



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 12:04 AM BST

PDB ID : 2KSC
Title : Solution structure of Synechococcus sp. PCC 7002 hemoglobin
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Deposited on : 2010-01-02

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

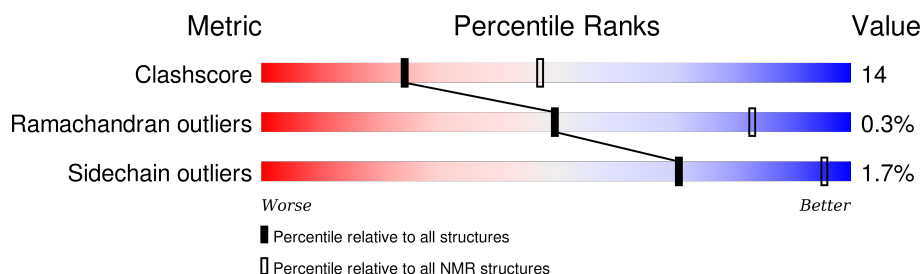
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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	123	

2 Ensemble composition and analysis

This entry contains 16 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:21-A:56, A:66-A:124 (95)	0.35	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 3 clusters and 4 single-model clusters were found.

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

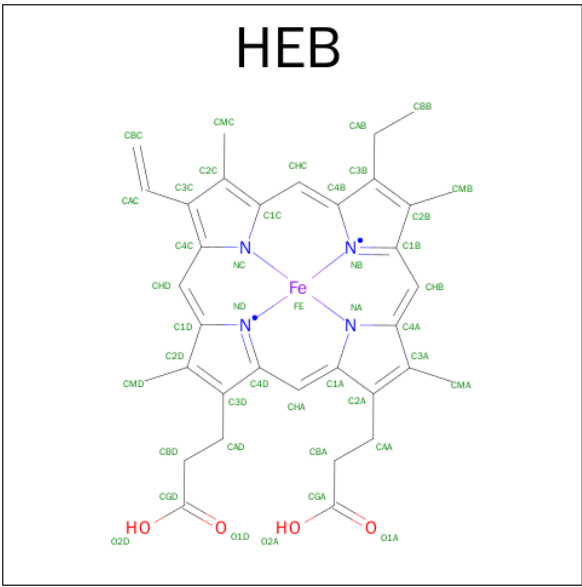
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1990 atoms, of which 980 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cyanoglobin.

Mol	Chain	Residues	Atoms						Trace
1	A	123	Total	C	H	N	O	S	0
			1916	605	949	172	187	3	

- Molecule 2 is HEME B/C (three-letter code: HEB) (formula: C₃₄H₃₄FeN₄O₄).



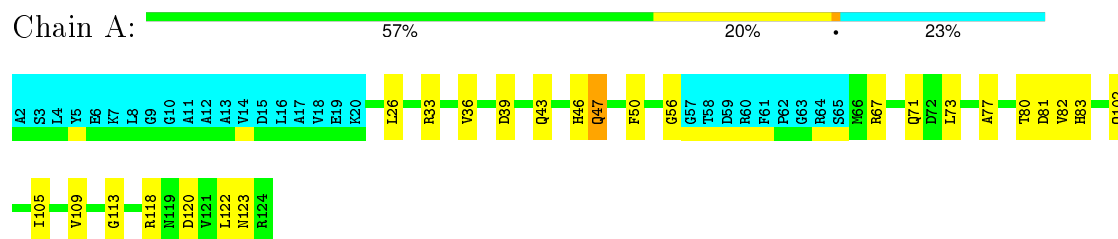
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	Fe	H	N	O
			74	34	1	31	4	4

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: Cyanoglobin

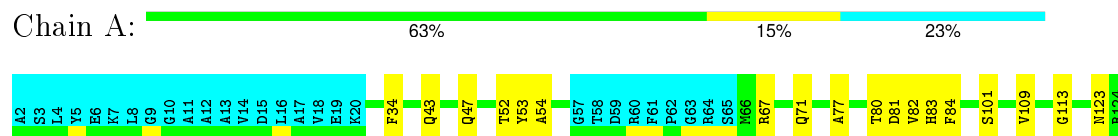


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

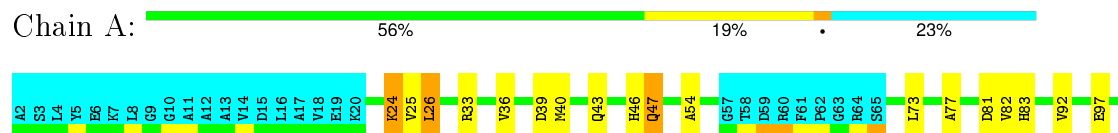
4.2.1 Score per residue for model 1 (medoid)

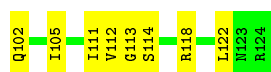
- Molecule 1: Cyanoglobin



4.2.2 Score per residue for model 2

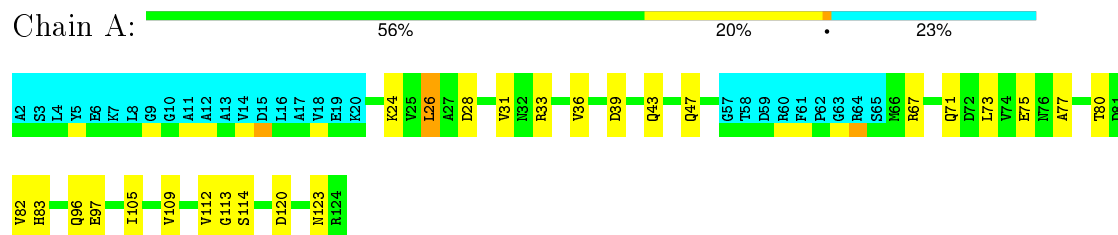
- Molecule 1: Cyanoglobin





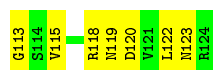
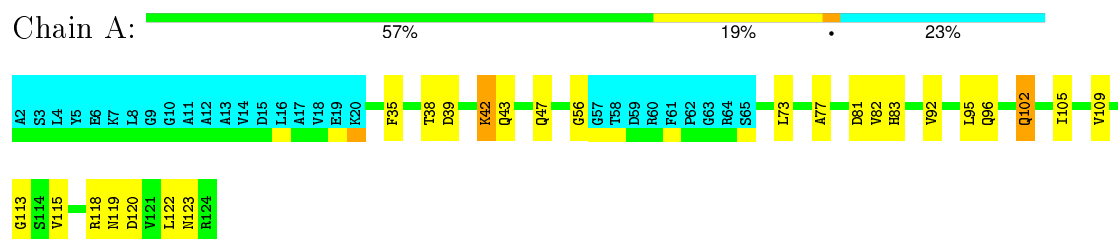
4.2.3 Score per residue for model 3

- Molecule 1: Cyanoglobin



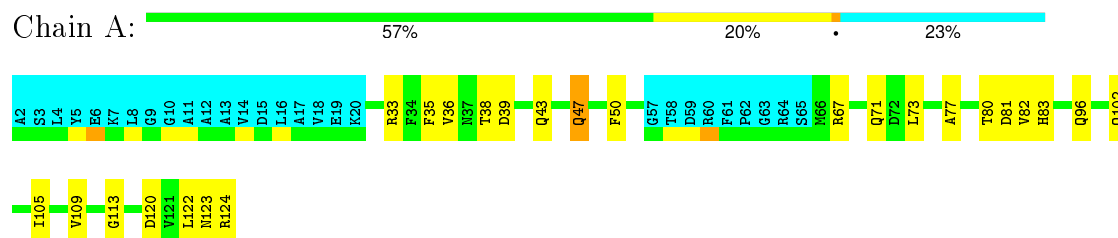
4.2.4 Score per residue for model 4

- Molecule 1: Cyanoglobin



4.2.5 Score per residue for model 5

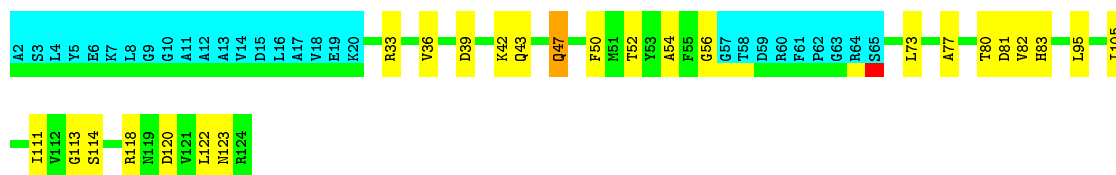
- Molecule 1: Cyanoglobin



4.2.6 Score per residue for model 6

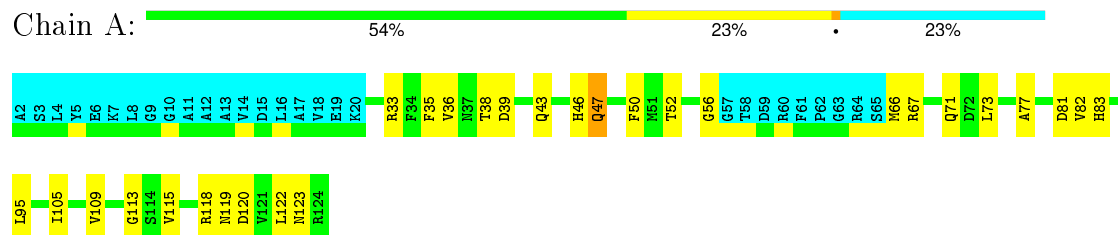
- Molecule 1: Cyanoglobin





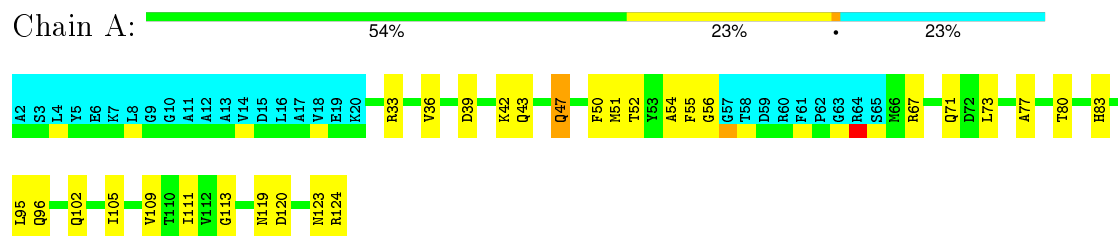
4.2.7 Score per residue for model 7

- Molecule 1: Cyanoglobin



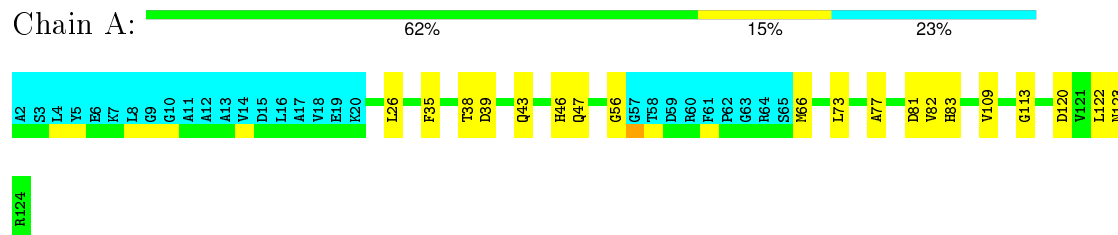
4.2.8 Score per residue for model 8

- Molecule 1: Cyanoglobin



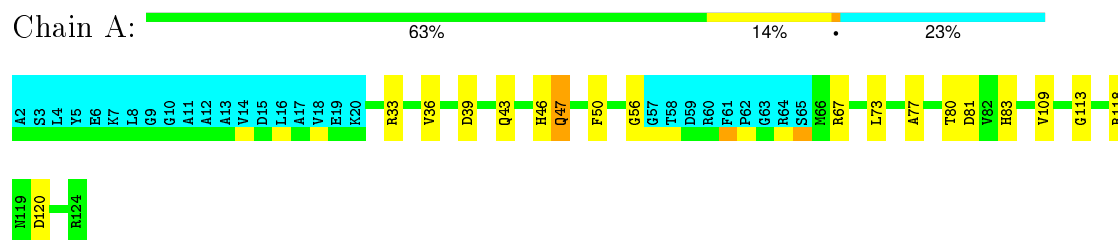
4.2.9 Score per residue for model 9

- Molecule 1: Cyanoglobin



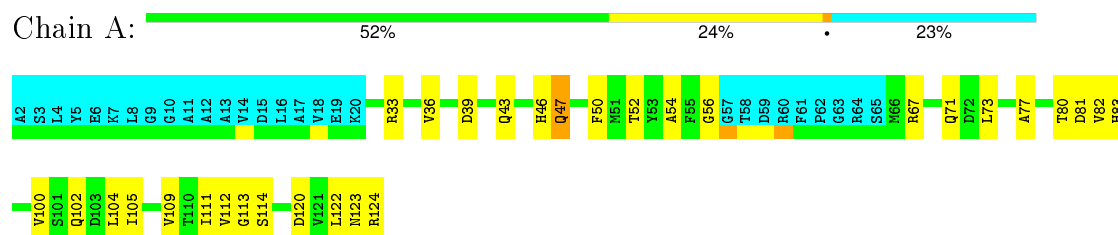
4.2.10 Score per residue for model 10

- Molecule 1: Cyanoglobin



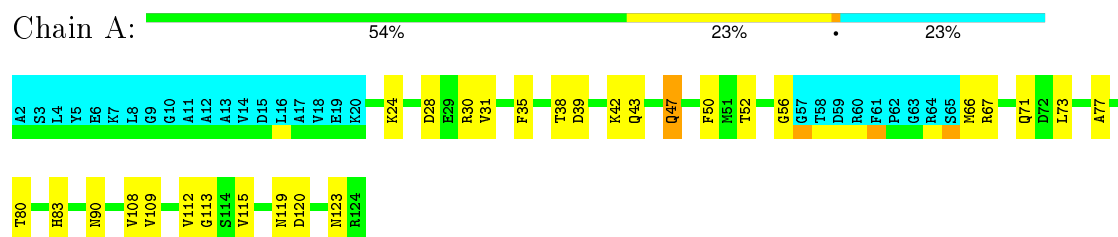
4.2.11 Score per residue for model 11

- Molecule 1: Cyanoglobin



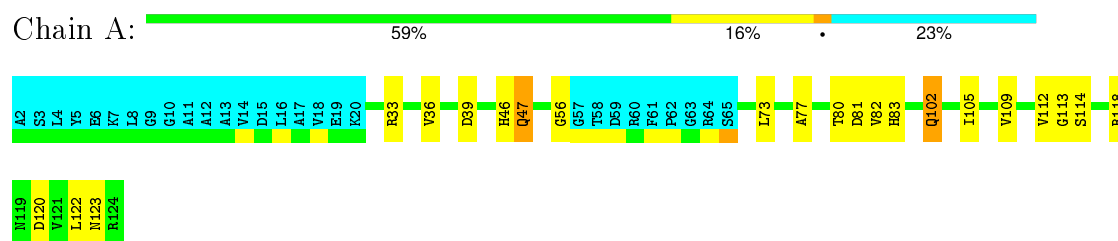
4.2.12 Score per residue for model 12

- Molecule 1: Cyanoglobin



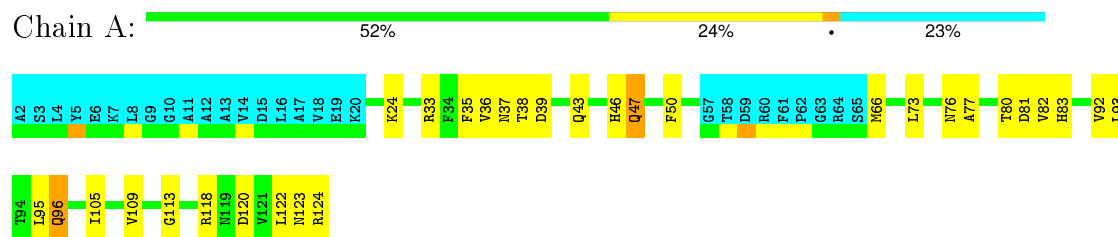
4.2.13 Score per residue for model 13

- Molecule 1: Cyanoglobin



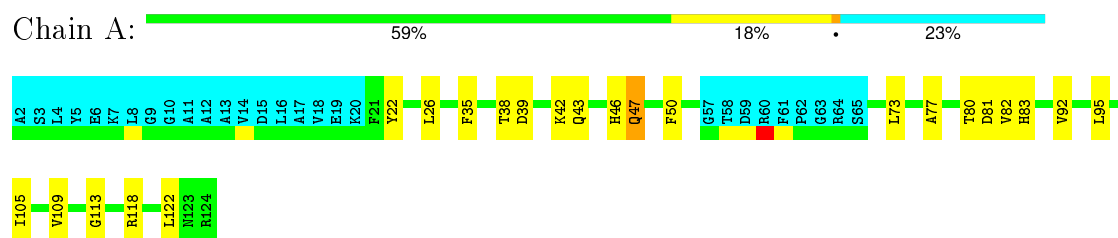
4.2.14 Score per residue for model 14

- Molecule 1: Cyanoglobin



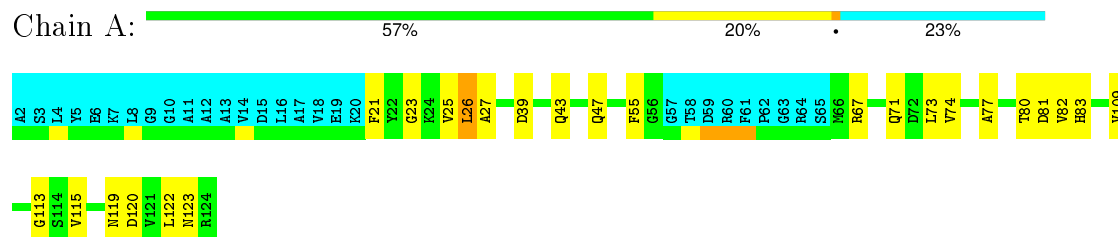
4.2.15 Score per residue for model 15

- Molecule 1: Cyanoglobin



4.2.16 Score per residue for model 16

- Molecule 1: Cyanoglobin



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing, torsion angle dynamics*.

Of the 30 calculated structures, 16 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
X-PLOR NIH	structure solution	2.23
X-PLOR NIH	refinement	2.23

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 16306
Number of chemical shift lists	1
Total number of shifts	1460
Number of shifts mapped to atoms	1429
Number of unparsed shifts	0
Number of shifts with mapping errors	31
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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: HEB

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 ⓘ

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	765	745	745	21±5
2	A	43	31	31	3±1
All	All	12928	12416	12416	358

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:LEU:HD13	1:A:27:ALA:N	0.94	1.77	16	1
1:A:26:LEU:O	1:A:26:LEU:HD22	0.82	1.73	16	1
1:A:73:LEU:HD11	2:A:125:HEB:HMD2	0.77	1.56	6	14
1:A:81:ASP:OD2	1:A:122:LEU:HD11	0.73	1.83	11	3
1:A:54:ALA:O	1:A:111:ILE:HG21	0.73	1.83	11	4
1:A:81:ASP:OD1	1:A:122:LEU:HD21	0.71	1.85	9	9
1:A:66:MET:SD	2:A:125:HEB:HMA2	0.66	2.29	9	2
1:A:26:LEU:C	1:A:26:LEU:HD12	0.66	2.10	2	1
1:A:26:LEU:HD22	1:A:26:LEU:C	0.66	2.10	16	1
1:A:26:LEU:HD13	1:A:26:LEU:C	0.64	2.13	16	1
1:A:33:ARG:O	1:A:36:VAL:HG13	0.63	1.93	10	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:ASP:OD1	1:A:122:LEU:HD11	0.63	1.94	2	3
1:A:96:GLN:NE2	1:A:105:ILE:HD13	0.62	2.09	14	1
1:A:26:LEU:O	1:A:26:LEU:HD12	0.62	1.95	2	1
1:A:47:GLN:N	1:A:47:GLN:OE1	0.61	2.33	9	5
1:A:96:GLN:NE2	1:A:105:ILE:CD1	0.61	2.64	8	3
2:A:125:HEB:HBB2	2:A:125:HEB:HMB1	0.61	1.72	1	11
1:A:47:GLN:OE1	1:A:47:GLN:N	0.61	2.33	2	7
1:A:43:GLN:O	1:A:47:GLN:NE2	0.61	2.34	7	13
1:A:102:GLN:NE2	1:A:105:ILE:HD12	0.60	2.11	11	5
1:A:115:VAL:HG12	1:A:119:ASN:ND2	0.60	2.12	7	4
1:A:38:THR:HG23	1:A:42:LYS:NZ	0.59	2.11	15	1
1:A:109:VAL:O	1:A:113:GLY:N	0.59	2.35	12	14
1:A:81:ASP:OD2	1:A:118:ARG:NH2	0.59	2.36	4	3
1:A:80:THR:OG1	1:A:83:HIS:CE1	0.58	2.56	3	3
2:A:125:HEB:HMB1	2:A:125:HEB:HBB2	0.58	1.73	7	5
1:A:73:LEU:O	1:A:77:ALA:N	0.58	2.36	9	13
1:A:81:ASP:CG	1:A:122:LEU:HD11	0.58	2.17	13	3
1:A:67:ARG:NH2	1:A:120:ASP:OD1	0.57	2.38	8	2
1:A:96:GLN:N	1:A:96:GLN:NE2	0.56	2.54	14	1
1:A:80:THR:OG1	1:A:83:HIS:ND1	0.55	2.38	3	5
1:A:47:GLN:CD	1:A:47:GLN:N	0.55	2.59	8	9
1:A:92:VAL:O	1:A:96:GLN:NE2	0.55	2.40	14	1
1:A:50:PHE:CE1	2:A:125:HEB:HBB3	0.55	2.37	5	8
1:A:33:ARG:O	1:A:36:VAL:HG22	0.55	2.00	10	2
1:A:47:GLN:N	1:A:47:GLN:CD	0.55	2.60	4	5
1:A:23:GLY:O	1:A:26:LEU:CD1	0.54	2.56	16	1
1:A:26:LEU:HD13	1:A:26:LEU:O	0.54	2.03	3	1
1:A:95:LEU:HD12	1:A:105:ILE:HG23	0.54	1.78	7	6
1:A:67:ARG:NH1	1:A:124:ARG:O	0.54	2.41	5	1
1:A:81:ASP:CG	1:A:118:ARG:NH2	0.54	2.61	10	1
1:A:24:LYS:NZ	1:A:90:ASN:OD1	0.53	2.40	12	1
1:A:115:VAL:HG12	1:A:119:ASN:HD21	0.52	1.64	7	1
1:A:54:ALA:O	1:A:111:ILE:CG2	0.51	2.57	11	1
1:A:73:LEU:O	1:A:77:ALA:O	0.51	2.29	12	15
1:A:26:LEU:C	1:A:26:LEU:CD1	0.51	2.77	2	1
1:A:71:GLN:O	1:A:75:GLU:OE1	0.51	2.28	3	1
1:A:46:HIS:CD2	2:A:125:HEB:ND	0.51	2.79	7	8
1:A:35:PHE:O	1:A:38:THR:O	0.51	2.29	5	7
1:A:120:ASP:O	1:A:123:ASN:OD1	0.51	2.29	11	12
1:A:33:ARG:O	1:A:36:VAL:HG23	0.50	2.06	6	7
1:A:37:ASN:ND2	1:A:76:ASN:HD22	0.50	2.04	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ARG:O	1:A:71:GLN:N	0.50	2.43	16	8
1:A:24:LYS:NZ	1:A:97:GLU:CD	0.50	2.65	2	1
1:A:39:ASP:OD1	1:A:39:ASP:O	0.50	2.29	15	2
1:A:25:VAL:HG11	1:A:47:GLN:NE2	0.50	2.21	2	1
1:A:81:ASP:OD1	1:A:122:LEU:CD2	0.49	2.60	9	3
1:A:21:PHE:CE2	1:A:25:VAL:CG2	0.49	2.95	16	1
1:A:43:GLN:O	1:A:47:GLN:OE1	0.49	2.30	2	2
1:A:67:ARG:HH12	1:A:124:ARG:C	0.49	2.11	11	1
1:A:119:ASN:O	1:A:123:ASN:N	0.49	2.45	8	1
1:A:112:VAL:O	1:A:114:SER:N	0.49	2.45	2	1
1:A:25:VAL:HG11	1:A:47:GLN:HE21	0.49	1.68	2	1
1:A:47:GLN:OE1	1:A:47:GLN:CA	0.48	2.61	13	5
1:A:50:PHE:CD1	2:A:125:HEB:HBB3	0.48	2.43	6	3
1:A:80:THR:OG1	1:A:82:VAL:HG12	0.48	2.07	6	7
1:A:75:GLU:N	1:A:75:GLU:OE1	0.48	2.47	3	1
1:A:26:LEU:CD2	1:A:26:LEU:C	0.48	2.80	16	1
1:A:82:VAL:CG1	1:A:83:HIS:N	0.48	2.76	16	12
1:A:92:VAL:O	1:A:96:GLN:OE1	0.48	2.31	14	1
1:A:81:ASP:CB	1:A:118:ARG:HH21	0.48	2.22	6	2
1:A:47:GLN:CA	1:A:47:GLN:OE1	0.48	2.62	6	5
1:A:81:ASP:O	1:A:83:HIS:N	0.47	2.47	1	1
1:A:100:VAL:CG1	1:A:104:LEU:HD12	0.47	2.39	11	1
1:A:28:ASP:OD1	1:A:30:ARG:CZ	0.47	2.63	12	1
1:A:24:LYS:NZ	1:A:93:LEU:CB	0.47	2.77	14	1
1:A:39:ASP:OD1	1:A:42:LYS:N	0.46	2.46	8	2
1:A:33:ARG:O	1:A:36:VAL:CG1	0.46	2.63	10	2
1:A:81:ASP:C	1:A:83:HIS:N	0.46	2.68	1	1
1:A:66:MET:SD	2:A:125:HEB:CMA	0.46	3.02	9	1
1:A:21:PHE:O	1:A:25:VAL:HG23	0.46	2.10	16	1
1:A:39:ASP:OD1	1:A:39:ASP:C	0.46	2.55	8	7
1:A:24:LYS:HZ3	1:A:93:LEU:CB	0.46	2.23	14	1
1:A:39:ASP:C	1:A:39:ASP:OD1	0.46	2.55	4	6
1:A:22:TYR:CE2	1:A:26:LEU:HD11	0.46	2.46	15	1
1:A:67:ARG:NE	1:A:120:ASP:OD1	0.45	2.50	10	1
1:A:53:TYR:CD1	1:A:53:TYR:O	0.45	2.69	1	1
1:A:24:LYS:HZ3	1:A:93:LEU:HB2	0.45	1.70	14	1
1:A:92:VAL:HG13	1:A:105:ILE:HG21	0.45	1.88	2	3
1:A:74:VAL:HG21	1:A:123:ASN:HD22	0.45	1.71	16	1
1:A:122:LEU:O	1:A:124:ARG:NH1	0.45	2.50	14	1
1:A:24:LYS:NZ	1:A:97:GLU:OE2	0.45	2.42	3	1
1:A:46:HIS:ND1	1:A:47:GLN:OE1	0.44	2.49	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:ASP:CG	1:A:118:ARG:HH22	0.44	2.13	10	1
1:A:39:ASP:O	1:A:39:ASP:OD1	0.44	2.35	4	1
1:A:81:ASP:CG	1:A:118:ARG:HE	0.44	2.15	7	2
1:A:112:VAL:C	1:A:114:SER:H	0.44	2.16	11	3
1:A:96:GLN:NE2	1:A:102:GLN:HE22	0.44	2.11	8	1
1:A:81:ASP:CG	1:A:122:LEU:HD21	0.43	2.34	9	2
1:A:39:ASP:N	1:A:39:ASP:OD1	0.43	2.50	6	2
1:A:39:ASP:OD1	1:A:42:LYS:CG	0.43	2.66	6	1
1:A:80:THR:HG1	1:A:83:HIS:CE1	0.43	2.27	3	1
1:A:96:GLN:HE21	1:A:105:ILE:CD1	0.43	2.25	8	1
1:A:113:GLY:O	1:A:114:SER:C	0.42	2.58	6	1
1:A:28:ASP:O	1:A:31:VAL:HG22	0.42	2.14	3	2
1:A:102:GLN:HA	1:A:105:ILE:HD12	0.41	1.91	2	1
1:A:108:VAL:O	1:A:112:VAL:HG22	0.41	2.15	12	1
1:A:96:GLN:OE1	1:A:105:ILE:HD11	0.41	2.14	4	1
1:A:33:ARG:O	1:A:36:VAL:CG2	0.41	2.68	10	1
1:A:54:ALA:O	1:A:111:ILE:CD1	0.40	2.69	11	1
1:A:123:ASN:O	1:A:124:ARG:C	0.40	2.58	8	1
1:A:52:THR:C	1:A:54:ALA:N	0.40	2.75	1	1
1:A:81:ASP:CB	1:A:118:ARG:NH2	0.40	2.84	4	1
1:A:96:GLN:HE21	1:A:105:ILE:HD13	0.40	1.77	3	1
1:A:34:PHE:CE2	1:A:77:ALA:HB1	0.40	2.52	1	1
1:A:81:ASP:O	1:A:84:PHE:N	0.40	2.54	1	1
1:A:92:VAL:O	1:A:96:GLN:CD	0.40	2.60	14	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	94/123 (76%)	92±2 (98±2%)	2±1 (2±1%)	0±1 (0±1%)	50	83
All	All	1504/1968 (76%)	1469 (98%)	31 (2%)	4 (0%)	50	83

All 4 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	123	ASN	1
1	A	113	GLY	1
1	A	82	VAL	1
1	A	101	SER	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	83/102 (81%)	82±1 (98±1%)	1±1 (2±1%)	71	95
All	All	1328/1632 (81%)	1306 (98%)	22 (2%)	71	95

All 7 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	47	GLN	11
1	A	26	LEU	4
1	A	42	LYS	2
1	A	102	GLN	2
1	A	96	GLN	1
1	A	24	LYS	1
1	A	40	MET	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

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	HEB	A	125	1	24,50,50	1.53±0.01	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	HEB	A	125	1	18,82,82	1.01±0.03	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	HEB	A	125	1	-	0±0,8,54,54	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 [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16306

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	1460
Number of shifts mapped to atoms	1429
Number of unparsed shifts	0
Number of shifts with mapping errors	31
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	39

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

- Chain not found in structure. All 31 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	HEB	HMB1	11.0	0.02	1
UNMAPPED	1	HEB	HBD1	0.46	0.02	2
UNMAPPED	1	HEB	HMD2	19.41	0.02	1
UNMAPPED	1	HEB	HMA1	13.27	0.02	1
UNMAPPED	1	HEB	HBB3	0.82	0.02	1
UNMAPPED	1	HEB	HAA2	2.63	0.02	2
UNMAPPED	1	HEB	HHH	-1.26	0.05	1
UNMAPPED	1	HEB	HMC1	12.05	0.02	1
UNMAPPED	1	HEB	HBD2	0.75	0.02	2
UNMAPPED	1	HEB	HMD1	19.41	0.02	1
UNMAPPED	1	HEB	HMC2	12.05	0.02	1
UNMAPPED	1	HEB	HAD2	7.75	0.02	2
UNMAPPED	1	HEB	HHC	1.06	0.05	1
UNMAPPED	1	HEB	HMA2	13.27	0.02	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	HEB	HMB3	11.0	0.02	1
UNMAPPED	1	HEB	HBC2	-2.44	0.02	1
UNMAPPED	1	HEB	HAC	6.67	0.02	1
UNMAPPED	1	HEB	HAB2	2.75	0.02	1
UNMAPPED	1	HEB	HBA2	-0.57	0.02	2
UNMAPPED	1	HEB	HBC1	-2.04	0.02	1
UNMAPPED	1	HEB	HMC3	12.05	0.02	1
UNMAPPED	1	HEB	HAD1	8.4	0.02	2
UNMAPPED	1	HEB	HHB	0.61	0.05	1
UNMAPPED	1	HEB	HMD3	19.41	0.02	1
UNMAPPED	1	HEB	HMA3	13.27	0.02	1
UNMAPPED	1	HEB	HBB1	0.82	0.02	1
UNMAPPED	1	HEB	HMB2	11.0	0.02	1
UNMAPPED	1	HEB	HHA	-2.3	0.05	1
UNMAPPED	1	HEB	HBA1	-0.11	0.02	2
UNMAPPED	1	HEB	HBB2	0.82	0.02	1
UNMAPPED	1	HEB	HAA1	3.52	0.02	2

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	116	-0.98 ± 0.21	Should be applied
$^{13}\text{C}_\beta$	109	0.28 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	115	-0.69 ± 0.16	Should be applied
^{15}N	118	0.15 ± 0.46	None needed (< 0.5 ppm)

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 88%, i.e. 1049 atoms were assigned a chemical shift out of a possible 1187. 14 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	475/475 (100%)	190/190 (100%)	190/190 (100%)	95/95 (100%)
Sidechain	494/614 (80%)	301/352 (86%)	175/229 (76%)	18/33 (55%)
Aromatic	80/98 (82%)	44/54 (81%)	34/40 (85%)	2/4 (50%)
Overall	1049/1187 (88%)	535/596 (90%)	399/459 (87%)	115/132 (87%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 1250 atoms were assigned a chemical shift out of a possible 1500. 18 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	583/613 (95%)	234/245 (96%)	231/246 (94%)	118/122 (97%)
Sidechain	570/772 (74%)	345/444 (78%)	207/287 (72%)	18/41 (44%)
Aromatic	97/115 (84%)	53/63 (84%)	42/48 (88%)	2/4 (50%)
Overall	1250/1500 (83%)	632/752 (84%)	480/581 (83%)	138/167 (83%)

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	46	HIS	HB2	11.84	4.91 – 1.31	24.2
1	A	70	HIS	HB2	9.92	4.91 – 1.31	18.9
1	A	70	HIS	HB3	9.45	5.00 – 1.10	16.4
1	A	46	HIS	HB3	9.20	5.00 – 1.10	15.8
1	A	121	VAL	HG12	4.15	2.13 – -0.47	12.8
1	A	121	VAL	HG13	4.15	2.13 – -0.47	12.8
1	A	121	VAL	HG11	4.15	2.13 – -0.47	12.8
1	A	46	HIS	CA	82.50	68.24 – 44.74	11.1
1	A	50	PHE	HD2	3.76	8.56 – 5.56	-11.0
1	A	50	PHE	HD1	3.76	8.56 – 5.56	-11.0
1	A	46	HIS	HA	9.41	6.81 – 2.41	10.9
1	A	121	VAL	HG22	3.78	2.20 – -0.60	10.6
1	A	121	VAL	HG21	3.78	2.20 – -0.60	10.6
1	A	121	VAL	HG23	3.78	2.20 – -0.60	10.6
1	A	69	ALA	HB3	-0.81	2.61 – 0.11	-8.7
1	A	69	ALA	HB2	-0.81	2.61 – 0.11	-8.7
1	A	69	ALA	HB1	-0.81	2.61 – 0.11	-8.7
1	A	50	PHE	HE2	4.54	8.69 – 5.49	-8.0
1	A	50	PHE	HE1	4.54	8.69 – 5.49	-8.0
1	A	87	ILE	HG21	-1.01	2.13 – -0.57	-6.6
1	A	87	ILE	HG22	-1.01	2.13 – -0.57	-6.6
1	A	87	ILE	HG23	-1.01	2.13 – -0.57	-6.6
1	A	87	ILE	HD11	-1.23	2.13 – -0.77	-6.6
1	A	87	ILE	HD12	-1.23	2.13 – -0.77	-6.6
1	A	87	ILE	HD13	-1.23	2.13 – -0.77	-6.6
1	A	70	HIS	CA	71.70	68.24 – 44.74	6.5
1	A	47	GLN	HA	6.96	6.41 – 2.11	6.3

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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	66	MET	HB3	4.09	3.70 – 0.30	6.1
1	A	121	VAL	HA	7.49	7.09 – 1.29	5.7
1	A	73	LEU	HD13	-0.80	2.16 – -0.64	-5.6
1	A	73	LEU	HD12	-0.80	2.16 – -0.64	-5.6
1	A	73	LEU	HD11	-0.80	2.16 – -0.64	-5.6
1	A	87	ILE	HB	0.23	3.24 – 0.34	-5.4
1	A	33	ARG	HG3	0.02	3.00 – 0.10	-5.3
1	A	47	GLN	HB2	3.35	3.30 – 0.80	5.2
1	A	79	LEU	HD11	-0.69	2.16 – -0.64	-5.2
1	A	79	LEU	HD13	-0.69	2.16 – -0.64	-5.2
1	A	79	LEU	HD12	-0.69	2.16 – -0.64	-5.2
1	A	121	VAL	HB	3.61	3.59 – 0.39	5.1

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:

