



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 03:59 PM BST

PDB ID : 1KX7
Title : Family of 30 conformers of a mono-heme ferrocyanochrome c from *Shewanella putrefaciens* solved by NMR
Authors : Bartalesi, I.; Bertini, I.; Hajieva, P.; Rosato, A.; Vasos, P.R.
Deposited on : 2002-01-31

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
<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 : 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

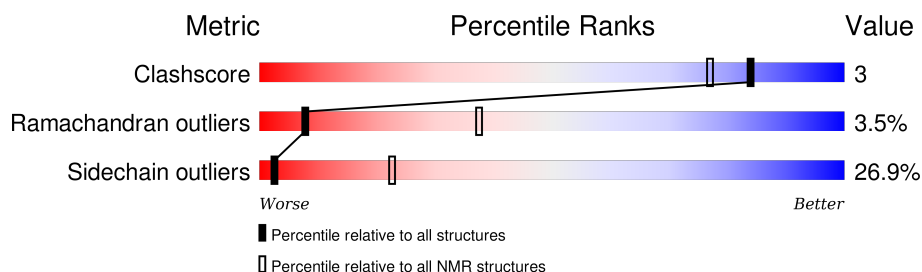
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 56%.

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	81	 73% 22% . .

2 Ensemble composition and analysis ⓘ

This entry contains 30 models. Model 12 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:-1, A:1-A:78 (79)	0.36	12

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

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

NmrClust was unable to cluster the ensemble.

Error message: 1 Unexpected character

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1249 atoms, of which 610 are hydrogens and 0 are deuteriums.

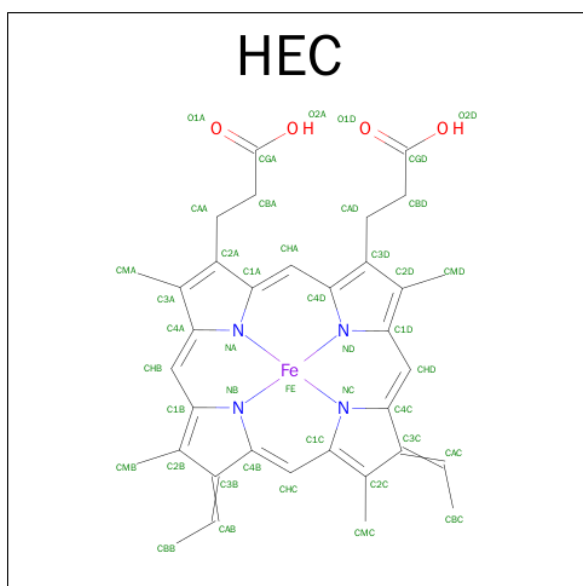
- Molecule 1 is a protein called mono-heme c-type cytochrome ScyA.

Mol	Chain	Residues	Atoms						Trace
1	A	81	Total	C	H	N	O	S	0
			1174	366	578	102	120	8	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ALA	-	CLONING ARTIFACT	UNP O52685
A	-2	ASP	-	CLONING ARTIFACT	UNP O52685
A	-1	LEU	-	CLONING ARTIFACT	UNP O52685

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



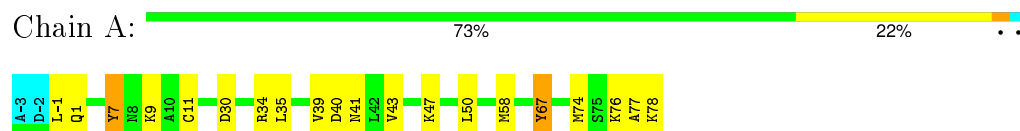
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	Fe	H	N	O
			75	34	1	32	4	4

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: mono-heme c-type cytochrome ScyA

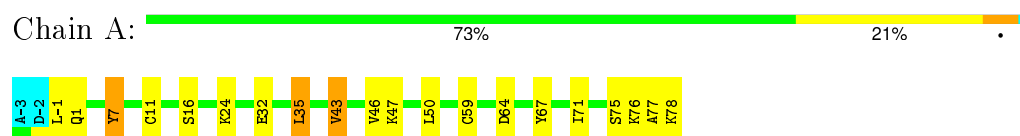


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

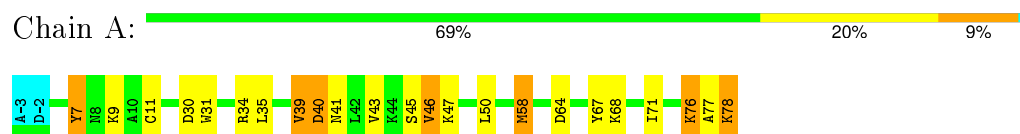
4.2.1 Score per residue for model 1

- Molecule 1: mono-heme c-type cytochrome ScyA



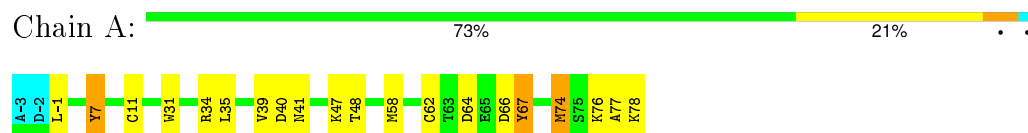
4.2.2 Score per residue for model 2

- Molecule 1: mono-heme c-type cytochrome ScyA



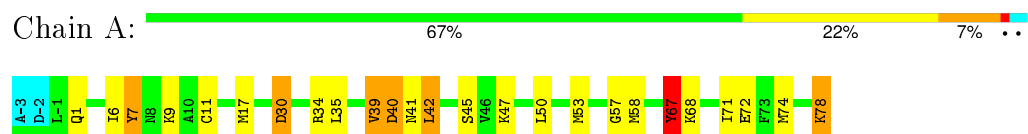
4.2.3 Score per residue for model 3

- Molecule 1: mono-heme c-type cytochrome ScyA



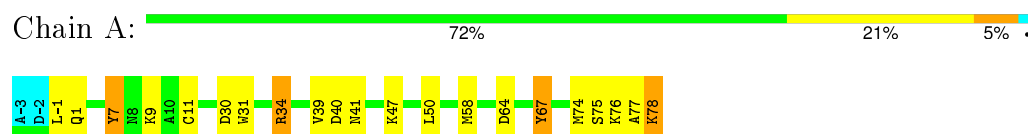
4.2.4 Score per residue for model 4

- Molecule 1: mono-heme c-type cytochrome ScyA



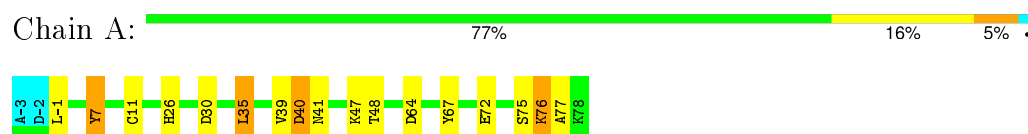
4.2.5 Score per residue for model 5

- Molecule 1: mono-heme c-type cytochrome ScyA



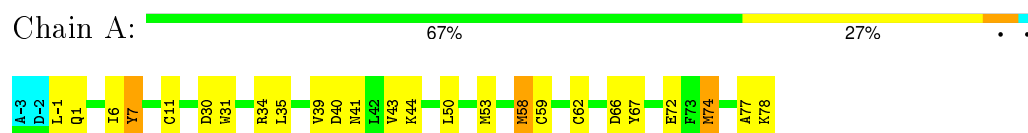
4.2.6 Score per residue for model 6

- Molecule 1: mono-heme c-type cytochrome ScyA



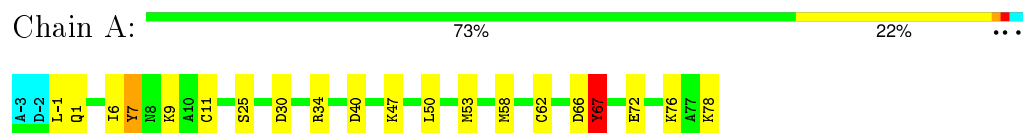
4.2.7 Score per residue for model 7

- Molecule 1: mono-heme c-type cytochrome ScyA



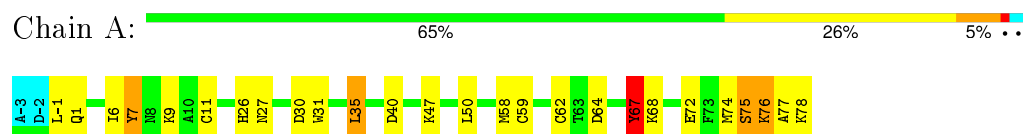
4.2.8 Score per residue for model 8

- Molecule 1: mono-heme c-type cytochrome ScyA



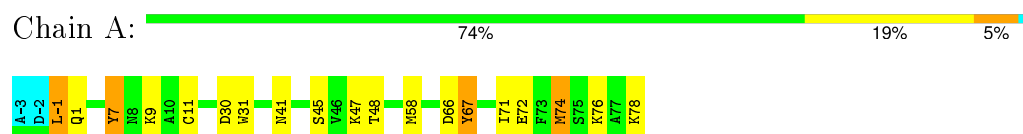
4.2.9 Score per residue for model 9

- Molecule 1: mono-heme c-type cytochrome ScyA



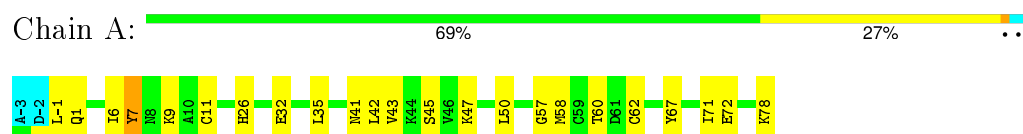
4.2.10 Score per residue for model 10

- Molecule 1: mono-heme c-type cytochrome ScyA



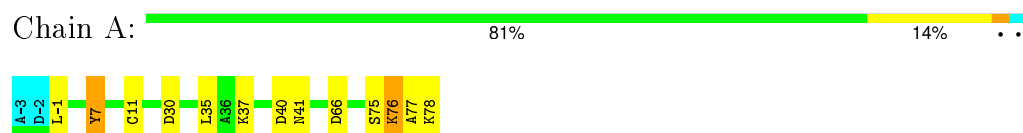
4.2.11 Score per residue for model 11

- Molecule 1: mono-heme c-type cytochrome ScyA



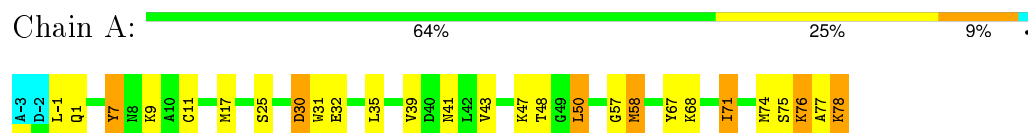
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: mono-heme c-type cytochrome ScyA



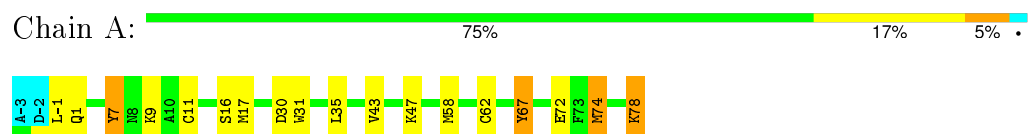
4.2.13 Score per residue for model 13

- Molecule 1: mono-heme c-type cytochrome ScyA



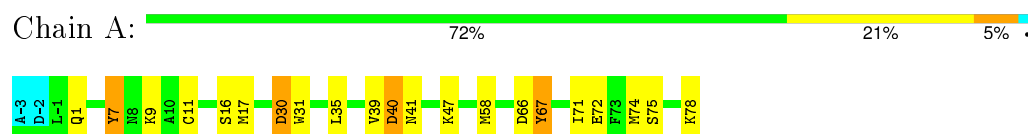
4.2.14 Score per residue for model 14

- Molecule 1: mono-heme c-type cytochrome ScyA



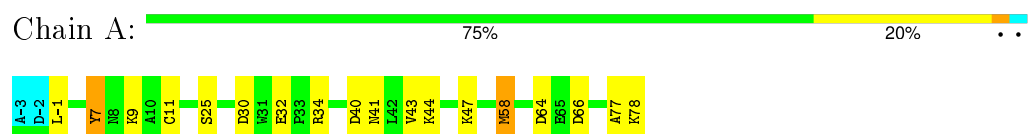
4.2.15 Score per residue for model 15

- Molecule 1: mono-heme c-type cytochrome ScyA



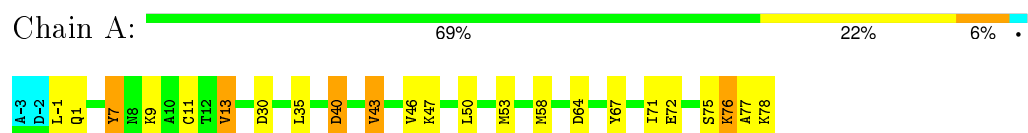
4.2.16 Score per residue for model 16

- Molecule 1: mono-heme c-type cytochrome ScyA



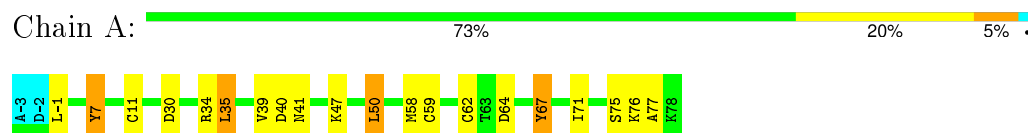
4.2.17 Score per residue for model 17

- Molecule 1: mono-heme c-type cytochrome ScyA



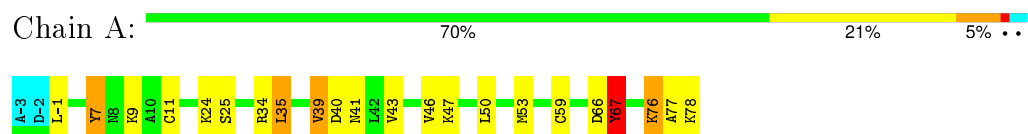
4.2.18 Score per residue for model 18

- Molecule 1: mono-heme c-type cytochrome ScyA



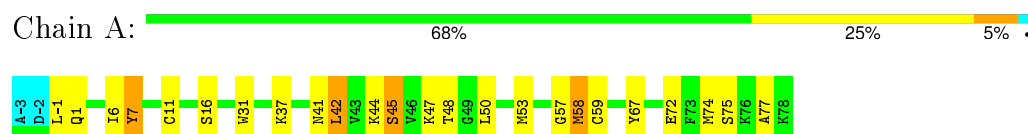
4.2.19 Score per residue for model 19

- Molecule 1: mono-heme c-type cytochrome ScyA



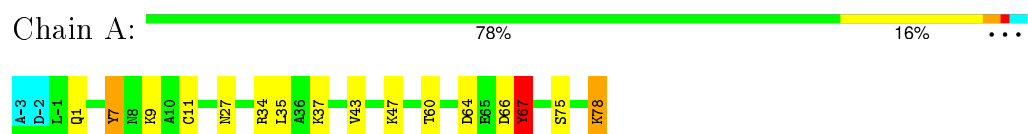
4.2.20 Score per residue for model 20

- Molecule 1: mono-heme c-type cytochrome ScyA



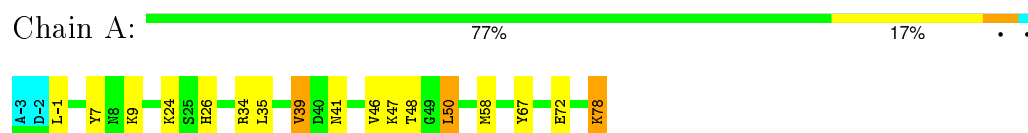
4.2.21 Score per residue for model 21

- Molecule 1: mono-heme c-type cytochrome ScyA



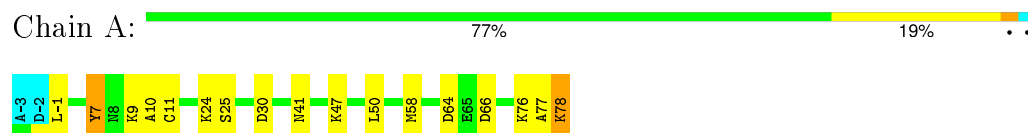
4.2.22 Score per residue for model 22

- Molecule 1: mono-heme c-type cytochrome ScyA



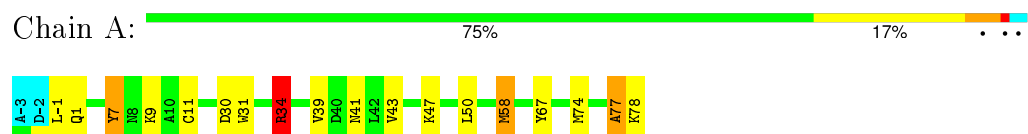
4.2.23 Score per residue for model 23

- Molecule 1: mono-heme c-type cytochrome ScyA



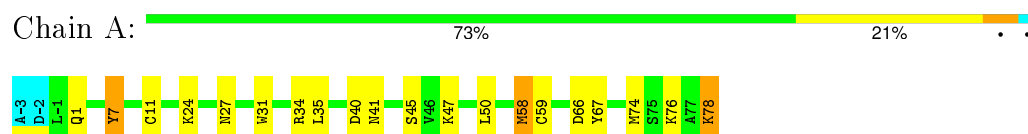
4.2.24 Score per residue for model 24

- Molecule 1: mono-heme c-type cytochrome ScyA



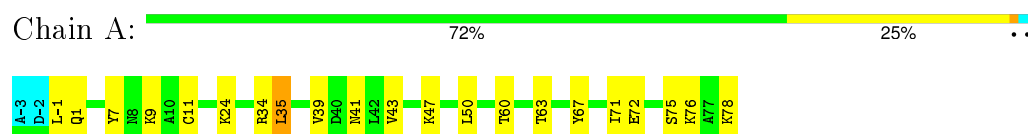
4.2.25 Score per residue for model 25

- Molecule 1: mono-heme c-type cytochrome ScyA



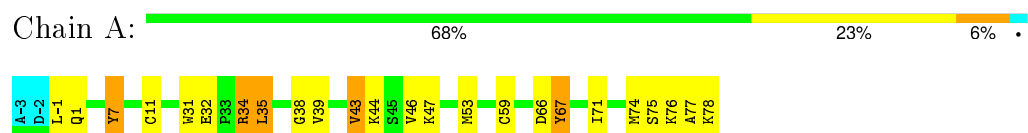
4.2.26 Score per residue for model 26

- Molecule 1: mono-heme c-type cytochrome ScyA



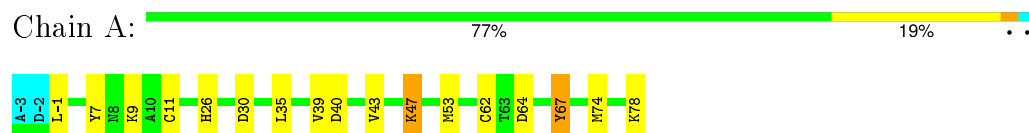
4.2.27 Score per residue for model 27

- Molecule 1: mono-heme c-type cytochrome ScyA



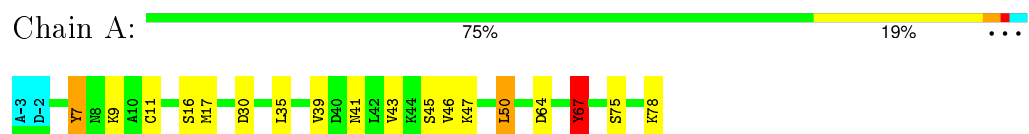
4.2.28 Score per residue for model 28

- Molecule 1: mono-heme c-type cytochrome ScyA



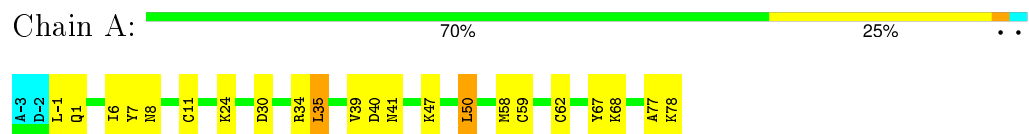
4.2.29 Score per residue for model 29

- Molecule 1: mono-heme c-type cytochrome ScyA



4.2.30 Score per residue for model 30

- Molecule 1: mono-heme c-type cytochrome ScyA



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing in the dihedral angle space in dyana in 15000 steps; 30 structures with the lowest target function out of a total number of 250 generated structures constitute the REM family - subject to restrained energy minimization in AMBER.*

Of the 250 calculated structures, 30 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
DYANA	structure solution	1.5
AMBER	refinement	6

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 5304
Number of chemical shift lists	2
Total number of shifts	615
Number of shifts mapped to atoms	591
Number of unparsed shifts	0
Number of shifts with mapping errors	24
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	56%

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

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	0.55±0.01	0±0/593 (0.0±0.0%)	1.01±0.02	1±1/799 (0.1±0.1%)
All	All	0.55	0/17790 (0.0%)	1.01	27/23970 (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
1	A	0.0±0.0	1.6±0.8
All	All	0	48

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
1	A	30	ASP	CB-CG-OD2	-7.53	111.52	118.30	7	16
1	A	67	TYR	CB-CG-CD2	-7.12	116.73	121.00	8	7
1	A	46	VAL	CG1-CB-CG2	-5.25	102.50	110.90	2	1
1	A	13	VAL	CG1-CB-CG2	-5.06	102.80	110.90	17	1
1	A	34	ARG	NE-CZ-NH1	5.05	122.83	120.30	2	1
1	A	50	LEU	CB-CG-CD1	5.04	119.57	111.00	29	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)
1	A	7	TYR	Sidechain	26
1	A	67	TYR	Sidechain	16
1	A	34	ARG	Sidechain	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	583	567	567	2±2
2	A	43	32	30	2±1
All	All	18780	17970	17910	107

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:90:HEC:HMC1	2:A:90:HEC:HBC3	0.72	1.61	11	12
2:A:90:HEC:HBC3	2:A:90:HEC:HMC1	0.72	1.62	13	16
1:A:78:LYS:HB2	2:A:90:HEC:HMA3	0.68	1.65	28	4
2:A:90:HEC:HMC1	2:A:90:HEC:CBC	0.64	2.22	2	13
2:A:90:HEC:CBC	2:A:90:HEC:HMC1	0.63	2.23	28	10
1:A:-1:LEU:H	1:A:-1:LEU:HD13	0.60	1.57	10	1
2:A:90:HEC:HMB1	2:A:90:HEC:HBB3	0.59	1.74	23	1
1:A:-1:LEU:HD13	1:A:6:ILE:CD1	0.56	2.29	8	1
1:A:-1:LEU:HD11	1:A:62:CYS:SG	0.56	2.41	8	1
1:A:42:LEU:HB3	2:A:90:HEC:HMA2	0.50	1.82	4	2
1:A:31:TRP:CH2	1:A:74:MET:CB	0.50	2.95	25	11
1:A:31:TRP:CZ2	1:A:78:LYS:HE3	0.49	2.43	2	3
1:A:31:TRP:CH2	1:A:74:MET:HB2	0.49	2.42	14	3
1:A:10:ALA:O	2:A:90:HEC:HMC3	0.48	2.07	23	1
1:A:34:ARG:HB2	1:A:77:ALA:HB1	0.47	1.85	24	3
1:A:31:TRP:CZ3	1:A:78:LYS:OXT	0.47	2.68	13	1
1:A:34:ARG:CB	1:A:77:ALA:HB1	0.46	2.41	24	1
1:A:30:ASP:OD1	1:A:78:LYS:NZ	0.46	2.49	9	4
1:A:34:ARG:HH12	2:A:90:HEC:CGD	0.45	2.24	27	1
1:A:45:SER:HA	1:A:48:THR:HG22	0.45	1.88	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:MET:HB2	2:A:90:HEC:HMC2	0.45	1.89	13	1
1:A:78:LYS:OXT	1:A:78:LYS:NZ	0.44	2.43	22	2
1:A:31:TRP:CH2	1:A:78:LYS:HG3	0.43	2.48	27	1
1:A:43:VAL:HA	1:A:46:VAL:HG12	0.43	1.89	27	4
1:A:78:LYS:NZ	1:A:78:LYS:OXT	0.42	2.51	25	1
1:A:-1:LEU:HD13	1:A:62:CYS:HA	0.42	1.91	18	1
1:A:35:LEU:HG	1:A:77:ALA:HB2	0.42	1.91	19	1
1:A:77:ALA:O	2:A:90:HEC:HMA3	0.41	2.16	20	1
1:A:78:LYS:O	2:A:90:HEC:CMA	0.41	2.69	13	1
1:A:47:LYS:NZ	1:A:64:ASP:OD1	0.41	2.52	28	1
1:A:78:LYS:NZ	1:A:78:LYS:O	0.41	2.48	14	1
2:A:90:HEC:HBB3	2:A:90:HEC:HMB1	0.40	1.92	27	1
1:A:71:ILE:HG12	1:A:78:LYS:OXT	0.40	2.16	13	1

6.3 Torsion angles

6.3.1 Protein backbone

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	78/81 (96%)	60±3 (77±4%)	16±3 (20±4%)	3±2 (3±2%)	8	37
All	All	2340/2430 (96%)	1794 (77%)	465 (20%)	81 (3%)	8	37

All 13 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	77	ALA	14
1	A	76	LYS	13
1	A	58	MET	8
1	A	35	LEU	7
1	A	50	LEU	7
1	A	39	VAL	7
1	A	40	ASP	7
1	A	75	SER	5
1	A	57	GLY	4

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Mol	Chain	Res	Type	Models (Total)
1	A	25	SER	3
1	A	60	THR	3
1	A	62	CYS	2
1	A	38	GLY	1

6.3.2 Protein sidechains ⓘ

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	62/63 (98%)	45±3 (73±5%)	17±3 (27±5%)	2	23
All	All	1860/1890 (98%)	1360 (73%)	500 (27%)	2	23

All 45 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	7	TYR	30
1	A	11	CYS	29
1	A	47	LYS	28
1	A	67	TYR	24
1	A	78	LYS	23
1	A	35	LEU	23
1	A	-1	LEU	22
1	A	41	ASN	22
1	A	9	LYS	20
1	A	1	GLN	19
1	A	58	MET	19
1	A	50	LEU	17
1	A	40	ASP	15
1	A	43	VAL	14
1	A	39	VAL	14
1	A	72	GLU	13
1	A	66	ASP	12
1	A	64	ASP	12
1	A	71	ILE	11
1	A	76	LYS	11
1	A	75	SER	10

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Mol	Chain	Res	Type	Models (Total)
1	A	59	CYS	9
1	A	34	ARG	9
1	A	53	MET	8
1	A	24	LYS	7
1	A	45	SER	7
1	A	74	MET	7
1	A	6	ILE	6
1	A	26	HIS	5
1	A	17	MET	5
1	A	48	THR	5
1	A	16	SER	5
1	A	62	CYS	5
1	A	32	GLU	5
1	A	68	LYS	5
1	A	44	LYS	4
1	A	30	ASP	3
1	A	27	ASN	3
1	A	37	LYS	3
1	A	46	VAL	3
1	A	42	LEU	3
1	A	25	SER	2
1	A	63	THR	1
1	A	13	VAL	1
1	A	8	ASN	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 carbohydrates 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.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	HEC	A	90	1	24,50,50	0.77±0.03	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.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	HEC	A	90	1	19,82,82	2.21±0.07	1±0 (7±2%)

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	90	1	-	0±0,6,54,54	0±0,0,8,8

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	A	90	HEC	CBB-CAB-C3B	6.88	112.31	127.34	20	30
2	A	90	HEC	CBC-CAC-C3C	5.70	114.88	127.34	29	10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

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 56% for the well-defined parts and 56% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5304

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	591
Number of shifts mapped to atoms	591
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	31

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	—
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	0	—	—
^{15}N	76	1.18 ± 0.88	None needed (imprecise)

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 56%, i.e. 497 atoms were assigned a chemical shift out of a possible 886. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	229/387 (59%)	154/154 (100%)	0/158 (0%)	75/75 (100%)
Sidechain	244/448 (54%)	239/263 (91%)	0/169 (0%)	5/16 (31%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	24/51 (47%)	23/27 (85%)	0/21 (0%)	1/3 (33%)
Overall	497/886 (56%)	416/444 (94%)	0/348 (0%)	81/94 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 56%, i.e. 502 atoms were assigned a chemical shift out of a possible 902. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	232/397 (58%)	156/158 (99%)	0/162 (0%)	76/77 (99%)
Sidechain	246/454 (54%)	241/266 (91%)	0/172 (0%)	5/16 (31%)
Aromatic	24/51 (47%)	23/27 (85%)	0/21 (0%)	1/3 (33%)
Overall	502/902 (56%)	420/451 (93%)	0/355 (0%)	82/96 (85%)

7.1.4 Statistically unusual chemical shifts ⓘ

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	53	MET	HG2	-3.94	4.23 – 0.63	-17.7
1	A	15	HIS	HE1	0.00	10.53 – 5.43	-15.6
1	A	15	HIS	HD2	0.87	9.28 – 4.78	-13.7
1	A	22	ALA	HB3	-1.39	2.61 – 0.11	-11.0
1	A	22	ALA	HB2	-1.39	2.61 – 0.11	-11.0
1	A	22	ALA	HB1	-1.39	2.61 – 0.11	-11.0
1	A	53	MET	HE1	-3.34	4.28 – -0.52	-10.9
1	A	53	MET	HE2	-3.34	4.28 – -0.52	-10.9
1	A	53	MET	HE3	-3.34	4.28 – -0.52	-10.9
1	A	-1	LEU	HG	4.74	3.16 – -0.14	9.8
1	A	53	MET	HG3	-1.24	4.30 – 0.50	-9.6
1	A	20	ALA	N	155.14	141.07 – 105.37	8.9
1	A	53	MET	HB2	-0.88	3.73 – 0.33	-8.6
1	A	53	MET	HB3	-0.88	3.70 – 0.30	-8.5
1	A	71	ILE	HD13	2.93	2.13 – -0.77	7.8
1	A	71	ILE	HD12	2.93	2.13 – -0.77	7.8
1	A	71	ILE	HD11	2.93	2.13 – -0.77	7.8
1	A	23	PRO	HB3	-0.62	3.81 – 0.21	-7.3
1	A	44	LYS	HE2	1.58	3.87 – 1.97	-7.1
1	A	32	GLU	HG2	3.76	3.33 – 1.23	7.0
1	A	44	LYS	HE3	1.58	3.86 – 1.96	-7.0
1	A	32	GLU	HG3	3.67	3.31 – 1.21	6.7

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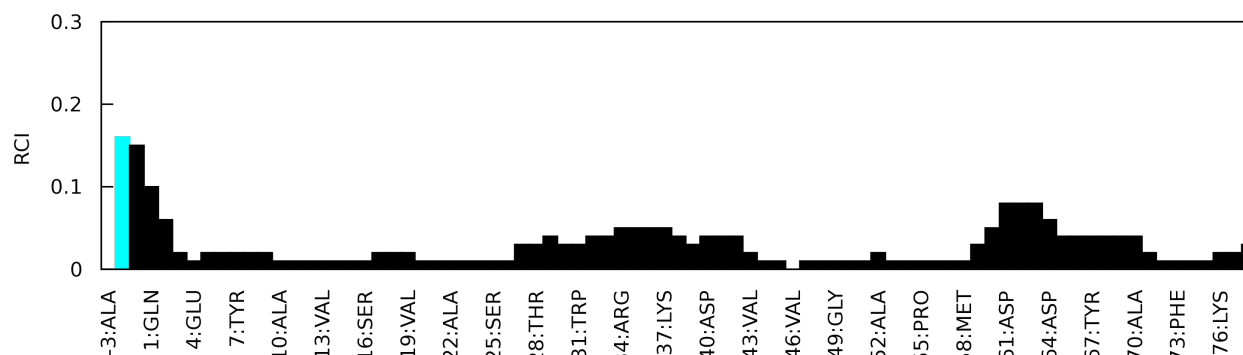
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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	23	PRO	HG3	-0.01	3.56 – 0.26	-5.8
1	A	49	GLY	HA3	1.90	5.80 – 2.00	-5.3
1	A	64	ASP	HB3	1.24	4.07 – 1.27	-5.1
1	A	15	HIS	HB2	1.28	4.91 – 1.31	-5.1
1	A	6	ILE	HG22	2.15	2.13 – -0.57	5.1
1	A	6	ILE	HG21	2.15	2.13 – -0.57	5.1
1	A	6	ILE	HG23	2.15	2.13 – -0.57	5.1
1	A	57	GLY	HA3	1.98	5.80 – 2.00	-5.1
1	A	15	HIS	HA	2.39	6.81 – 2.41	-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:



7.2 Chemical shift list 2

File name: BMRB entry 5304

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	24
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Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	24
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. All 24 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	HEM	3HBC	2.44	0.01	1
UNMAPPED	1	HEM	3HMC	3.64	0.01	1
UNMAPPED	1	HEM	2HAD	3.58	0.01	1
UNMAPPED	1	HEM	1HBC	2.44	0.01	1
UNMAPPED	1	HEM	HAB	6.35	0.01	1
UNMAPPED	1	HEM	2HMC	3.64	0.01	1
UNMAPPED	1	HEM	1HBB	2.47	0.01	1
UNMAPPED	1	HEM	HHA	9.41	0.01	1
UNMAPPED	1	HEM	3HMA	2.93	0.01	1
UNMAPPED	1	HEM	2HBB	2.47	0.01	1
UNMAPPED	1	HEM	2HMD	3.39	0.01	1
UNMAPPED	1	HEM	HAC	6.33	0.01	1
UNMAPPED	1	HEM	1HAD	3.58	0.01	1
UNMAPPED	1	HEM	1HMD	3.39	0.01	1
UNMAPPED	1	HEM	2HMB	3.7	0.01	1
UNMAPPED	1	HEM	1HMA	2.93	0.01	1
UNMAPPED	1	HEM	1HMB	3.7	0.01	1
UNMAPPED	1	HEM	3HMB	3.7	0.01	1
UNMAPPED	1	HEM	2HBC	2.44	0.01	1
UNMAPPED	1	HEM	3HMD	3.39	0.01	1
UNMAPPED	1	HEM	HHB	10.2	0.01	1
UNMAPPED	1	HEM	2HMA	2.93	0.01	1
UNMAPPED	1	HEM	1HMC	3.64	0.01	1
UNMAPPED	1	HEM	HHC	9.4	0.01	1

7.2.2 Chemical shift referencing

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

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 886. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/387 (0%)	0/154 (0%)	0/158 (0%)	0/75 (0%)
Sidechain	0/448 (0%)	0/263 (0%)	0/169 (0%)	0/16 (0%)
Aromatic	0/51 (0%)	0/27 (0%)	0/21 (0%)	0/3 (0%)
Overall	0/886 (0%)	0/444 (0%)	0/348 (0%)	0/94 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 902. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/397 (0%)	0/158 (0%)	0/162 (0%)	0/77 (0%)
Sidechain	0/454 (0%)	0/266 (0%)	0/172 (0%)	0/16 (0%)
Aromatic	0/51 (0%)	0/27 (0%)	0/21 (0%)	0/3 (0%)
Overall	0/902 (0%)	0/451 (0%)	0/355 (0%)	0/96 (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.