



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 07:24 pm GMT

PDB ID : 1N9C
Title : Structure and dynamics of reduced *Bacillus pasteurii* cytochrome c: oxidation state dependent properties and implications for electron transfer processes
Authors : Bartalesi, I.; Bertini, I.; Rosato, A.
Deposited on : 2002-11-23

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	:	1.7.2 (RC1), CSD as538be (2017)
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

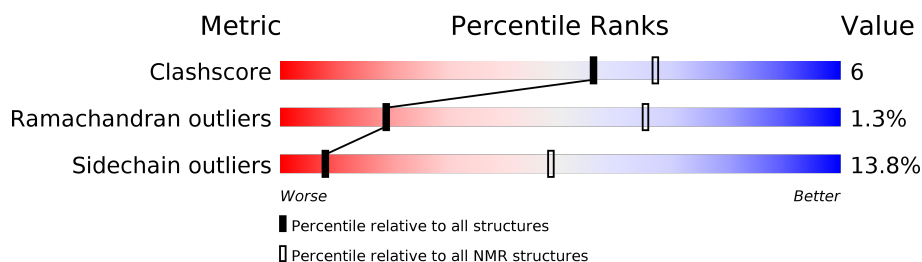
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 57%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	71	 87% 8% ..

2 Ensemble composition and analysis

This entry contains 30 models. Model 4 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:23-A:92 (70)	0.16	4

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 4 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 14, 15, 16, 19, 20, 22, 25, 28, 29
2	8, 9, 11, 23, 24, 27
3	10, 13, 30
4	12, 17
Single-model clusters	18; 21; 26

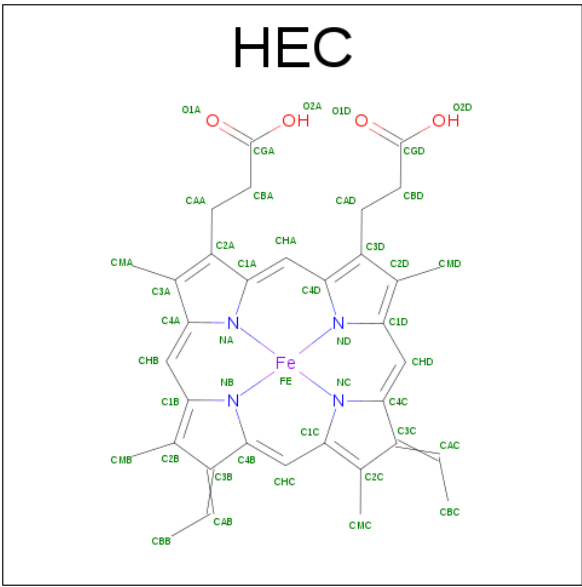
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1058 atoms, of which 518 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cytochrome c-553.

Mol	Chain	Residues	Atoms						Trace
1	A	71	Total	C	H	N	O	S	0
			983	306	486	84	104	3	

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



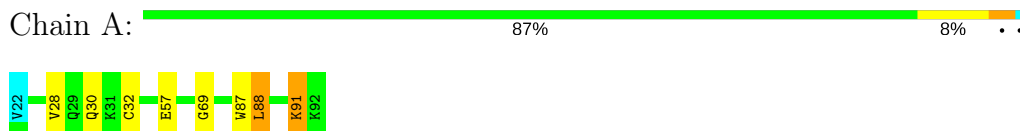
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	Fe	H	N	O
			75	34	1	32	4	4

4 Residue-property plots

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: Cytochrome c-553

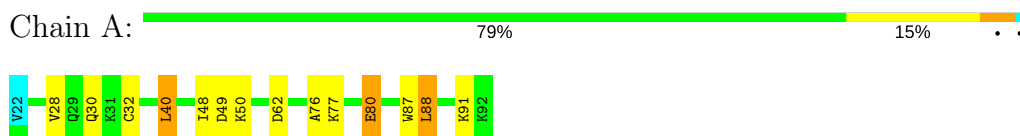


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

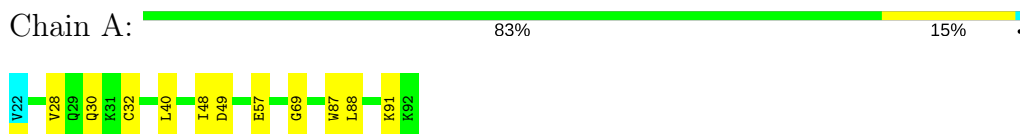
4.2.1 Score per residue for model 1

- Molecule 1: Cytochrome c-553



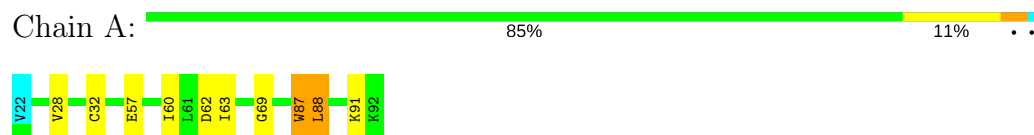
4.2.2 Score per residue for model 2

- Molecule 1: Cytochrome c-553



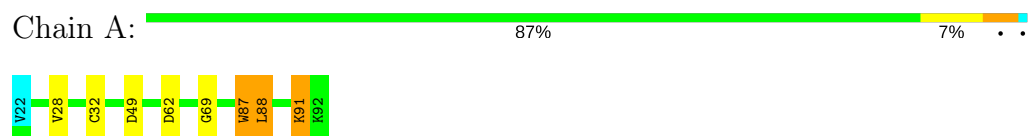
4.2.3 Score per residue for model 3

- Molecule 1: Cytochrome c-553



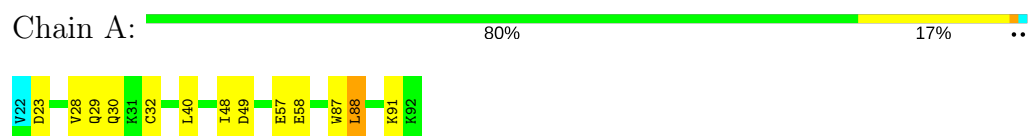
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Cytochrome c-553



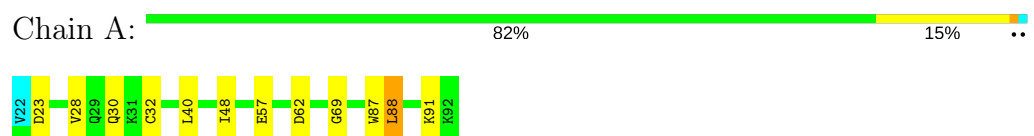
4.2.5 Score per residue for model 5

- Molecule 1: Cytochrome c-553



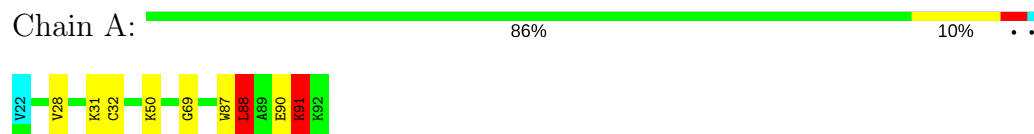
4.2.6 Score per residue for model 6

- Molecule 1: Cytochrome c-553



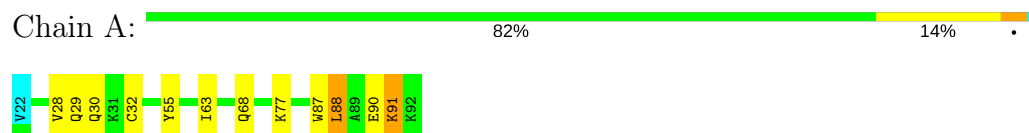
4.2.7 Score per residue for model 7

- Molecule 1: Cytochrome c-553



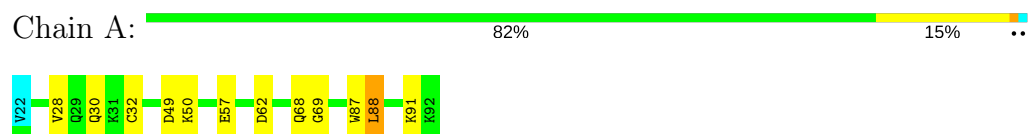
4.2.8 Score per residue for model 8

- Molecule 1: Cytochrome c-553



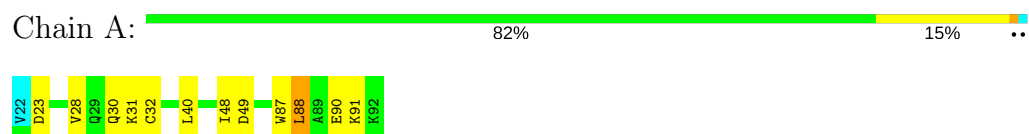
4.2.9 Score per residue for model 9

- Molecule 1: Cytochrome c-553



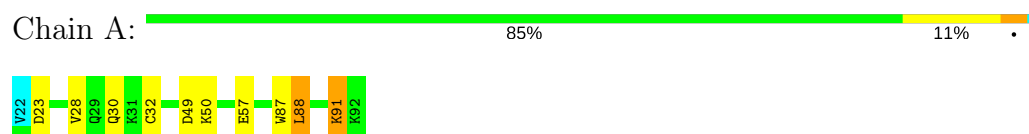
4.2.10 Score per residue for model 10

- Molecule 1: Cytochrome c-553



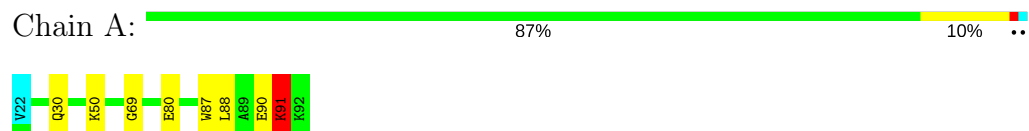
4.2.11 Score per residue for model 11

- Molecule 1: Cytochrome c-553



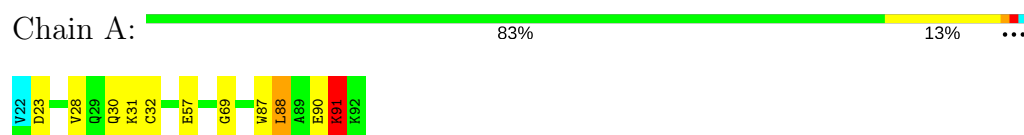
4.2.12 Score per residue for model 12

- Molecule 1: Cytochrome c-553



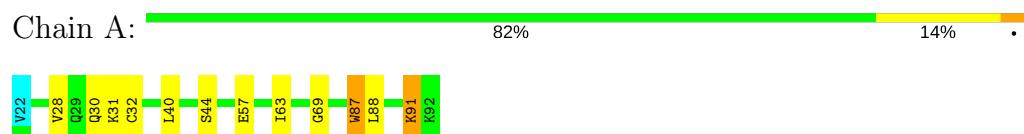
4.2.13 Score per residue for model 13

- Molecule 1: Cytochrome c-553



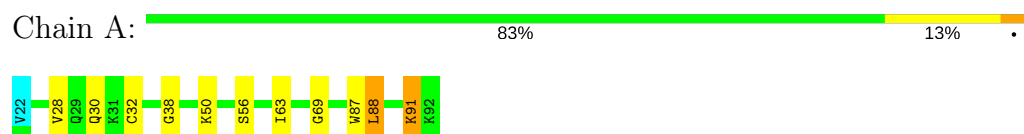
4.2.14 Score per residue for model 14

- Molecule 1: Cytochrome c-553



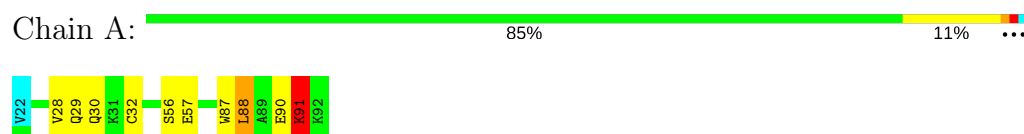
4.2.15 Score per residue for model 15

- Molecule 1: Cytochrome c-553



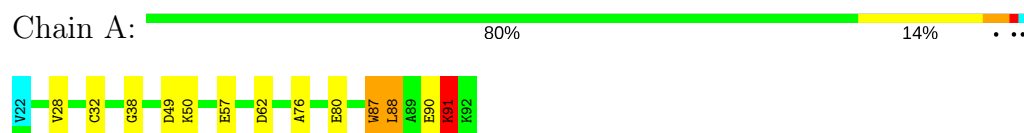
4.2.16 Score per residue for model 16

- Molecule 1: Cytochrome c-553



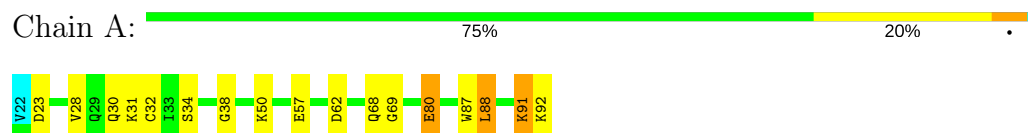
4.2.17 Score per residue for model 17

- Molecule 1: Cytochrome c-553



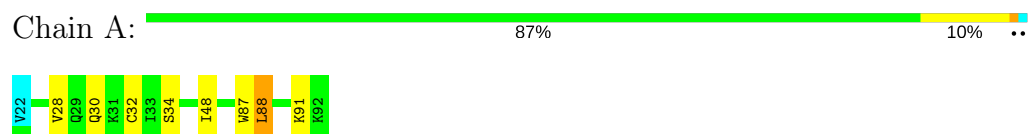
4.2.18 Score per residue for model 18

- Molecule 1: Cytochrome c-553



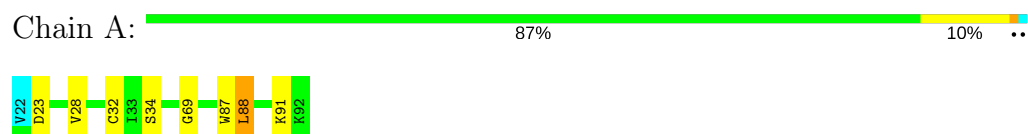
4.2.19 Score per residue for model 19

- Molecule 1: Cytochrome c-553



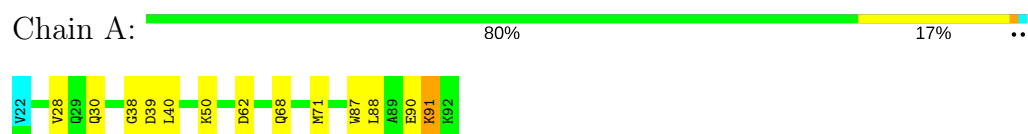
4.2.20 Score per residue for model 20

- Molecule 1: Cytochrome c-553



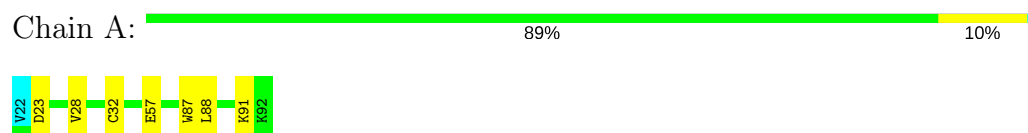
4.2.21 Score per residue for model 21

- Molecule 1: Cytochrome c-553



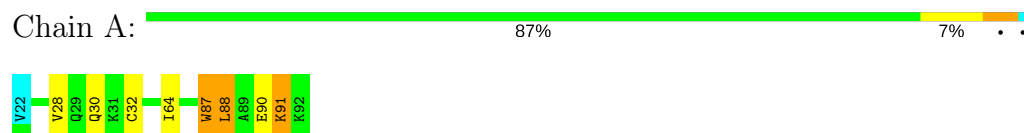
4.2.22 Score per residue for model 22

- Molecule 1: Cytochrome c-553



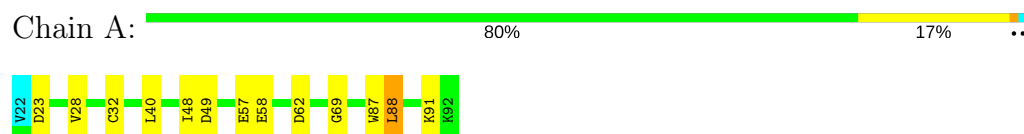
4.2.23 Score per residue for model 23

- Molecule 1: Cytochrome c-553



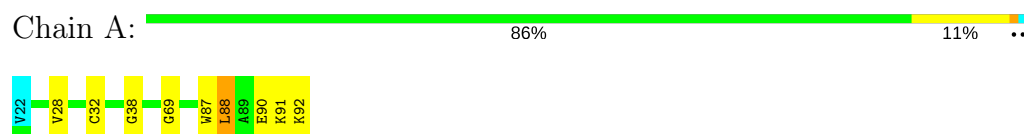
4.2.24 Score per residue for model 24

- Molecule 1: Cytochrome c-553



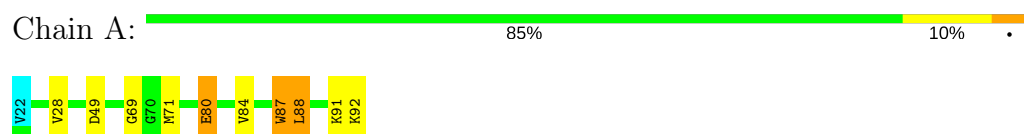
4.2.25 Score per residue for model 25

- Molecule 1: Cytochrome c-553



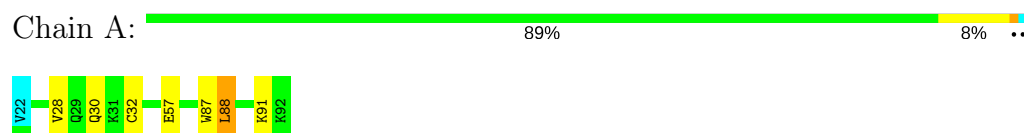
4.2.26 Score per residue for model 26

- Molecule 1: Cytochrome c-553



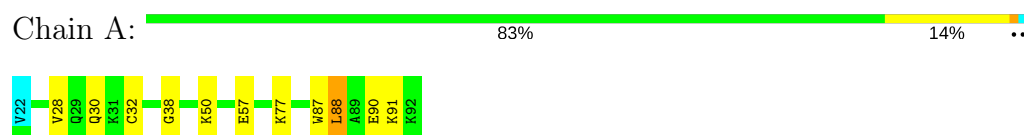
4.2.27 Score per residue for model 27

- Molecule 1: Cytochrome c-553



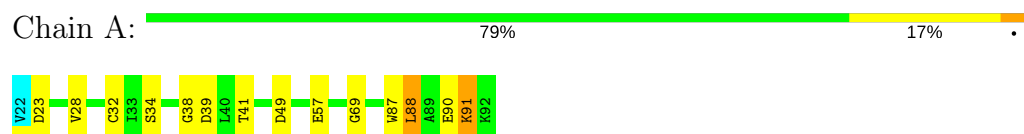
4.2.28 Score per residue for model 28

- Molecule 1: Cytochrome c-553



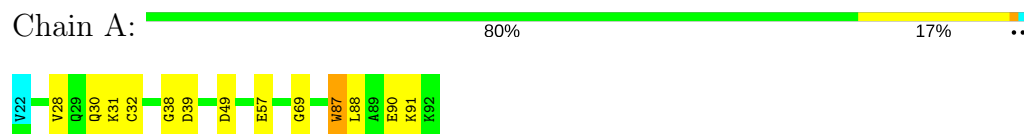
4.2.29 Score per residue for model 29

- Molecule 1: Cytochrome c-553



4.2.30 Score per residue for model 30

- Molecule 1: Cytochrome c-553



5 Refinement protocol and experimental data overview

The models were refined using the following method: *restrained energy minimization*.

Of the 130 calculated structures, 30 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
DYANA	structure solution	1.5
DYANA	refinement	1.5

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 5597
Number of chemical shift lists	2
Total number of shifts	537
Number of shifts mapped to atoms	517
Number of unparsed shifts	0
Number of shifts with mapping errors	20
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	57%

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

6 Model quality

6.1 Standard geometry

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	0.47±0.01	0±0/495 (0.0±0.0%)	0.98±0.02	0±0/666 (0.0±0.1%)
All	All	0.47	0/14850 (0.0%)	0.99	9/19980 (0.0%)

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	0.4±0.6
All	All	0	13

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	87	TRP	CZ3-CH2-CZ2	-5.96	114.45	121.60	14	7
1	A	87	TRP	NE1-CE2-CZ2	5.30	136.23	130.40	26	1
1	A	88	LEU	CB-CG-CD2	5.22	119.88	111.00	7	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	91	LYS	Peptide	11
1	A	55	TYR	Sidechain	1
1	A	90	GLU	Peptide	1

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	490	475	475	5±2
2	A	43	32	30	1±0
All	All	15990	15210	15150	186

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:87:TRP:CZ3	1:A:88:LEU:HD23	0.85	2.07	7	17
1:A:87:TRP:CH2	1:A:88:LEU:HD23	0.78	2.13	7	4
1:A:28:VAL:HG21	1:A:87:TRP:CZ3	0.72	2.19	19	20
2:A:93:HEC:CGD	2:A:93:HEC:HMD1	0.70	2.17	30	16
1:A:28:VAL:HG21	1:A:87:TRP:HZ3	0.68	1.46	18	13
2:A:93:HEC:HMD1	2:A:93:HEC:CGD	0.67	2.20	21	14
1:A:28:VAL:HG13	1:A:32:CYS:SG	0.66	2.29	11	8
1:A:28:VAL:HG22	1:A:32:CYS:SG	0.63	2.33	16	10
1:A:28:VAL:HG13	1:A:32:CYS:HB2	0.60	1.72	5	8
1:A:48:ILE:HD13	1:A:88:LEU:HD11	0.57	1.75	2	3
1:A:87:TRP:CE3	1:A:88:LEU:HD23	0.57	2.34	18	1
1:A:76:ALA:HB1	1:A:80:GLU:HB3	0.55	1.77	17	2
1:A:87:TRP:CE3	1:A:88:LEU:HD12	0.54	2.37	17	1
1:A:87:TRP:CZ3	1:A:88:LEU:CD2	0.54	2.88	18	10
1:A:28:VAL:HG11	1:A:87:TRP:CH2	0.51	2.40	24	2
1:A:28:VAL:HA	1:A:32:CYS:SG	0.50	2.46	13	22
1:A:48:ILE:O	1:A:88:LEU:HD11	0.50	2.07	19	1
1:A:40:LEU:HD22	1:A:48:ILE:HD11	0.49	1.85	1	6
1:A:28:VAL:HB	1:A:87:TRP:CZ3	0.49	2.43	23	1
1:A:91:LYS:CE	1:A:91:LYS:HA	0.46	2.41	13	2
1:A:64:ILE:HD11	2:A:93:HEC:HMB2	0.46	1.86	23	1
1:A:87:TRP:CZ3	1:A:88:LEU:CD1	0.46	2.99	17	1
1:A:87:TRP:CZ3	1:A:88:LEU:HG	0.45	2.46	24	3
1:A:60:ILE:HG23	2:A:93:HEC:HMA1	0.44	1.88	3	1
1:A:28:VAL:CG2	1:A:87:TRP:CZ3	0.44	3.01	14	3
1:A:28:VAL:CG1	1:A:40:LEU:HD21	0.44	2.43	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:LYS:HE2	1:A:91:LYS:O	0.43	2.14	18	1
1:A:87:TRP:CE3	1:A:88:LEU:CD1	0.43	3.02	17	1
1:A:91:LYS:HA	1:A:91:LYS:CE	0.42	2.44	7	3
1:A:28:VAL:HG12	1:A:40:LEU:HD21	0.42	1.91	14	1
1:A:28:VAL:HG13	1:A:32:CYS:CB	0.41	2.45	6	1
1:A:71:MET:HB2	2:A:93:HEC:C1D	0.41	2.45	21	1
1:A:31:LYS:NZ	1:A:80:GLU:OE2	0.41	2.53	18	1
1:A:28:VAL:CB	1:A:87:TRP:CZ3	0.40	3.05	23	1
1:A:91:LYS:HE3	1:A:91:LYS:HA	0.40	1.93	12	1
1:A:71:MET:HB2	2:A:93:HEC:C4D	0.40	2.46	26	1
1:A:91:LYS:HE2	1:A:91:LYS:CA	0.40	2.46	17	1
1:A:80:GLU:O	1:A:84:VAL:HG23	0.40	2.17	26	1
1:A:91:LYS:HA	1:A:91:LYS:HE3	0.40	1.93	16	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	69/71 (97%)	59±2 (85±2%)	9±2 (13±3%)	1±1 (1±1%)	19	65
All	All	2070/2130 (97%)	1764 (85%)	279 (13%)	27 (1%)	19	65

All 3 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	69	GLY	17
1	A	38	GLY	8
1	A	91	LYS	2

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	46/47 (98%)	40±2 (86±4%)	6±2 (14±4%)	8	48
All	All	1380/1410 (98%)	1190 (86%)	190 (14%)	8	48

All 23 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	91	LYS	30
1	A	88	LEU	29
1	A	30	GLN	20
1	A	57	GLU	17
1	A	90	GLU	12
1	A	49	ASP	12
1	A	50	LYS	10
1	A	23	ASP	10
1	A	62	ASP	9
1	A	31	LYS	5
1	A	68	GLN	4
1	A	34	SER	4
1	A	63	ILE	4
1	A	80	GLU	4
1	A	92	LYS	3
1	A	29	GLN	3
1	A	39	ASP	3
1	A	77	LYS	3
1	A	56	SER	2
1	A	40	LEU	2
1	A	58	GLU	2
1	A	44	SER	1
1	A	41	THR	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	93	1	28,50,50	0.83±0.02	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	93	1	16,82,82	1.64±0.16	0±0 (0±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	93	1	-	0±0,6,54,54	0±0,0,8,8

There are no bond-length outliers.

There are no bond-angle outliers.

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

The completeness of assignment taking into account all chemical shift lists is 57% for the well-defined parts and 56% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5597

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	517
Number of shifts mapped to atoms	517
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	24

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	68	1.58 ± 0.33	Should be applied

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 57%, i.e. 417 atoms were assigned a chemical shift out of a possible 737. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	206/346 (60%)	138/138 (100%)	0/140 (0%)	68/68 (100%)
Sidechain	199/364 (55%)	193/210 (92%)	1/144 (1%)	5/10 (50%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	12/27 (44%)	10/14 (71%)	0/11 (0%)	2/2 (100%)
Overall	417/737 (57%)	341/362 (94%)	1/295 (0%)	75/80 (94%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 56%, i.e. 421 atoms were assigned a chemical shift out of a possible 748. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	207/351 (59%)	139/140 (99%)	0/142 (0%)	68/69 (99%)
Sidechain	202/370 (55%)	196/213 (92%)	1/147 (1%)	5/10 (50%)
Aromatic	12/27 (44%)	10/14 (71%)	0/11 (0%)	2/2 (100%)
Overall	421/748 (56%)	345/367 (94%)	1/300 (0%)	75/81 (93%)

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	36	HIS	HE1	0.50	10.53 – 5.43	-14.7
1	A	36	HIS	HD2	0.47	9.28 – 4.78	-14.6
1	A	71	MET	HB3	-2.70	3.70 – 0.30	-13.8
1	A	45	ALA	HB3	-1.64	2.61 – 0.11	-12.0
1	A	45	ALA	HB1	-1.64	2.61 – 0.11	-12.0
1	A	45	ALA	HB2	-1.64	2.61 – 0.11	-12.0
1	A	33	ILE	CG2	0.79	24.63 – 10.43	-11.8
1	A	71	MET	HG2	-1.77	4.23 – 0.63	-11.7
1	A	72	PRO	HD2	7.67	5.45 – 1.85	11.2
1	A	71	MET	HE3	-3.18	4.28 – -0.52	-10.5
1	A	71	MET	HE1	-3.18	4.28 – -0.52	-10.5
1	A	71	MET	HE2	-3.18	4.28 – -0.52	-10.5
1	A	71	MET	HB2	-0.59	3.73 – 0.33	-7.7
1	A	63	ILE	HG21	-1.22	2.13 – -0.57	-7.4
1	A	63	ILE	HG22	-1.22	2.13 – -0.57	-7.4
1	A	63	ILE	HG23	-1.22	2.13 – -0.57	-7.4
1	A	48	ILE	HG13	-1.37	3.26 – -0.84	-6.3
1	A	48	ILE	HG23	-0.84	2.13 – -0.57	-6.0
1	A	48	ILE	HG22	-0.84	2.13 – -0.57	-6.0
1	A	48	ILE	HG21	-0.84	2.13 – -0.57	-6.0
1	A	36	HIS	HB3	0.87	5.00 – 1.10	-5.6
1	A	48	ILE	HG12	-0.95	3.27 – -0.73	-5.5

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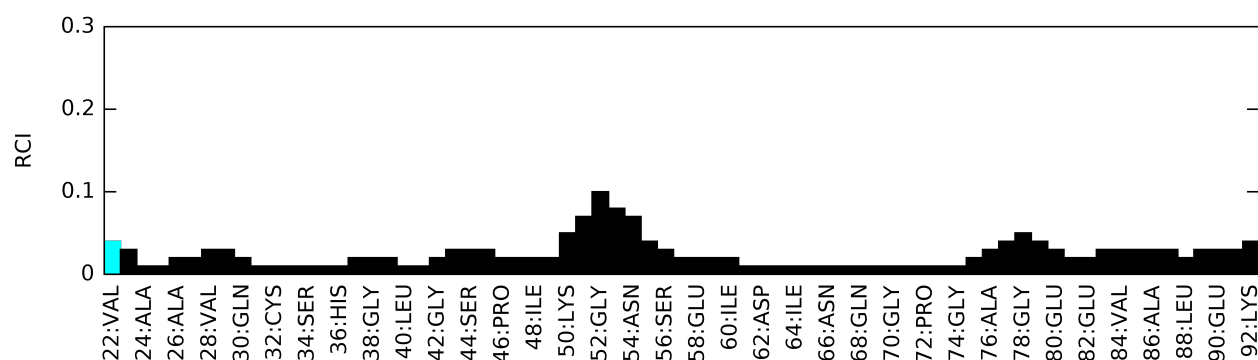
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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	36	HIS	HB2	1.30	4.91 – 1.31	-5.0
1	A	67	GLY	HA2	2.06	5.87 – 2.07	-5.0

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 5597

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	20
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	20
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 20 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	HEM	HAP62	3.85	-1.0	1
UNMAPPED	1	HEM	HAP71	4.39	-1.0	1
UNMAPPED	1	HEM	HBP64	2.82	-1.0	1
UNMAPPED	1	HEM	HDM	8.99	-1.0	1
UNMAPPED	1	HEM	QM1	3.3	-1.0	1
UNMAPPED	1	HEM	HBP73	3.17	-1.0	1
UNMAPPED	1	HEM	HT2A	5.83	-1.0	1
UNMAPPED	1	HEM	QM5	3.3	-1.0	1
UNMAPPED	1	HEM	HT4A	6.25	-1.0	1
UNMAPPED	1	HEM	HBP63	3.07	-1.0	1
UNMAPPED	1	HEM	HBM	9.37	-1.0	1
UNMAPPED	1	HEM	HBP74	2.94	-1.0	1
UNMAPPED	1	HEM	HAP61	4.31	-1.0	1
UNMAPPED	1	HEM	QT2	1.82	-1.0	1
UNMAPPED	1	HEM	QM3	3.77	-1.0	1
UNMAPPED	1	HEM	HGM	9.58	-1.0	1
UNMAPPED	1	HEM	HAP72	4.49	-1.0	1
UNMAPPED	1	HEM	QM8	2.94	-1.0	1
UNMAPPED	1	HEM	HAM	9.79	-1.0	1
UNMAPPED	1	HEM	QT4	2.19	-1.0	1

7.2.2 Chemical shift referencing [i](#)

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 737. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/346 (0%)	0/138 (0%)	0/140 (0%)	0/68 (0%)
Sidechain	0/364 (0%)	0/210 (0%)	0/144 (0%)	0/10 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	0/737 (0%)	0/362 (0%)	0/295 (0%)	0/80 (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 748. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	0/351 (0%)	0/140 (0%)	0/142 (0%)	0/69 (0%)
Sidechain	0/370 (0%)	0/213 (0%)	0/147 (0%)	0/10 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	0/748 (0%)	0/367 (0%)	0/300 (0%)	0/81 (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.