

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID : 1E0Z

Title : [2Fe-2S]-Ferredoxin from Halobacterium salinarum

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This is a wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)

NmrClust : Kelley et al. (1996)

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

wwPDB-RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

wwPDB-ShiftChecker : v1.2

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

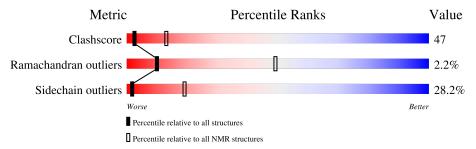
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment was not calculated.

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 $(\# \mathrm{Entries})$	m NMR archive $(# m Entries)$
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 <=5%

Mol	Chain	Length		Quality of chain				
1	A	128	29%	55%	9%	7%		



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues						
Well-defined core Residue range (total) Backbone RMSD (Å) Medoid mod						
1	A:1-A:117, (119)	A:119-A:120	0.77	6		
	(119)					

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters. No single-model clusters were found.

Cluster number	Models
1	9, 10, 11, 12, 15, 19
2	1, 5, 7, 14, 16
3	2, 4, 6, 13
4	3, 8, 20
5	17, 18



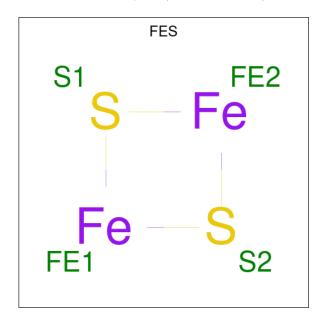
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1914 atoms, of which 908 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called FERREDOXIN.

Mol	Chain	Residues	Atoms				Trace		
1	Λ	190	Total	С	Н	N	О	S	0
1 A	128	1910	619	908	155	220	8	U	

• Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms		
9	٨	1	Total	Fe	S
	2 A	1	4	2	2

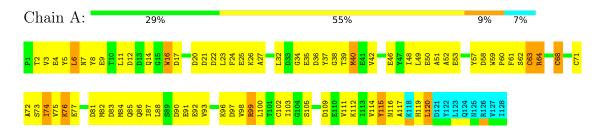


4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

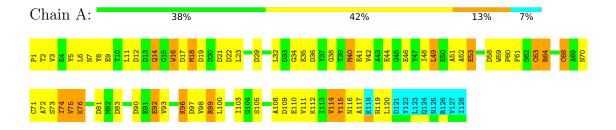
• Molecule 1: FERREDOXIN



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 6. Colouring as in section 4.1 above.

• Molecule 1: FERREDOXIN





5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: simulated annealing.

Of the 60 calculated structures, 20 were deposited, based on the following criterion: LEAST RESTRAINT VIOLATION, LOWEST ENERGY.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	3.851
NMRView	structure solution	
NDEE	structure solution	

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

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

There are no covalent bond-length or bond-angle outliers.

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	Planarity
1	A	0.0 ± 0.0	1.9 ± 0.3
All	All	0	38

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	99	ARG	Sidechain	20
1	A	64	ARG	Sidechain	18

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	918	824	824	83±11
2	A	4	0	0	2±1
All	All	18440	16480	16480	1655

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 47.

5 of 671 unique clashes are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Clash(Å)	$Distance(\mathring{A})$	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:87:ILE:HG23	1:A:88:LEU:HD23	1.01	1.26	2	2
1:A:87:ILE:O	1:A:87:ILE:HD13	0.91	1.65	3	2
1:A:102:CYS:C	1:A:103:ILE:HD13	0.90	1.87	15	1
1:A:93:VAL:HG21	1:A:99:ARG:NH2	0.87	1.84	14	1
1:A:3:VAL:HG13	1:A:40:MET:HB3	0.86	1.47	13	1

6.3 Torsion angles (i)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	118/128 (92%)	102±2 (87±2%)	13±2 (11±2%)	3±1 (2±1%)	10 49
All	All	$2360/2560 \ (92\%)$	2046 (87%)	262 (11%)	52 (2%)	10 49

5 of 17 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	74	ILE	10
1	A	109	ASP	6
1	A	32	LEU	5
1	A	48	ILE	5
1	A	72	ALA	4

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	96/104 (92%)	69±3 (72±4%)	27±3 (28±4%)	2 19		
All	All	1920/2080 (92%)	1378 (72%)	542 (28%)	2 19		



5 of 76 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	68	CYS	20
1	A	63	CYS	19
1	A	115	TYR	19
1	A	6	LEU	17
1	A	99	ARG	15

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Trmo	Chain	Peg	Link		Bond lengths Counts RMSZ 7		
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	#Z>2	
1	ALY	A	118	1	10,11,12	0.80 ± 0.01	0±0 (0±0%)	

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mal	Tuno	Chain	Peg	Link		Bond angles			
IVIOI	туре	Chain	nes	Lilik	$\begin{array}{c c} \textbf{Bond angles} \\ \textbf{Counts} & \textbf{RMSZ} & \#\textbf{Z}{>}2 \end{array}$		#Z>2		
1	ALY	A	118	1	7,12,14	2.14 ± 0.73	$2\pm0 \ (27\pm4\%)$		

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
1	ALY	A	118	1	-	$0\pm0,9,10,12$	-

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mal	Chain	Dog	Ттто	Atoma	$oxed{Atoms} oxed{f Z} oxed{f Observed}({}^o)$	Ideal(0)	Mod	dels	
MIOI	Chain	nes	Туре	Atoms	L	Observed()	ideai()	Worst	Total
1	A	118	ALY	CE-NZ-CH	8.81	109.01	122.56	19	18
1	A	118	ALY	CD-CE-NZ	2.60	104.79	112.21	19	20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mal	Type	Chain	Pos	Link	В	Bond lengths	
IVIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	#Z>2
2	FES	A	130	1	0,4,4	0.00 ± 0.00	-

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard



deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Pog	Link	Bo	nd angl	es
WIOI	Type	Chain	rtes	Lilik	Bo Counts	RMSZ	#Z>2
2	FES	A	130	1	-	-	-

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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FES	A	130	1	=	-	$0\pm0,1,1,1$

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

No chemical shift data were provided

