



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:51 am GMT

PDB ID : 1B25
Title : FORMALDEHYDE FERREDOXIN OXIDOREDUCTASE FROM PYRO-
COCCUS FURIOSUS
Authors : Hu, Y.L.; Faham, S.; Roy, R.; Adams, M.W.W.; Rees, D.C.
Deposited on : 1998-12-04
Resolution : 1.85 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

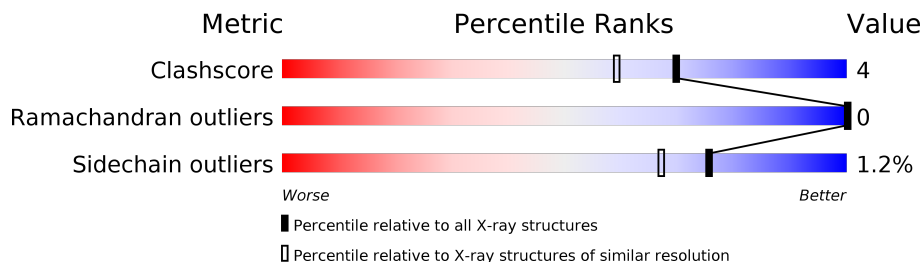
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	112137	2083 (1.86-1.86)
Ramachandran outliers	110173	2060 (1.86-1.86)
Sidechain outliers	110143	2060 (1.86-1.86)

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	619	
1	B	619	
1	C	619	
1	D	619	

2 Entry composition [i](#)

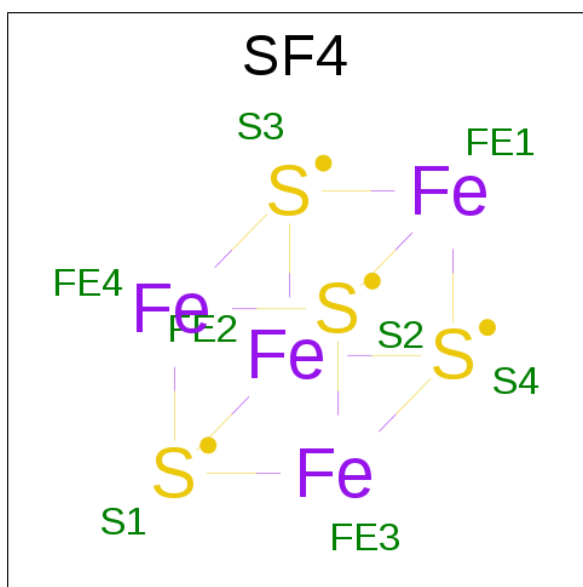
There are 4 unique types of molecules in this entry. The entry contains 20733 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (FORMALDEHYDE FERREDOXIN OXIDOREDUCTASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	611	Total	C	N	O	S	0	0	0
			4786	3067	809	888	22			
1	B	611	Total	C	N	O	S	0	0	0
			4786	3067	809	888	22			
1	C	611	Total	C	N	O	S	0	0	0
			4786	3067	809	888	22			
1	D	611	Total	C	N	O	S	0	0	0
			4786	3067	809	888	22			

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



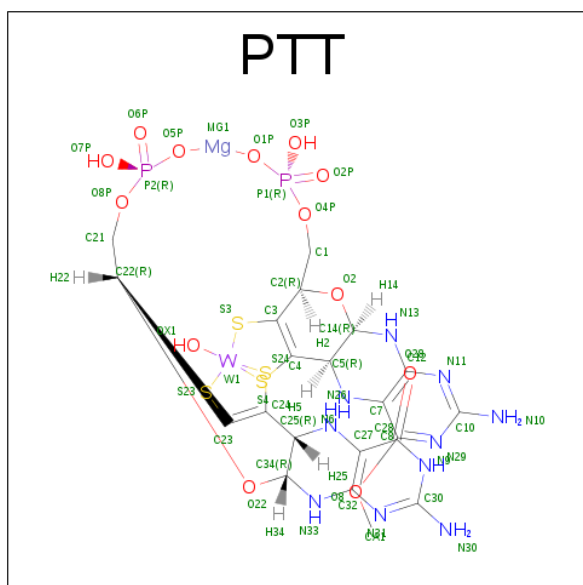
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is TUNGSTOPTERIN (three-letter code: PTT) (formula: $C_{21}H_{25}MgN_{10}O_{13}P_2S_4W$).



Mol	Chain	Residues	Atoms								ZeroOcc	AltConf
3	A	1	Total	C	Mg	N	O	P	S	W	0	0
			52	21	1	10	13	2	4	1		
3	B	1	Total	C	Mg	N	O	P	S	W	0	0
			52	21	1	10	13	2	4	1		
3	C	1	Total	C	Mg	N	O	P	S	W	0	0
			52	21	1	10	13	2	4	1		
3	D	1	Total	C	Mg	N	O	P	S	W	0	0
			52	21	1	10	13	2	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	285	Total	O	0	0
			285	285		
4	B	318	Total	O	0	0
			318	318		
4	C	393	Total	O	0	0
			393	393		

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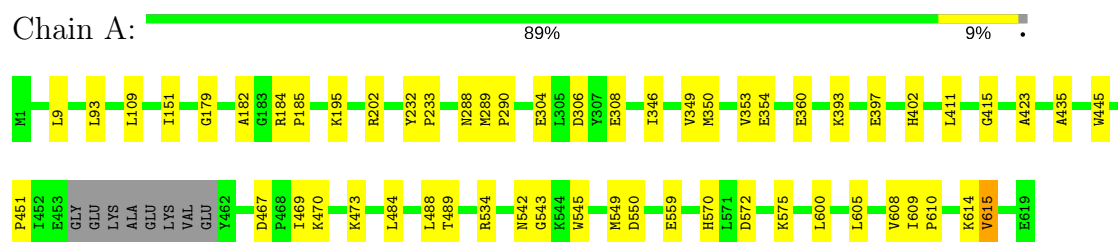
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	353	Total	O	0	0
			353	353		

3 Residue-property plots [i](#)

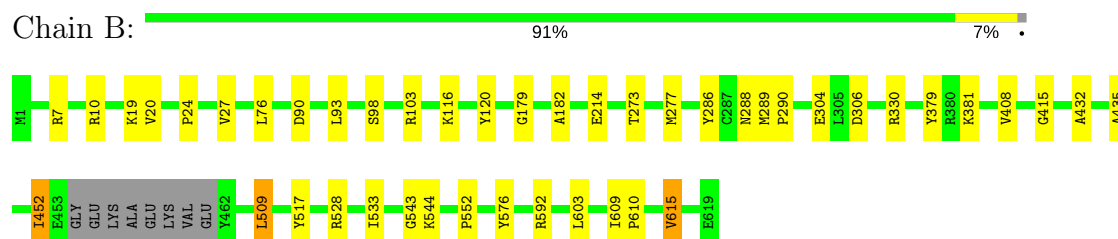
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

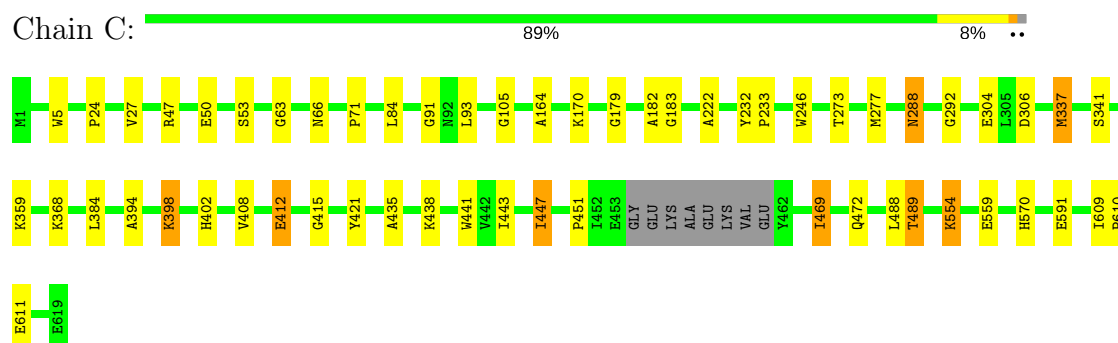
• Molecule 1: PROTEIN (FORMALDEHYDE FERREDOXIN OXIDOREDUCTASE)



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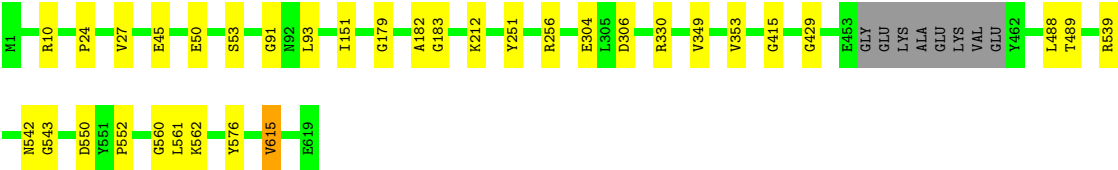


• Molecule 1: PROTEIN (FORMALDEHYDE FERREDOXIN OXIDOREDUCTASE)



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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.34Å 170.85Å 180.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.85	Depositor
% Data completeness (in resolution range)	91.4 (20.00-1.85)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.174 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	20733	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, PTT

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	0.49	0/4896	0.68	1/6619 (0.0%)
1	B	0.48	0/4896	0.69	2/6619 (0.0%)
1	C	0.52	0/4896	0.70	1/6619 (0.0%)
1	D	0.51	0/4896	0.69	2/6619 (0.0%)
All	All	0.50	0/19584	0.69	6/26476 (0.0%)

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	B	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	90	ASP	CB-CG-OD1	5.85	123.56	118.30
1	D	539	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	D	415	GLY	N-CA-C	5.43	126.67	113.10
1	A	415	GLY	N-CA-C	5.22	126.14	113.10
1	C	415	GLY	N-CA-C	5.09	125.81	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	120	TYR	Sidechain

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	4786	0	4773	39	0
1	B	4786	0	4773	30	0
1	C	4786	0	4773	44	0
1	D	4786	0	4773	26	0
2	A	8	0	0	0	0
2	B	8	0	0	1	0
2	C	8	0	0	0	0
2	D	8	0	0	1	0
3	A	52	0	22	12	0
3	B	52	0	22	12	0
3	C	52	0	22	11	0
3	D	52	0	22	13	0
4	A	285	0	0	8	0
4	B	318	0	0	11	0
4	C	393	0	0	6	0
4	D	353	0	0	8	0
All	All	20733	0	19180	160	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 4.

The worst 5 of 160 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:D:179:GLY:O	3:D:803:PTT:HA12	1.43	1.17
1:C:179:GLY:O	3:C:802:PTT:HA12	1.46	1.13
1:B:179:GLY:O	3:B:801:PTT:HA12	1.46	1.12
1:A:179:GLY:O	3:A:800:PTT:HA12	1.50	1.11
3:A:800:PTT:HA13	4:A:1084:HOH:O	1.57	1.04

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	607/619 (98%)	588 (97%)	19 (3%)	0	100	100
1	B	607/619 (98%)	588 (97%)	19 (3%)	0	100	100
1	C	607/619 (98%)	588 (97%)	19 (3%)	0	100	100
1	D	607/619 (98%)	591 (97%)	16 (3%)	0	100	100
All	All	2428/2476 (98%)	2355 (97%)	73 (3%)	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	493/499 (99%)	488 (99%)	5 (1%)	80	74
1	B	493/499 (99%)	488 (99%)	5 (1%)	80	74
1	C	493/499 (99%)	482 (98%)	11 (2%)	57	40
1	D	493/499 (99%)	491 (100%)	2 (0%)	93	91
All	All	1972/1996 (99%)	1949 (99%)	23 (1%)	75	67

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	288	ASN
1	C	384	LEU
1	D	212	LYS

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Mol	Chain	Res	Type
1	C	337	MET
1	C	398	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	288	ASN
1	A	542	ASN
1	C	66	ASN
1	C	288	ASN
1	C	372	GLN

5.3.3 RNA [i](#)

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](#)

8 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	$\# Z > 2$
2	SF4	A	700	1	0,12,12	0.00	-	0,24,24	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PTT	A	800	1,4	48,60,60	4.51	13 (27%)	33,98,98	9.06	14 (42%)
2	SF4	B	701	1	0,12,12	0.00	-	0,24,24	0.00	-
3	PTT	B	801	1,4	48,60,60	4.54	14 (29%)	33,98,98	8.76	15 (45%)
2	SF4	C	702	1	0,12,12	0.00	-	0,24,24	0.00	-
3	PTT	C	802	1,4	48,60,60	4.75	17 (35%)	33,98,98	8.75	16 (48%)
2	SF4	D	703	1	0,12,12	0.00	-	0,24,24	0.00	-
3	PTT	D	803	1,4	48,60,60	4.29	14 (29%)	33,98,98	8.06	13 (39%)

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
2	SF4	A	700	1	-	0/0/48/48	0/6/5/5
3	PTT	A	800	1,4	-	0/14/102/102	0/0/9/9
2	SF4	B	701	1	-	0/0/48/48	0/6/5/5
3	PTT	B	801	1,4	-	0/14/102/102	0/0/9/9
2	SF4	C	702	1	-	0/0/48/48	0/6/5/5
3	PTT	C	802	1,4	-	0/14/102/102	0/0/9/9
2	SF4	D	703	1	-	0/0/48/48	0/6/5/5
3	PTT	D	803	1,4	-	0/14/102/102	0/0/9/9

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	802	PTT	O2-C14	-4.06	1.37	1.43
3	C	802	PTT	O2-C2	-3.52	1.38	1.43
3	B	801	PTT	O2-C14	-3.47	1.38	1.43
3	A	800	PTT	O2-C14	-3.46	1.38	1.43
3	A	800	PTT	O22-C22	-3.28	1.39	1.43

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	800	PTT	O22-C34-C25	-14.34	99.40	108.96
3	C	802	PTT	O2-C14-C5	-11.43	101.34	108.96
3	C	802	PTT	O22-C34-C25	-9.18	102.84	108.96
3	B	801	PTT	O22-C34-C25	-7.21	104.15	108.96
3	B	801	PTT	N29-C30-N31	-4.32	118.44	125.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	800	PTT	12	0
2	B	701	SF4	1	0
3	B	801	PTT	12	0
3	C	802	PTT	11	0
2	D	703	SF4	1	0
3	D	803	PTT	13	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.