wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2MZ9
Title	:	Solution structure of oxidized triheme cytochrome PpcA from Geobacter sulfurreducens
Authors	:	Morgado, L.; Bruix, M.; Pokkuluri, R.; Salgueiro, C.A.; Turner, D.L.
Deposited on	:	2015-02-08

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 (i) symbol.

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

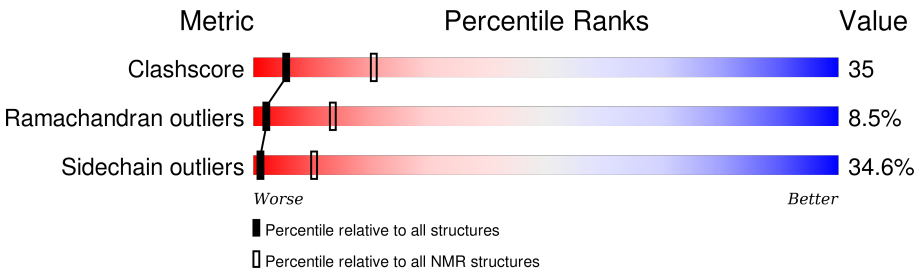
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	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 (i)

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

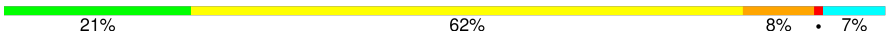
The overall completeness of chemical shifts assignment is 47%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	71	

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:2-A:23, A:28-A:71 (66)	0.31	10

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 2 clusters. No single-model clusters were found.

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

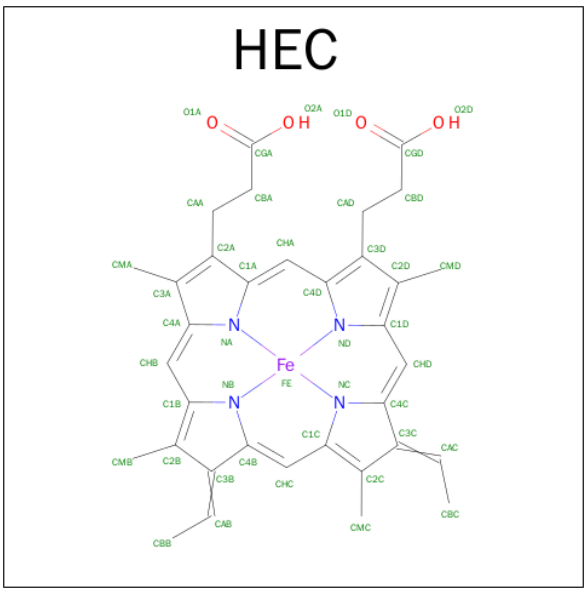
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1166 atoms, of which 502 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PpcA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	71	1037	331	502	102	94	8	0

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



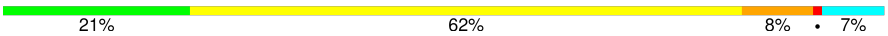
Mol	Chain	Residues	Atoms				
			Total	C	Fe	N	O
2	A	1	43	34	1	4	4
2	A	1	43	34	1	4	4
2	A	1	43	34	1	4	4

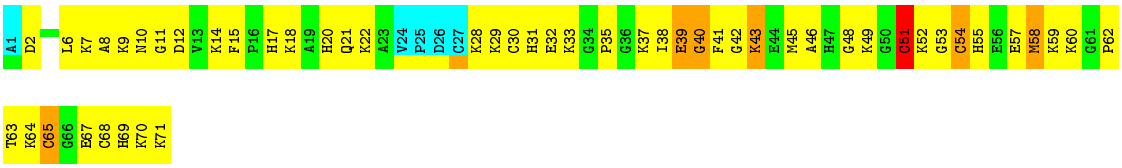
4 Residue-property plots (i)

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: PpcA

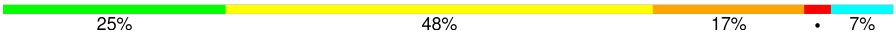
Chain A: 

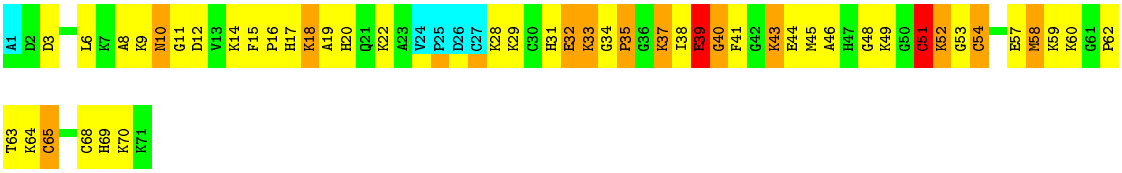


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 10. Colouring as in section 4.1 above.

- Molecule 1: PpcA

Chain A: 



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 500 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
PARADYANA	structure solution	
PARADYANA	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)	2mz9_cs.str
Number of chemical shift lists	1
Total number of shifts	504
Number of shifts mapped to atoms	445
Number of unparsed shifts	0
Number of shifts with mapping errors	59
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	47%

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: HEC

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	502	476	510	37±7
2	A	129	0	90	20±5
All	All	12620	9520	12000	869

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 35.

5 of 267 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:PRO:HG2	2:A:102:HEC:HMA3	0.89	1.40	7	7
1:A:8:ALA:HB3	1:A:11:GLY:O	0.89	1.68	9	19
2:A:102:HEC:HMC1	2:A:102:HEC:HBC3	0.88	1.46	18	2
2:A:101:HEC:HMB1	2:A:101:HEC:HBB2	0.87	1.47	19	9
2:A:101:HEC:HBB2	2:A:101:HEC:HMB1	0.87	1.46	3	6

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	65/71 (92%)	43±3 (66±5%)	17±3 (26±5%)	6±2 (8±3%)	2 13
All	All	1300/1420 (92%)	856 (66%)	334 (26%)	110 (8%)	2 13

5 of 19 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	51	CYS	19
1	A	39	GLU	17
1	A	35	PRO	14
1	A	40	GLY	13
1	A	33	LYS	8

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	52/56 (93%)	34±3 (65±6%)	18±3 (35±6%)	1 10
All	All	1040/1120 (93%)	680 (65%)	360 (35%)	1 10

5 of 36 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	65	CYS	20
1	A	43	LYS	20
1	A	51	CYS	19
1	A	45	MET	19
1	A	54	CYS	18

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)

3 ligands are 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	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	HEC	A	101	1	24,50,50	1.83±0.05	2±0 (8±0%)
2	HEC	A	102	1	24,50,50	1.80±0.04	2±0 (8±0%)
2	HEC	A	103	1	24,50,50	1.76±0.03	2±0 (8±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.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	HEC	A	101	1	19,82,82	2.33±0.01	2±0 (10±0%)
2	HEC	A	102	1	19,82,82	2.33±0.00	2±0 (10±0%)
2	HEC	A	103	1	19,82,82	2.33±0.00	2±0 (10±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
2	HEC	A	101	1	-	0±0,6,54,54	0±0,0,8,8
2	HEC	A	102	1	-	0±0,6,54,54	0±0,0,8,8
2	HEC	A	103	1	-	0±0,6,54,54	0±0,0,8,8

5 of 6 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
2	A	102	HEC	C3B-C2B	5.27	1.35	1.40	6	20
2	A	101	HEC	C3C-C2C	5.26	1.35	1.40	19	20
2	A	103	HEC	C3C-C2C	5.25	1.35	1.40	4	19
2	A	103	HEC	C3B-C2B	5.24	1.35	1.40	6	20
2	A	102	HEC	C3C-C2C	5.23	1.35	1.40	12	20

5 of 6 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	101	HEC	CBB-CAB-C3B	6.13	113.93	127.34	5	20
2	A	103	HEC	CBB-CAB-C3B	6.13	113.94	127.34	6	20
2	A	101	HEC	CBC-CAC-C3C	6.13	113.95	127.34	7	20
2	A	103	HEC	CBC-CAC-C3C	6.13	113.95	127.34	3	20
2	A	102	HEC	CBC-CAC-C3C	6.12	113.95	127.34	13	20

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)

The completeness of assignment taking into account all chemical shift lists is 47% for the well-defined parts and 47% for the entire structure.

7.1 Chemical shift list 1

File name: 2mz9_cs.str

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	504
Number of shifts mapped to atoms	445
Number of unparsed shifts	0
Number of shifts with mapping errors	59
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	85

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

- Residue not found in structure. First 5 (of 59) occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	168	HEC	HHD	1.212	0.003	1
A	130	HEC	HAB	0.91	0.005	1
A	154	HEC	HAA1	3.685	0.01	1
A	168	HEC	HBA1	-0.853	0.007	1
A	130	HEC	HBA2	-0.414	0.012	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	—
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	0	—	—

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Nucleus	# values	Correction ± precision, *ppm*	Suggested action
^{15}N	63	-0.08 ± 0.56	None needed (< 0.5 ppm)

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 47%, i.e. 377 atoms were assigned a chemical shift out of a possible 809. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	187/324 (58%)	127/129 (98%)	0/132 (0%)	60/63 (95%)
Sidechain	185/425 (44%)	185/257 (72%)	0/149 (0%)	0/19 (0%)
Aromatic	5/60 (8%)	5/34 (15%)	0/20 (0%)	0/6 (0%)
Overall	377/809 (47%)	317/420 (75%)	0/301 (0%)	60/88 (68%)

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	55	HIS	HB3	19.33	5.00 – 1.10	41.7
1	A	47	HIS	HB3	18.08	5.00 – 1.10	38.5
1	A	55	HIS	HB2	16.22	4.91 – 1.31	36.4
1	A	47	HIS	HB2	15.25	4.91 – 1.31	33.7
1	A	17	HIS	HB3	15.70	5.00 – 1.10	32.4
1	A	31	HIS	HB3	12.90	5.00 – 1.10	25.2
1	A	17	HIS	HB2	11.35	4.91 – 1.31	22.9
1	A	69	HIS	HB3	11.97	5.00 – 1.10	22.9
1	A	13	VAL	HG23	6.50	2.20 – -0.60	20.3
1	A	13	VAL	HG22	6.50	2.20 – -0.60	20.3
1	A	13	VAL	HG21	6.50	2.20 – -0.60	20.3
1	A	31	HIS	HB2	10.29	4.91 – 1.31	19.9
1	A	46	ALA	HB2	-3.38	2.61 – 0.11	-19.0
1	A	46	ALA	HB3	-3.38	2.61 – 0.11	-19.0
1	A	46	ALA	HB1	-3.38	2.61 – 0.11	-19.0
1	A	61	GLY	HA2	-2.60	5.87 – 2.07	-17.3
1	A	20	HIS	HB3	9.63	5.00 – 1.10	16.9
1	A	69	HIS	HB2	8.53	4.91 – 1.31	15.1
1	A	69	HIS	HA	10.51	6.81 – 2.41	13.4

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Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	31	HIS	HA	10.23	6.81 – 2.41	12.8
1	A	8	ALA	HB3	4.33	2.61 – 0.11	11.9
1	A	8	ALA	HB1	4.33	2.61 – 0.11	11.9
1	A	8	ALA	HB2	4.33	2.61 – 0.11	11.9
1	A	51	CYS	HA	-1.92	7.47 – 1.87	-11.8
1	A	65	CYS	HA	-1.39	7.47 – 1.87	-10.8
1	A	18	LYS	HB3	4.59	3.10 – 0.40	10.5
1	A	43	LYS	HA	-0.12	6.46 – 2.06	-9.9
1	A	18	LYS	HB2	4.15	3.03 – 0.53	9.5
1	A	43	LYS	HG2	3.83	2.67 – 0.07	9.5
1	A	16	PRO	HA	7.38	6.05 – 2.75	9.0
1	A	55	HIS	HA	8.56	6.81 – 2.41	9.0
1	A	43	LYS	HB2	-0.44	3.03 – 0.53	-8.9
1	A	3	ASP	HA	7.28	6.15 – 3.05	8.6
1	A	17	HIS	HA	8.38	6.81 – 2.41	8.6
1	A	2	ASP	HA	7.25	6.15 – 3.05	8.5
1	A	65	CYS	HB2	-0.85	5.20 – 0.70	-8.5
1	A	47	HIS	HA	8.27	6.81 – 2.41	8.3
1	A	20	HIS	HB2	6.07	4.91 – 1.31	8.2
1	A	35	PRO	HB2	-0.79	3.82 – 0.32	-8.2
1	A	11	GLY	HA3	6.96	5.80 – 2.00	8.1
1	A	18	LYS	H	12.97	11.24 – 5.14	7.8
1	A	36	GLY	HA2	1.01	5.87 – 2.07	-7.8
1	A	12	ASP	HA	6.99	6.15 – 3.05	7.7
1	A	38	ILE	HG12	4.30	3.27 – -0.73	7.6
1	A	20	HIS	HA	7.92	6.81 – 2.41	7.5
1	A	18	LYS	HA	7.45	6.46 – 2.06	7.2
1	A	21	GLN	HG3	4.37	3.75 – 0.85	7.1
1	A	4	ILE	HG13	4.08	3.26 – -0.84	7.0
1	A	62	PRO	HG2	-0.23	3.48 – 0.38	-7.0
1	A	18	LYS	HD2	3.16	2.76 – 0.46	6.7
1	A	19	ALA	HB1	3.02	2.61 – 0.11	6.6
1	A	19	ALA	HB3	3.02	2.61 – 0.11	6.6
1	A	19	ALA	HB2	3.02	2.61 – 0.11	6.6
1	A	41	PHE	HE2	5.00	8.69 – 5.49	-6.5
1	A	18	LYS	HG2	3.06	2.67 – 0.07	6.5
1	A	2	ASP	HB3	4.49	4.07 – 1.27	6.5
1	A	41	PHE	HE1	5.01	8.69 – 5.49	-6.5
1	A	16	PRO	HB3	4.34	3.81 – 0.21	6.5
1	A	52	LYS	HE2	4.14	3.87 – 1.97	6.4
1	A	18	LYS	HG3	3.15	2.76 – -0.04	6.4
1	A	41	PHE	HZ	4.35	9.11 – 4.91	-6.3

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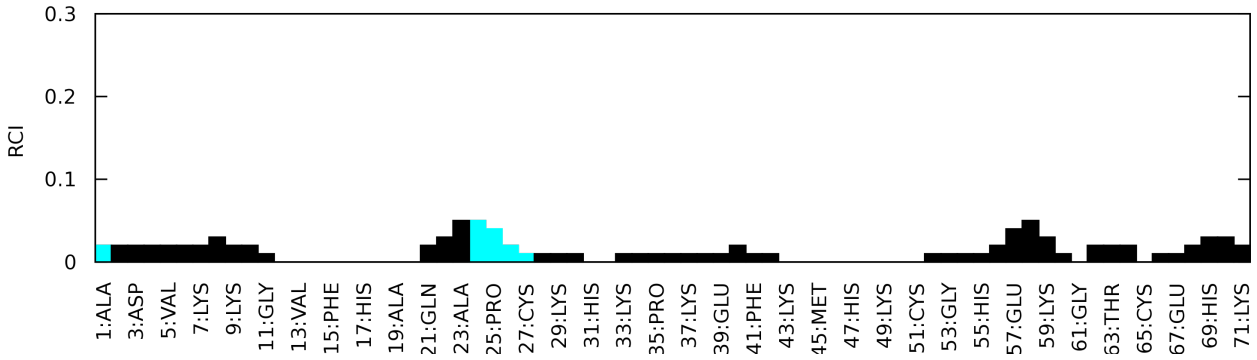
Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	35	PRO	HB3	-0.27	3.81 – 0.21	-6.3
1	A	54	CYS	HB2	0.11	5.20 – 0.70	-6.3
1	A	51	CYS	HB2	0.13	5.20 – 0.70	-6.3
1	A	50	GLY	HA2	1.60	5.87 – 2.07	-6.2
1	A	21	GLN	HG2	0.67	3.67 – 0.97	-6.1
1	A	43	LYS	HE3	4.07	3.86 – 1.96	6.1
1	A	18	LYS	HE2	4.07	3.87 – 1.97	6.0
1	A	62	PRO	HD2	1.50	5.45 – 1.85	-6.0
1	A	33	LYS	HE3	4.01	3.86 – 1.96	5.8
1	A	46	ALA	HA	1.73	6.46 – 2.06	-5.8
1	A	20	HIS	H	12.11	11.68 – 4.78	5.6
1	A	35	PRO	HA	6.24	6.05 – 2.75	5.6
1	A	30	CYS	HB2	0.47	5.20 – 0.70	-5.5
1	A	42	GLY	H	4.70	11.63 – 5.03	-5.5
1	A	50	GLY	HA3	1.83	5.80 – 2.00	-5.4
1	A	31	HIS	H	11.95	11.68 – 4.78	5.4
1	A	21	GLN	HB3	3.46	3.37 – 0.67	5.3
1	A	56	GLU	HG3	3.33	3.31 – 1.21	5.1
1	A	51	CYS	H	4.99	11.75 – 5.05	-5.1
1	A	63	THR	HG21	2.30	2.29 – -0.01	5.1
1	A	63	THR	HG23	2.30	2.29 – -0.01	5.1
1	A	63	THR	HG22	2.30	2.29 – -0.01	5.1
1	A	51	CYS	HB3	0.54	5.25 – 0.55	-5.0
1	A	47	HIS	H	11.69	11.68 – 4.78	5.0

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:


RCI
0.3
0.2
0.1
0
1:ALA
3:ASP
5:VAL
7:LYS
9:LYS
11:GLY
13:VAL
15:PHE
17:HIS
19:ALA
21:GLN
23:ALA
25:PRO
27:CYS
29:LYS
31:HIS
33:LYS
35:PRO
37:LYS
39:GLU
41:PHE
43:LYS
45:MET
47:HIS
49:LYS
51:CYS
53:GLY
55:HIS
57:GLU
59:LYS
61:GLY
63:THR
65:CYS
67:GLU
69:HIS
71:LYS