



wwPDB NMR Structure Validation Summary Report ⓘ

Apr 26, 2016 – 06:50 PM BST

PDB ID : 1ZRP
Title : SOLUTION-STATE STRUCTURE BY NMR OF ZINC-SUBSTITUTED RUBREDOXIN FROM THE MARINE HYPERTHERMOPHILIC ARCHAE-BACTERIUM PYROCOCCLUS FURIOSUS
Authors : Blake, P.R.; Park, J.B.; Zhou, Z.H.; Hare, D.R.; Adams, M.W.W.; Summers, M.F.
Deposited on : 1992-07-10

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
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

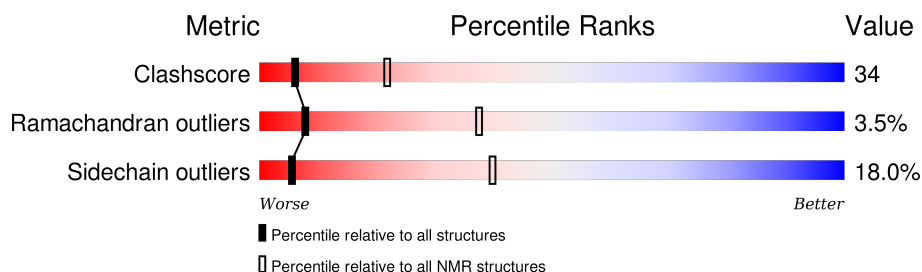
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 97%.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	53	

2 Ensemble composition and analysis

This entry contains 40 models. Model 9 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 model
1	A:1-A:50 (50)	0.23	9

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 6 clusters and 5 single-model clusters were found.

Cluster number	Models
1	1, 4, 5, 6, 7, 8, 9, 10, 13, 14, 15, 16, 17, 18, 21, 23, 24, 25, 27, 28, 35, 36, 39, 40
2	32, 34, 37
3	12, 26
4	30, 33
5	2, 3
6	31, 38
Single-model clusters	11; 19; 20; 22; 29

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 789 atoms, of which 375 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RUBREDOXIN.

Mol	Chain	Residues	Atoms							Trace
1	A	53	Total	C	H	N	O	S		0
			788	262	375	61	86	4		

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

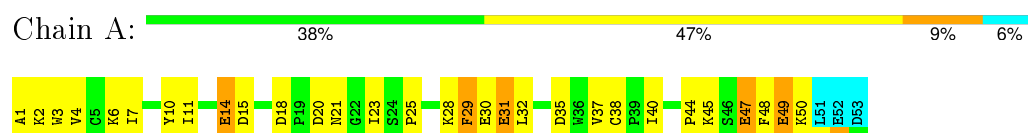
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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.

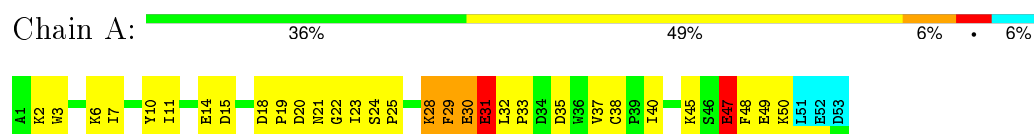
- Molecule 1: RUBREDOXIN



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

The representative model is number 9. Colouring as in section 4.1 above.

- Molecule 1: RUBREDOXIN



5 Refinement protocol and experimental data overview

Of the ? calculated structures, 40 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
DSPACE	refinement	

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)	BMRB entry 5601
Number of chemical shift lists	3
Total number of shifts	1239
Number of shifts mapped to atoms	660
Number of unparsed shifts	0
Number of shifts with mapping errors	579
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	97%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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: ZN

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 (average) 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	0.83±0.00	5±0/400 (1.2±0.0%)	1.12±0.00	7±0/545 (1.3±0.0%)
All	All	0.83	200/16000 (1.2%)	1.12	280/21800 (1.3%)

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	2.3±1.0
All	All	0	91

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	30	GLU	CB-CG	-5.28	1.42	1.52	32	40
1	A	49	GLU	CB-CG	-5.25	1.42	1.52	32	40
1	A	47	GLU	CB-CG	-5.24	1.42	1.52	14	40
1	A	14	GLU	CB-CG	-5.24	1.42	1.52	20	40
1	A	31	GLU	CB-CG	-5.23	1.42	1.52	14	40

5 of 7 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	29	PHE	CB-CG-CD1	-5.83	116.72	120.80	30	40
1	A	48	PHE	CB-CG-CD2	-5.51	116.94	120.80	3	40
1	A	31	GLU	CA-CB-CG	5.31	125.08	113.40	28	40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	47	GLU	CA-CB-CG	5.17	124.77	113.40	14	40
1	A	49	GLU	CA-CB-CG	5.17	124.77	113.40	24	40

There are no chirality outliers.

5 of 12 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	38	CYS	Mainchain	40
1	A	4	VAL	Mainchain	12
1	A	5	CYS	Mainchain	11
1	A	15	ASP	Mainchain	9
1	A	13	ASP	Mainchain	6

6.2 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 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	387	354	354	25±4
All	All	15520	14160	14160	1001

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 34.

5 of 147 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:ILE:HD11	1:A:47:GLU:HB3	0.82	1.51	24	18
1:A:7:ILE:HD11	1:A:47:GLU:CB	0.80	2.04	22	20
1:A:27:THR:HG21	1:A:32:LEU:HD23	0.80	1.52	30	2
1:A:17:GLY:HA2	1:A:23:ILE:HG22	0.76	1.57	38	2
1:A:4:VAL:HG23	1:A:11:ILE:CD1	0.76	2.10	26	13

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	49/53 (92%)	41±1 (84±2%)	6±1 (13±3%)	2±1 (3±2%)	8	37
All	All	1960/2120 (92%)	1644 (84%)	248 (13%)	68 (3%)	8	37

All 5 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	25	PRO	37
1	A	44	PRO	14
1	A	26	GLY	11
1	A	15	ASP	5
1	A	49	GLU	1

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	42/45 (93%)	34±2 (82±5%)	8±2 (18±5%)	5	40
All	All	1680/1800 (93%)	1378 (82%)	302 (18%)	5	40

5 of 21 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	45	LYS	31
1	A	50	LYS	30
1	A	35	ASP	23
1	A	6	LYS	22
1	A	2	LYS	21

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

The completeness of assignment taking into account all chemical shift lists is 97% for the well-defined parts and 97% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5601

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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	677
Number of shifts mapped to atoms	660
Number of unparsed shifts	0
Number of shifts with mapping errors	17
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. First 5 (of 17) occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	1	FME	CN	167.25	0.1	1
A	1	FME	N	129.2	0.05	1
A	1	FME	HB3	2.0	0.01	2
A	1	FME	CB	33.1	0.1	1
A	1	FME	HCN	8.19	0.01	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	54	0.47 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	49	0.85 ± 0.30	Should be applied
$^{13}\text{C}'$	54	-0.06 ± 0.29	None needed (< 0.5 ppm)

Continued on next page...

Continued from previous page...

Nucleus	# values	Correction \pm precision, ppm	Suggested action
^{15}N	54	-1.65 \pm 0.53	Should be applied

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 97%, i.e. 561 atoms were assigned a chemical shift out of a possible 577. 1 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	240/240 (100%)	95/95 (100%)	100/100 (100%)	45/45 (100%)
Sidechain	271/279 (97%)	165/166 (99%)	105/107 (98%)	1/6 (17%)
Aromatic	50/58 (86%)	30/30 (100%)	18/26 (69%)	2/2 (100%)
Overall	561/577 (97%)	290/291 (100%)	223/233 (96%)	48/53 (91%)

7.1.4 Statistically unusual chemical shifts [i](#)

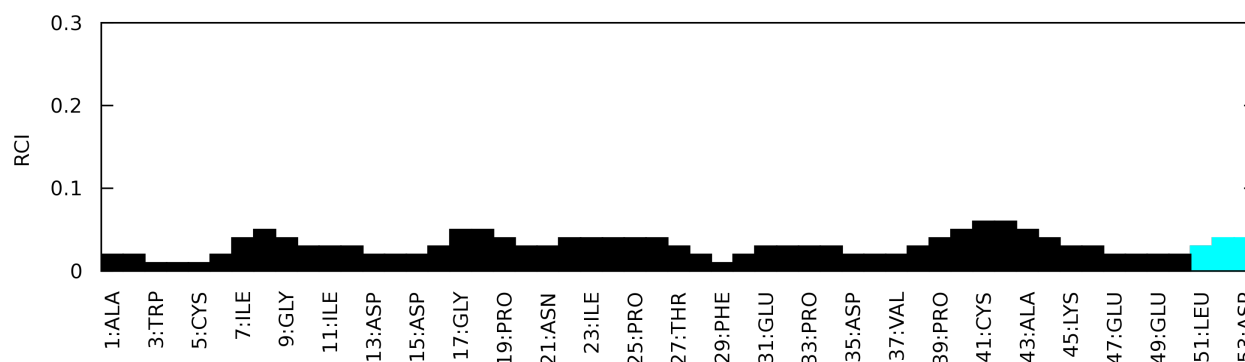
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	32	LEU	HD13	-1.76	2.16 – -0.64	-9.0
1	A	32	LEU	HD11	-1.76	2.16 – -0.64	-9.0
1	A	32	LEU	HD12	-1.76	2.16 – -0.64	-9.0
1	A	50	LYS	HB3	0.01	3.10 – 0.40	-6.4

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.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: BMRB entry 5601

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	281
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	281
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Chain not found in structure. First 5 (of 281) occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	45	PRO	CA	61.48	-1.0	1
UNMAPPED	38	VAL	H	6.17	-1.0	1
UNMAPPED	10	GLY	N	113.6	-1.0	1
UNMAPPED	8	ILE	H	9.08	-1.0	1
UNMAPPED	12	ILE	CB	38.78	-1.0	1

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	53	0.00 \pm 0.00	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	48	0.00 \pm 0.00	None needed (< 0.5 ppm)
$^{13}\text{C}'$	46	0.00 \pm 0.00	None needed (< 0.5 ppm)
^{15}N	48	0.00 \pm 0.00	None needed (< 0.5 ppm)

7.2.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 577. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	0/240 (0%)	0/95 (0%)	0/100 (0%)	0/45 (0%)
Sidechain	0/279 (0%)	0/166 (0%)	0/107 (0%)	0/6 (0%)
Aromatic	0/58 (0%)	0/30 (0%)	0/26 (0%)	0/2 (0%)
Overall	0/577 (0%)	0/291 (0%)	0/233 (0%)	0/53 (0%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_2). RCI is only applicable to proteins.

7.3 Chemical shift list 3

File name: BMRB entry 5601

Chemical shift list name: *assigned_chem_shift_list_3*

7.3.1 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	281
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	281

Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Chain not found in structure. First 5 (of 281) occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	12	TYR	CA	57.34	-1.0	1
UNMAPPED	21	ASN	H	7.67	-1.0	1
UNMAPPED	47	GLU	HA	4.76	-1.0	1
UNMAPPED	12	TYR	N	127.38	-1.0	5
UNMAPPED	35	ASP	N	114.26	-1.0	1

7.3.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	53	0.00 \pm 0.00	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	48	0.00 \pm 0.00	None needed (< 0.5 ppm)
$^{13}\text{C}'$	46	0.00 \pm 0.00	None needed (< 0.5 ppm)
^{15}N	48	0.00 \pm 0.00	None needed (< 0.5 ppm)

7.3.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 577. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	0/240 (0%)	0/95 (0%)	0/100 (0%)	0/45 (0%)
Sidechain	0/279 (0%)	0/166 (0%)	0/107 (0%)	0/6 (0%)
Aromatic	0/58 (0%)	0/30 (0%)	0/26 (0%)	0/2 (0%)
Overall	0/577 (0%)	0/291 (0%)	0/233 (0%)	0/53 (0%)

7.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.3.5 Random Coil Index (RCI) plots

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_3). RCI is only applicable to proteins.