



Full wwPDB NMR Structure Validation Report ⓘ

Apr 15, 2026 – 10:32 AM UTC

PDB ID : 2LK6 / pdb_00002lk6
BMRB ID : 17997
Title : NMR determination of the global structure of the Cd-113 derivative of desulforedoxin
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Deposited on : 2011-10-07

This is a Full wwPDB NMR Structure Validation 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 26%.

There are no overall percentile quality scores available for this entry.

The sequence quality summary graphics cannot be shown.

2 Ensemble composition and analysis

This entry contains 18 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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 model
1	A:3-A:36, B:1-B:36 (70)	0.34	17

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 3 clusters and 5 single-model clusters were found.

Cluster number	Models
1	1, 8, 9, 16, 18
2	2, 7, 15, 17
3	4, 10, 13, 14
Single-model clusters	3; 5; 6; 11; 12

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1016 atoms, of which 494 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Desulforedoxin.

Mol	Chain	Residues	Atoms						Trace
1	A	36	Total	C	H	N	O	S	0
			507	158	247	42	55	5	
1	B	36	Total	C	H	N	O	S	0
			507	158	247	42	55	5	

- Molecule 2 is CADMIUM ION (CCD ID: CD) (formula: Cd).

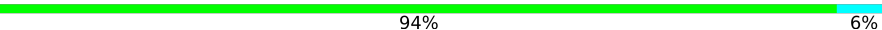
Mol	Chain	Residues	Atoms	
2	A	1	Total	Cd
			1	1
2	B	1	Total	Cd
			1	1

4 Residue-property plots

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: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

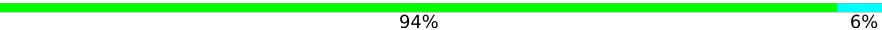
There are no outlier residues in this chain.

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.2 Score per residue for model 2

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.3 Score per residue for model 3

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



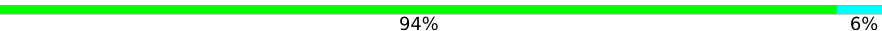
- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

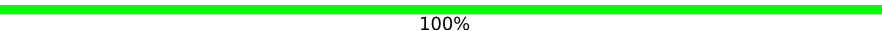
4.2.4 Score per residue for model 4

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

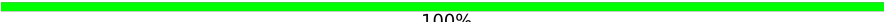
4.2.5 Score per residue for model 5

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.6 Score per residue for model 6

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

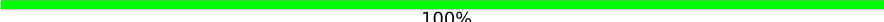
4.2.7 Score per residue for model 7

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.8 Score per residue for model 8

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.9 Score per residue for model 9

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.10 Score per residue for model 10

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.11 Score per residue for model 11

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



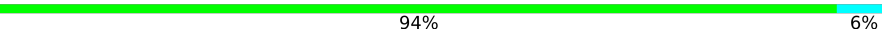
- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.12 Score per residue for model 12

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



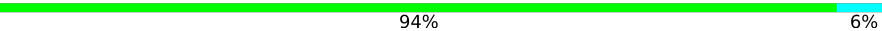
- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.13 Score per residue for model 13

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



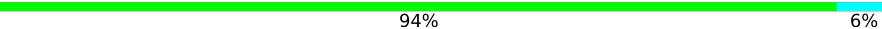
- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.14 Score per residue for model 14

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

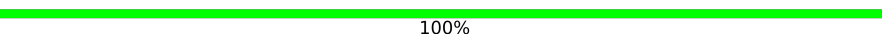
4.2.15 Score per residue for model 15

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

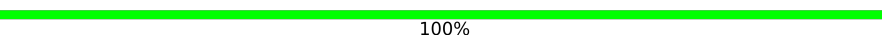
4.2.16 Score per residue for model 16

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



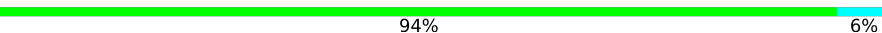
- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

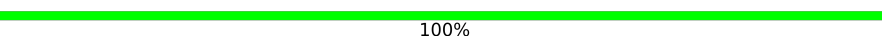
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

4.2.18 Score per residue for model 18

- Molecule 1: Desulforedoxin

Chain A:  94% 6%



- Molecule 1: Desulforedoxin

Chain B:  100%

There are no outlier residues in this chain.

5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 300 calculated structures, 18 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
DIANA	structure solution	2.8
DIANA	refinement	2.8

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	234
Number of shifts mapped to atoms	234
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	26%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.3 RNA [i](#)

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

6.5 Carbohydrates [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.6 Ligand geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.7 Other polymers [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 26% for the well-defined parts and 27% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	234
Number of shifts mapped to atoms	234
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 26%, i.e. 224 atoms were assigned a chemical shift out of a possible 855. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	74/362 (20%)	74/152 (49%)	0/140 (0%)	0/70 (0%)
Sidechain	146/475 (31%)	146/307 (48%)	0/157 (0%)	0/11 (0%)
Aromatic	4/18 (22%)	4/8 (50%)	0/10 (0%)	0/0 (—%)
Overall	224/855 (26%)	224/467 (48%)	0/307 (0%)	0/81 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 27%, i.e. 234 atoms were assigned a chemical shift out of a possible 876. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	77/372 (21%)	77/156 (49%)	0/144 (0%)	0/72 (0%)
Sidechain	153/486 (31%)	153/314 (49%)	0/160 (0%)	0/12 (0%)
Aromatic	4/18 (22%)	4/8 (50%)	0/10 (0%)	0/0 (—%)
Overall	234/876 (27%)	234/478 (49%)	0/314 (0%)	0/84 (0%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

