



Full wwPDB NMR Structure Validation Report ⓘ

Nov 2, 2021 – 08:57 AM EDT

PDB ID : 2IPA
Title : solution structure of Trx-ArsC complex
Authors : Jin, C.; Hu, Y.; Li, Y.; Zhang, X.
Deposited on : 2006-10-12

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

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.23.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

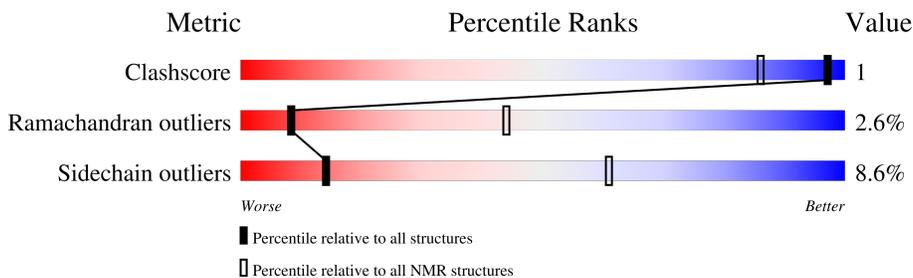
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

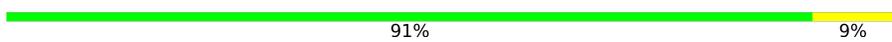
The overall completeness of chemical shifts assignment was not calculated.

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 (#Entries)	NMR archive (#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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	104	 91% 9%
2	B	139	 89% 8% ..

2 Ensemble composition and analysis

This entry contains 21 models. Model 1 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:104, B:1-B:82, B:86-B:139 (240)	0.40	1

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 and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 17, 18, 20
2	19, 21
Single-model clusters	11

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3743 atoms, of which 1853 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Thioredoxin.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	104	1604	509	807	124	159	5	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	SER	CYS	engineered mutation	UNP P14949

- Molecule 2 is a protein called Protein arsC.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
2	B	139	2139	682	1046	190	216	5	0

There are 3 discrepancies between the modelled and reference sequences:

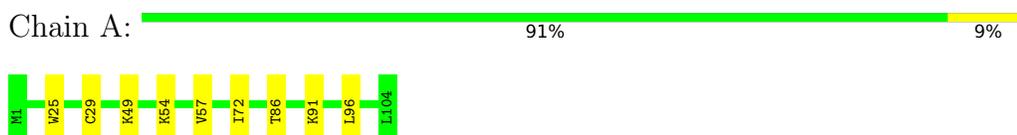
Chain	Residue	Modelled	Actual	Comment	Reference
B	10	SER	CYS	engineered mutation	UNP P45947
B	15	ALA	CYS	engineered mutation	UNP P45947
B	82	SER	CYS	engineered mutation	UNP P45947

4 Residue-property plots [i](#)

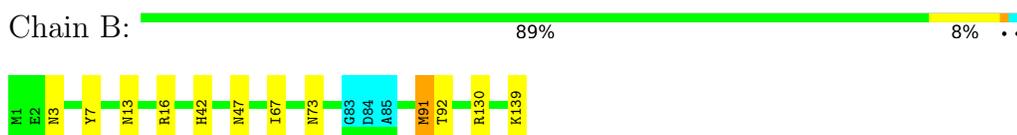
4.1 Average score per residue in the NMR ensemble

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: Thioredoxin



- Molecule 2: Protein arsC

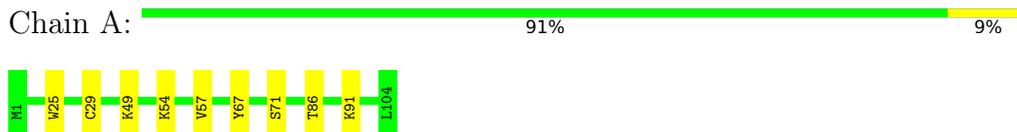


4.2 Scores per residue for each member of the ensemble

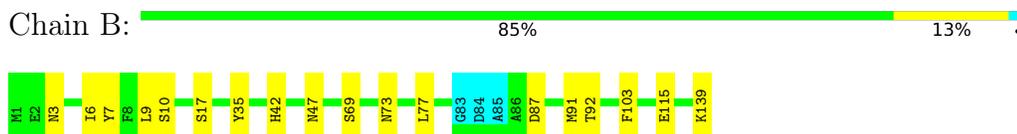
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Thioredoxin

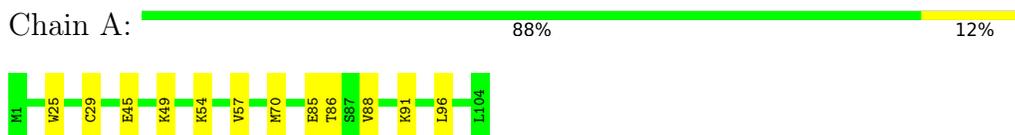


- Molecule 2: Protein arsC

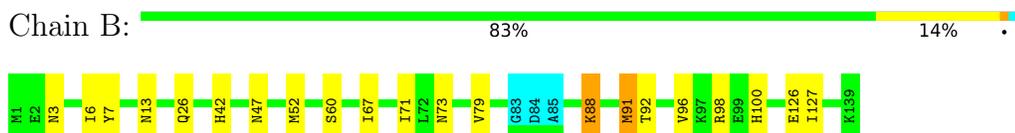


4.2.2 Score per residue for model 2

- Molecule 1: Thioredoxin

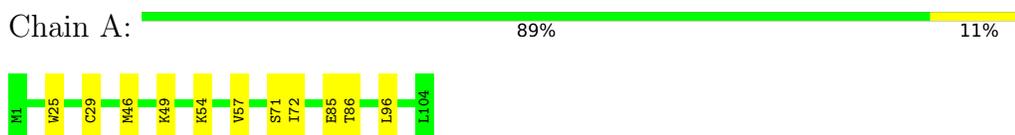


- Molecule 2: Protein arsC

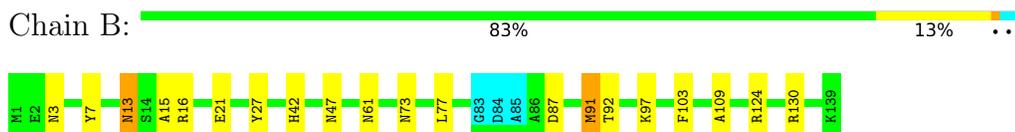


4.2.3 Score per residue for model 3

- Molecule 1: Thioredoxin

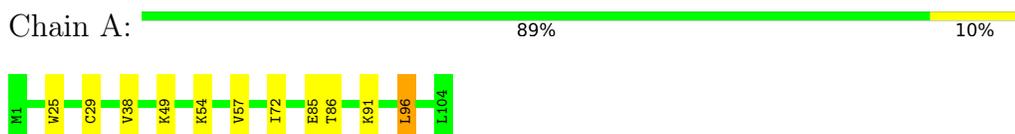


- Molecule 2: Protein arsC

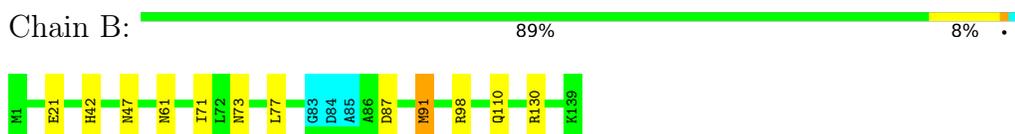


4.2.4 Score per residue for model 4

- Molecule 1: Thioredoxin

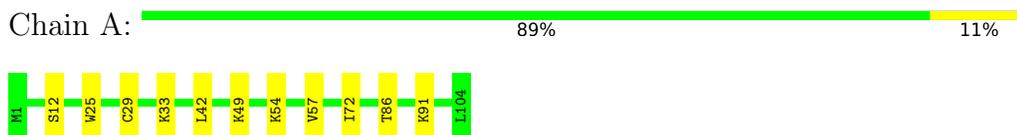


- Molecule 2: Protein arsC

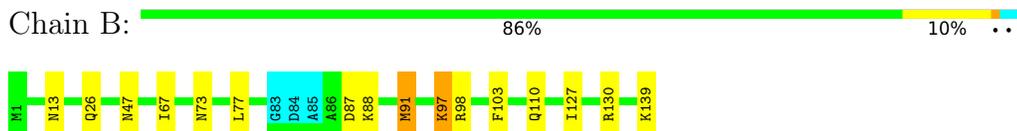


4.2.5 Score per residue for model 5

- Molecule 1: Thioredoxin

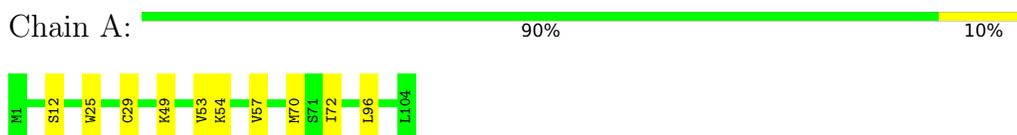


- Molecule 2: Protein arsC

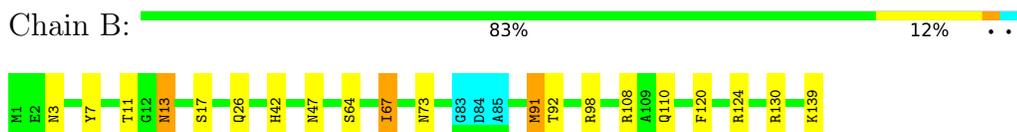


4.2.6 Score per residue for model 6

- Molecule 1: Thioredoxin

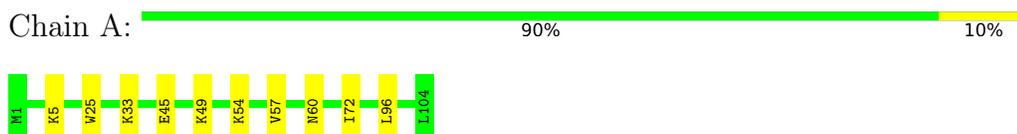


- Molecule 2: Protein arsC

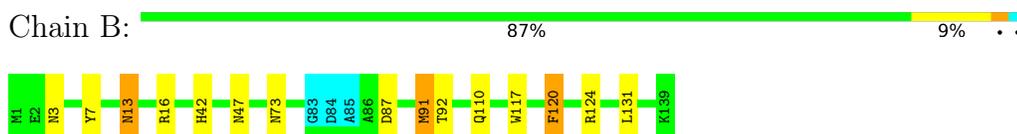


4.2.7 Score per residue for model 7

- Molecule 1: Thioredoxin

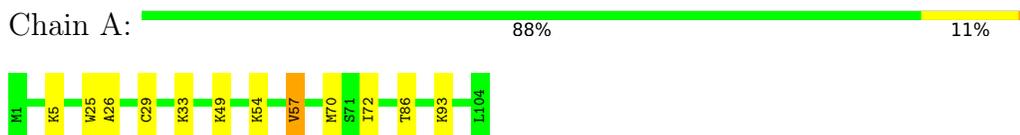


- Molecule 2: Protein arsC

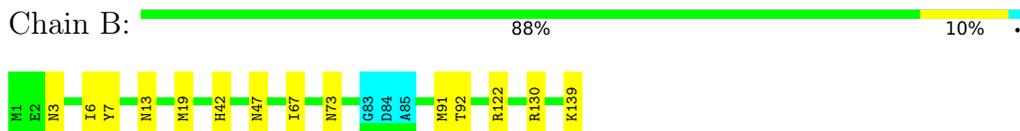


4.2.8 Score per residue for model 8

- Molecule 1: Thioredoxin

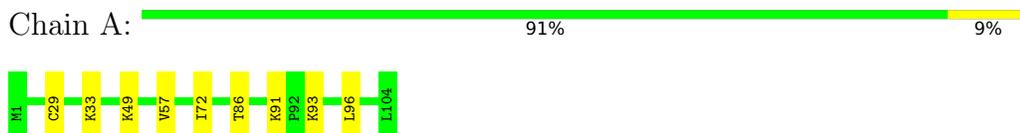


- Molecule 2: Protein arsC

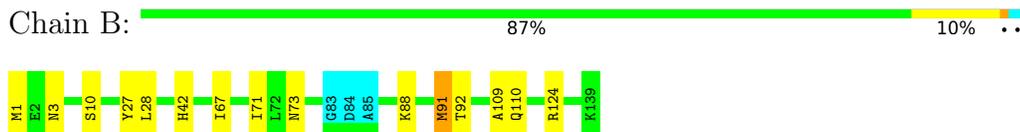


4.2.9 Score per residue for model 9

- Molecule 1: Thioredoxin

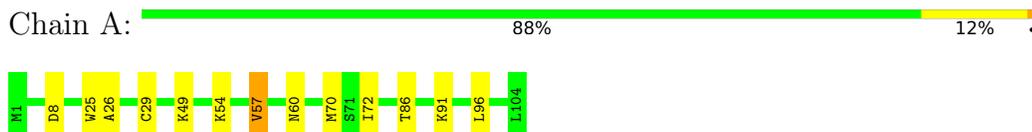


- Molecule 2: Protein arsC

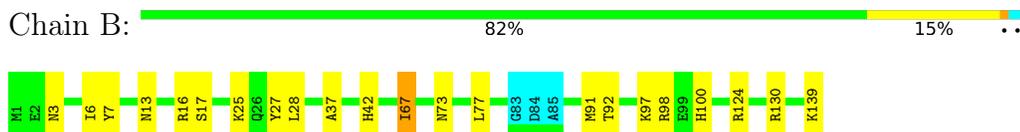


4.2.10 Score per residue for model 10

- Molecule 1: Thioredoxin

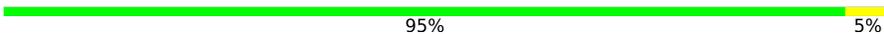


- Molecule 2: Protein arsC



4.2.11 Score per residue for model 11

- Molecule 1: Thioredoxin

Chain A:  95% 5%



- Molecule 2: Protein arsC

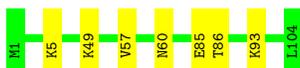
Chain B:  85% 12% ..



4.2.12 Score per residue for model 12

- Molecule 1: Thioredoxin

Chain A:  93% 7%



- Molecule 2: Protein arsC

Chain B:  88% 9% ..



4.2.13 Score per residue for model 13

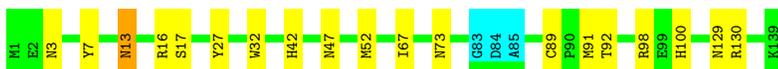
- Molecule 1: Thioredoxin

Chain A:  91% 9%



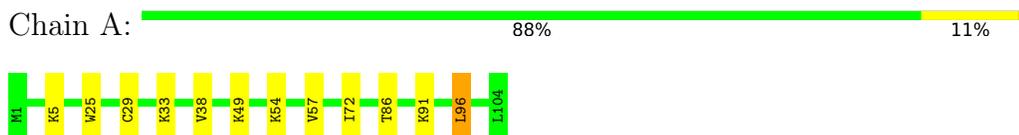
- Molecule 2: Protein arsC

Chain B:  84% 13% ..

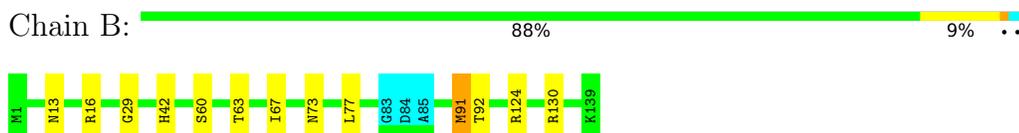


4.2.14 Score per residue for model 14

- Molecule 1: Thioredoxin

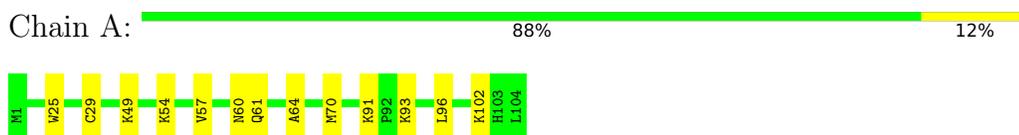


- Molecule 2: Protein arsC

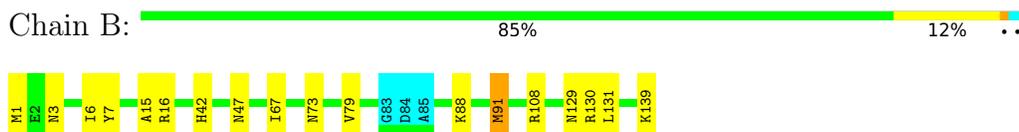


4.2.15 Score per residue for model 15

- Molecule 1: Thioredoxin

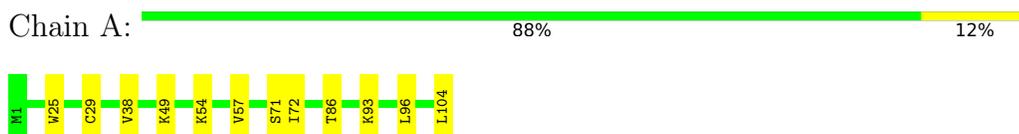


- Molecule 2: Protein arsC

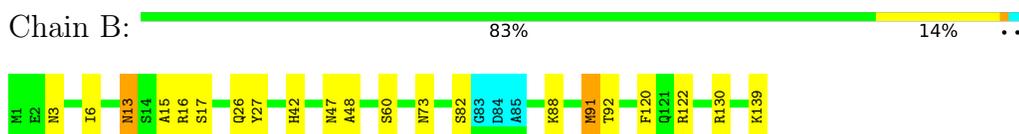


4.2.16 Score per residue for model 16

- Molecule 1: Thioredoxin

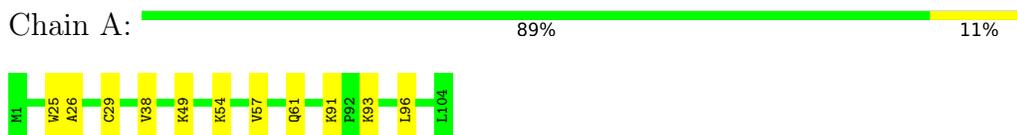


- Molecule 2: Protein arsC

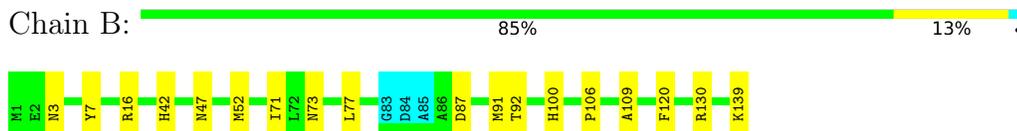


4.2.17 Score per residue for model 17

- Molecule 1: Thioredoxin

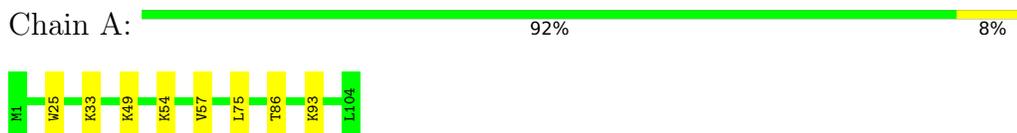


- Molecule 2: Protein arsC

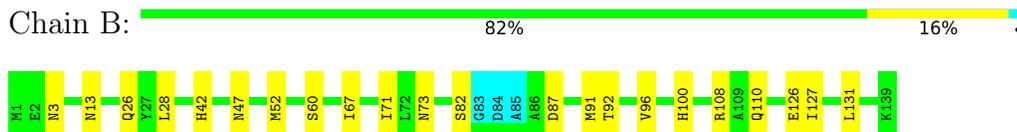


4.2.18 Score per residue for model 18

- Molecule 1: Thioredoxin

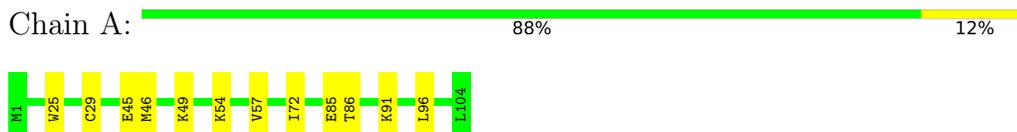


- Molecule 2: Protein arsC

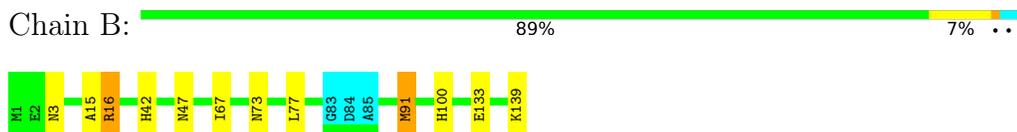


4.2.19 Score per residue for model 19

- Molecule 1: Thioredoxin

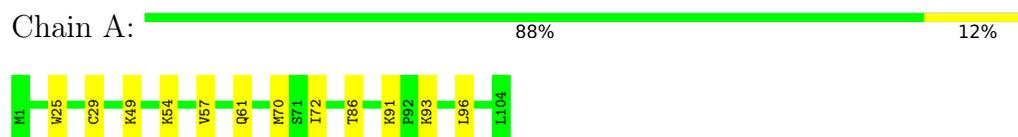


- Molecule 2: Protein arsC

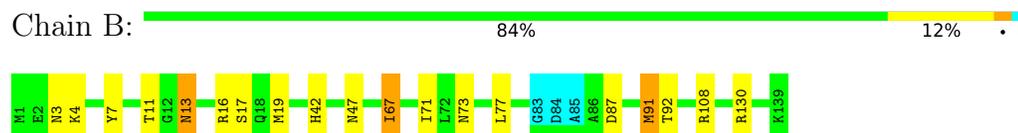


4.2.20 Score per residue for model 20

- Molecule 1: Thioredoxin

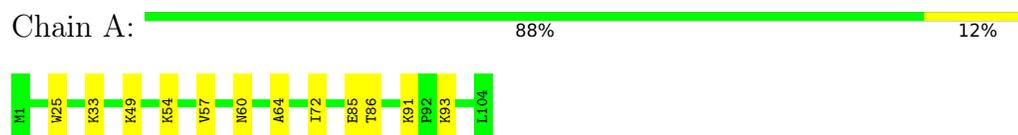


- Molecule 2: Protein arsC

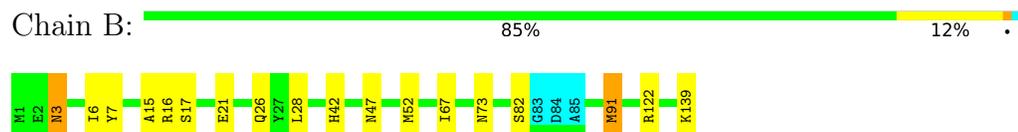


4.2.21 Score per residue for model 21

- Molecule 1: Thioredoxin



- Molecule 2: Protein arsC



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics*.

Of the 200 calculated structures, 21 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
CNS	structure solution	1.1
Amber	refinement	7

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

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	0.58±0.00	0±0/810 (0.0± 0.0%)	0.98±0.03	0±0/1095 (0.0± 0.0%)
2	B	0.63±0.00	0±0/1099 (0.0± 0.0%)	1.06±0.11	2±1/1483 (0.1± 0.1%)
All	All	0.61	0/40089 (0.0%)	1.03	42/54138 (0.1%)

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
2	B	0.0±0.0	0.3±0.5
All	All	0	7

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.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	115	GLU	OE1-CD-OE2	-37.45	78.35	123.30	1	1
2	B	115	GLU	CG-CD-OE1	22.02	162.34	118.30	1	1
2	B	115	GLU	CG-CD-OE2	-17.15	83.99	118.30	1	1
2	B	108	ARG	NE-CZ-NH2	-7.86	116.37	120.30	20	2
2	B	130	ARG	NE-CZ-NH2	-7.17	116.71	120.30	20	10
2	B	98	ARG	NE-CZ-NH2	-6.38	117.11	120.30	4	6
2	B	124	ARG	NE-CZ-NH2	-5.99	117.30	120.30	9	4
2	B	91	MET	CG-SD-CE	-5.78	90.96	100.20	4	11
2	B	122	ARG	NE-CZ-NH2	-5.42	117.59	120.30	16	3
2	B	16	ARG	NE-CZ-NH1	5.34	122.97	120.30	15	2
1	A	46	MET	CB-CA-C	-5.33	99.75	110.40	19	1

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)
2	B	7	TYR	Sidechain	5
2	B	108	ARG	Sidechain	1
2	B	16	ARG	Sidechain	1

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	797	807	807	2±1
2	B	1076	1034	1034	1±1
All	All	39333	38661	38661	46

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:57:VAL:HG21	1:A:72:ILE:HD11	0.68	1.66	8	2
1:A:70:MET:HG3	2:B:67:ILE:HD12	0.64	1.69	11	3
1:A:25:TRP:CD1	1:A:54:LYS:HE3	0.60	2.32	2	5
2:B:47:ASN:ND2	2:B:120:PHE:CE1	0.57	2.72	17	1
1:A:38:VAL:HG12	1:A:96:LEU:HD22	0.56	1.78	16	4
1:A:26:ALA:HB2	1:A:57:VAL:HG22	0.51	1.82	17	3
1:A:26:ALA:HB2	1:A:57:VAL:CG2	0.51	2.35	17	1
1:A:88:VAL:HG12	2:B:88:LYS:HD3	0.51	1.80	2	1
1:A:25:TRP:CD1	1:A:54:LYS:HE2	0.50	2.41	19	12
1:A:72:ILE:HD11	2:B:91:MET:HB3	0.49	1.84	21	1
2:B:77:LEU:HD13	2:B:97:LYS:HD2	0.47	1.86	3	3
2:B:106:PRO:C	2:B:120:PHE:CE1	0.45	2.90	17	1
2:B:15:ALA:HA	2:B:48:ALA:HB2	0.44	1.90	16	1
2:B:47:ASN:ND2	2:B:120:PHE:CZ	0.44	2.85	17	1
1:A:70:MET:CE	2:B:72:LEU:HD13	0.43	2.43	11	1
2:B:37:ALA:HB1	2:B:67:ILE:HA	0.43	1.91	10	1
1:A:25:TRP:CD1	1:A:54:LYS:CE	0.42	3.01	18	1
1:A:25:TRP:CG	1:A:54:LYS:HE3	0.42	2.49	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ALA:HB1	2:B:91:MET:HE2	0.41	1.92	21	2
2:B:117:TRP:CD1	2:B:120:PHE:CZ	0.41	3.08	7	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	102/104 (98%)	92±2 (91±2%)	8±2 (8±2%)	1±1 (1±1%)	16	63
2	B	134/139 (96%)	115±3 (86±2%)	14±3 (11±2%)	5±2 (4±1%)	6	34
All	All	4956/5103 (97%)	4356 (88%)	471 (10%)	129 (3%)	8	44

All 21 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	42	HIS	20
1	A	57	VAL	19
2	B	3	ASN	15
2	B	92	THR	15
2	B	13	ASN	13
2	B	87	ASP	8
2	B	60	SER	4
2	B	15	ALA	4
2	B	109	ALA	4
1	A	70	MET	4
2	B	28	LEU	4
2	B	88	LYS	3
2	B	103	PHE	3
1	A	12	SER	3
2	B	82	SER	3
2	B	11	THR	2
2	B	64	SER	1
1	A	8	ASP	1
2	B	29	GLY	1

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Mol	Chain	Res	Type	Models (Total)
2	B	63	THR	1
2	B	67	ILE	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	89/89 (100%)	82±1 (93±1%)	7±1 (7±1%)	17	65
2	B	113/114 (99%)	102±2 (91±2%)	11±2 (9±2%)	12	58
All	All	4242/4263 (100%)	3879 (91%)	363 (9%)	14	61

All 70 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	49	LYS	21
2	B	73	ASN	21
2	B	91	MET	21
1	A	86	THR	16
1	A	29	CYS	15
2	B	47	ASN	15
2	B	67	ILE	14
1	A	91	LYS	12
2	B	139	LYS	12
1	A	96	LEU	12
2	B	16	ARG	11
1	A	72	ILE	10
1	A	93	LYS	10
2	B	6	ILE	8
2	B	7	TYR	8
2	B	17	SER	7
2	B	77	LEU	7
2	B	71	ILE	7
2	B	110	GLN	7
1	A	33	LYS	7
1	A	85	GLU	6
2	B	26	GLN	6

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Mol	Chain	Res	Type	Models (Total)
2	B	52	MET	6
2	B	100	HIS	6
2	B	13	ASN	6
2	B	27	TYR	6
1	A	60	ASN	5
1	A	5	LYS	4
1	A	71	SER	3
1	A	45	GLU	3
2	B	96	VAL	3
2	B	127	ILE	3
2	B	21	GLU	3
2	B	124	ARG	3
2	B	130	ARG	3
2	B	97	LYS	3
2	B	120	PHE	3
2	B	131	LEU	3
2	B	3	ASN	3
1	A	61	GLN	3
2	B	10	SER	2
2	B	79	VAL	2
2	B	126	GLU	2
2	B	61	ASN	2
2	B	88	LYS	2
2	B	19	MET	2
2	B	1	MET	2
2	B	33	LYS	2
2	B	89	CYS	2
1	A	102	LYS	2
2	B	129	ASN	2
1	A	67	TYR	1
2	B	9	LEU	1
2	B	35	TYR	1
2	B	69	SER	1
2	B	103	PHE	1
1	A	70	MET	1
1	A	46	MET	1
1	A	42	LEU	1
1	A	53	VAL	1
2	B	108	ARG	1
2	B	25	LYS	1
1	A	79	LYS	1
1	A	101	ASN	1

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Mol	Chain	Res	Type	Models (Total)
2	B	81	LEU	1
2	B	32	TRP	1
1	A	104	LEU	1
1	A	75	LEU	1
2	B	133	GLU	1
2	B	4	LYS	1

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 monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

No chemical shift data were provided