406/429 (95%)	344 (85%)	62 (15%)	4	12
1	C	405/429 (94%)	343 (85%)	62 (15%)	4	12
1	D	407/429 (95%)	346 (85%)	61 (15%)	4	12
All	All	1627/1716 (95%)	1383 (85%)	244 (15%)	4	12

5 of 244 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	480	GLU
1	C	145	ARG
1	D	395	MET
1	B	494	TYR
1	C	17	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	410	GLN
1	C	35	ASN
1	D	388	ASN
1	B	411	GLN
1	B	478	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 ⓘ

23 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	$\# Z  > 2$
4	FAD	A	600	-	58,58,58	3.96	12 (20%)	85,89,89	3.35	30 (35%)
3	HEM	A	601	1	49,50,50	2.53	12 (24%)	46,82,82	2.87	17 (36%)
3	HEM	A	602	1	49,50,50	2.47	16 (32%)	46,82,82	1.94	11 (23%)
3	HEM	A	603	1	49,50,50	2.38	10 (20%)	46,82,82	1.86	8 (17%)
3	HEM	A	604	1	49,50,50	2.31	13 (26%)	46,82,82	2.35	11 (23%)
3	HEM	B	601	1	49,50,50	2.25	10 (20%)	46,82,82	2.28	12 (26%)
3	HEM	B	602	1	49,50,50	2.42	10 (20%)	46,82,82	1.94	9 (19%)
3	HEM	B	603	1	49,50,50	2.15	11 (22%)	46,82,82	1.98	9 (19%)
3	HEM	B	604	1	49,50,50	2.18	10 (20%)	46,82,82	2.36	16 (34%)
4	FAD	B	700	-	58,58,58	3.89	9 (15%)	85,89,89	3.19	32 (37%)
2	SO4	B	714	-	4,4,4	0.71	0	6,6,6	0.62	0
3	HEM	C	601	1	49,50,50	2.19	10 (20%)	46,82,82	2.17	8 (17%)
3	HEM	C	602	1	49,50,50	2.45	13 (26%)	46,82,82	2.33	12 (26%)
3	HEM	C	603	1	49,50,50	2.23	9 (18%)	46,82,82	1.77	9 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	HEM	C	604	1	49,50,50	2.28	11 (22%)	46,82,82	3.15	16 (34%)
4	FAD	C	800	-	58,58,58	4.03	10 (17%)	85,89,89	3.37	27 (31%)
2	SO4	C	814	-	4,4,4	1.03	0	6,6,6	0.86	0
3	HEM	D	601	1	49,50,50	2.41	13 (26%)	46,82,82	2.26	13 (28%)
3	HEM	D	602	1	49,50,50	2.36	13 (26%)	46,82,82	2.05	10 (21%)
3	HEM	D	603	1	49,50,50	2.24	12 (24%)	46,82,82	1.80	6 (13%)
3	HEM	D	604	1	49,50,50	2.11	9 (18%)	46,82,82	2.51	13 (28%)
4	FAD	D	900	-	58,58,58	3.99	8 (13%)	85,89,89	3.27	28 (32%)
2	SO4	D	914	-	4,4,4	0.78	0	6,6,6	0.68	0

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
4	FAD	A	600	-	2/2/9/9	0/34/50/50	0/1/6/6
3	HEM	A	601	1	-	0/14/114/114	0/0/8/8
3	HEM	A	602	1	-	0/14/114/114	0/0/8/8
3	HEM	A	603	1	-	0/14/114/114	0/0/8/8
3	HEM	A	604	1	-	0/14/114/114	0/0/8/8
3	HEM	B	601	1	-	0/14/114/114	0/0/8/8
3	HEM	B	602	1	-	0/14/114/114	0/0/8/8
3	HEM	B	603	1	-	0/14/114/114	0/0/8/8
3	HEM	B	604	1	-	0/14/114/114	0/0/8/8
4	FAD	B	700	-	2/2/9/9	0/34/50/50	0/1/6/6
2	SO4	B	714	-	-	0/0/0/0	0/0/0/0
3	HEM	C	601	1	-	0/14/114/114	0/0/8/8
3	HEM	C	602	1	-	0/14/114/114	0/0/8/8
3	HEM	C	603	1	-	0/14/114/114	0/0/8/8
3	HEM	C	604	1	-	0/14/114/114	0/0/8/8
4	FAD	C	800	-	3/3/9/9	0/34/50/50	0/1/6/6
2	SO4	C	814	-	-	0/0/0/0	0/0/0/0
3	HEM	D	601	1	-	0/14/114/114	0/0/8/8
3	HEM	D	602	1	-	0/14/114/114	0/0/8/8
3	HEM	D	603	1	-	0/14/114/114	0/0/8/8
3	HEM	D	604	1	-	0/14/114/114	0/0/8/8
4	FAD	D	900	-	2/2/9/9	0/34/50/50	0/1/6/6
2	SO4	D	914	-	-	0/0/0/0	0/0/0/0



The worst 5 of 221 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	800	FAD	C1'-C2'	28.57	1.78	1.51
4	D	900	FAD	C1'-C2'	27.94	1.78	1.51
4	A	600	FAD	C1'-C2'	27.75	1.78	1.51
4	B	700	FAD	C1'-C2'	27.01	1.77	1.51
3	A	601	HEM	C2B-C1B	7.37	1.46	1.44

The worst 5 of 297 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	600	FAD	O4B-C1B-N9A	-18.36	91.36	108.44
4	C	800	FAD	O5B-C5B-C4B	15.28	165.03	108.94
4	C	800	FAD	O4B-C4B-C5B	15.22	163.68	109.36
3	C	604	HEM	CBD-CAD-C3D	11.65	139.81	114.37
4	D	900	FAD	O5B-C5B-C4B	10.80	148.57	108.94

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	800	FAD	C4B
4	C	800	FAD	C4'
4	C	800	FAD	C3'
4	B	700	FAD	C4'
4	B	700	FAD	C3'

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.