



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 12:30 AM BST

PDB ID : 2L22
Title : Mupirocin didomain ACP
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Deposited on : 2010-08-10

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 : unknown
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

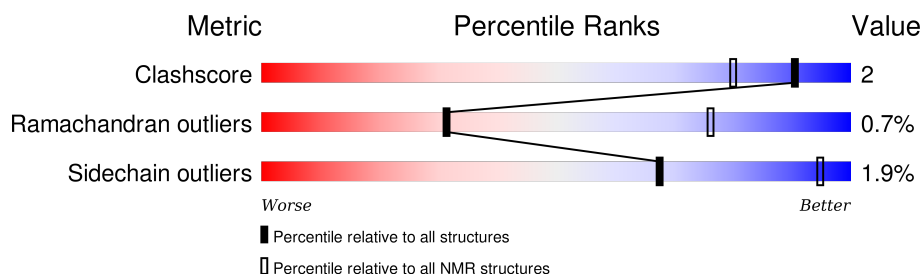
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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	212	

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:4-A:78 (75)	0.65	9
2	A:104-A:183 (80)	0.99	5

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2850 atoms, of which 1414 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Mupirocin didomain Acyl Carrier Protein.

Mol	Chain	Residues	Atoms						Trace
1	A	183	Total	C	H	N	O	S	0
			2850	910	1414	250	271	5	

There are 29 discrepancies between the modelled and reference sequences:

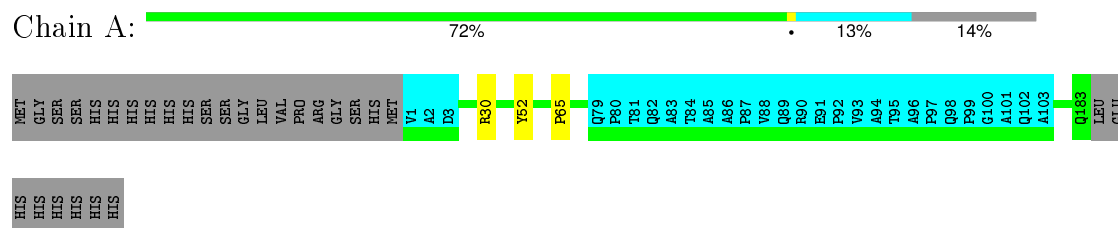
Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP Q8RL76
A	-19	GLY	-	EXPRESSION TAG	UNP Q8RL76
A	-18	SER	-	EXPRESSION TAG	UNP Q8RL76
A	-17	SER	-	EXPRESSION TAG	UNP Q8RL76
A	-16	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-15	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-14	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-13	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-12	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-11	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	-10	SER	-	EXPRESSION TAG	UNP Q8RL76
A	-9	SER	-	EXPRESSION TAG	UNP Q8RL76
A	-8	GLY	-	EXPRESSION TAG	UNP Q8RL76
A	-7	LEU	-	EXPRESSION TAG	UNP Q8RL76
A	-6	VAL	-	EXPRESSION TAG	UNP Q8RL76
A	-5	PRO	-	EXPRESSION TAG	UNP Q8RL76
A	-4	ARG	-	EXPRESSION TAG	UNP Q8RL76
A	-3	GLY	-	EXPRESSION TAG	UNP Q8RL76
A	-2	SER	-	EXPRESSION TAG	UNP Q8RL76
A	-1	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	0	MET	-	EXPRESSION TAG	UNP Q8RL76
A	184	LEU	-	EXPRESSION TAG	UNP Q8RL76
A	185	GLU	-	EXPRESSION TAG	UNP Q8RL76
A	186	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	187	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	188	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	189	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	190	HIS	-	EXPRESSION TAG	UNP Q8RL76
A	191	HIS	-	EXPRESSION TAG	UNP Q8RL76

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: Mupirocin didomain Acyl Carrier Protein

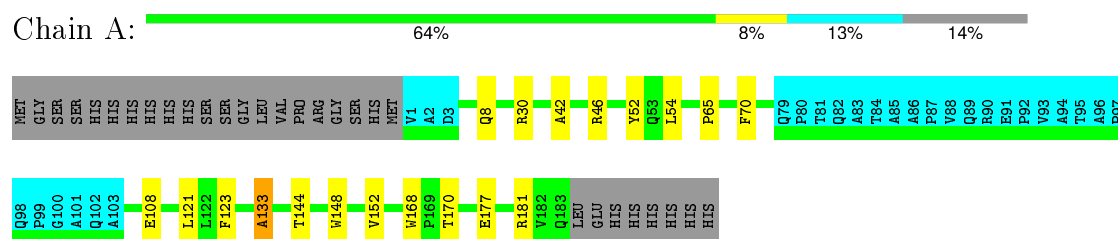


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

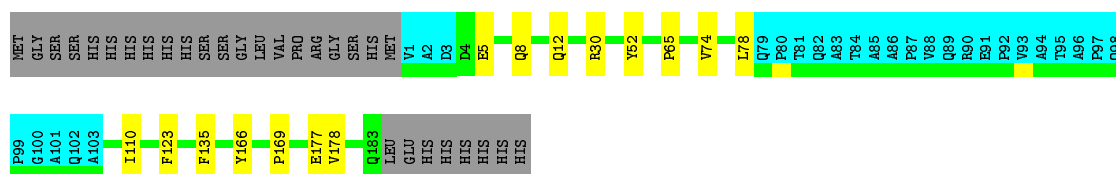
- Molecule 1: Mupirocin didomain Acyl Carrier Protein



4.2.2 Score per residue for model 2

- Molecule 1: Mupirocin didomain Acyl Carrier Protein

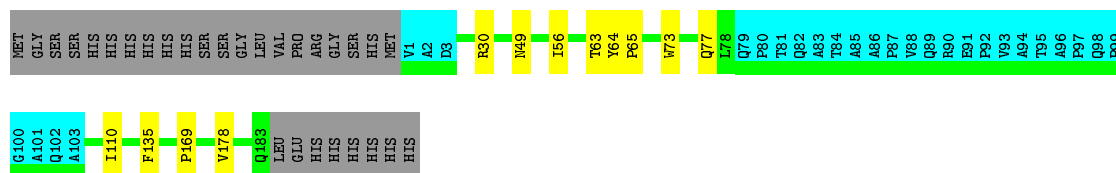




4.2.3 Score per residue for model 3

- Molecule 1: Mupirocin didomain Acyl Carrier Protein

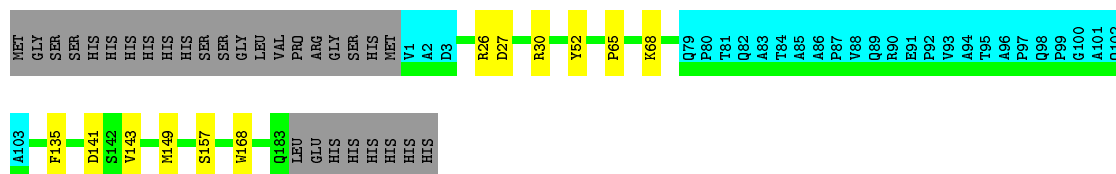
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Mupirocin didomain Acyl Carrier Protein

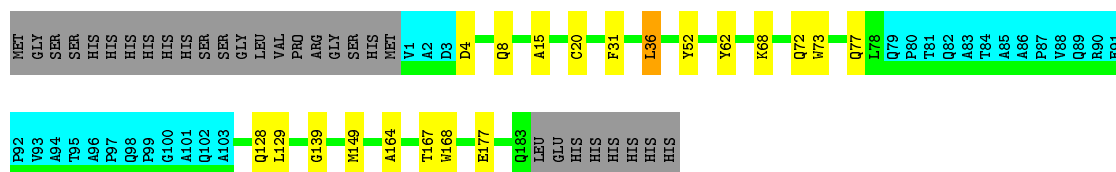
Chain A:



4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Mupirocin didomain Acyl Carrier Protein

Chain A:



4.2.6 Score per residue for model 6

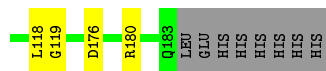
- Molecule 1: Mupirocin didomain Acyl Carrier Protein



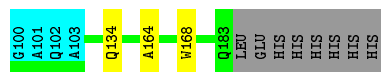
- ar:



- ar:

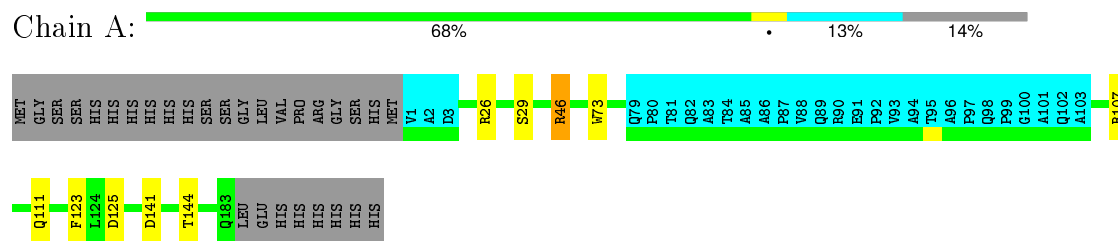


- ar:



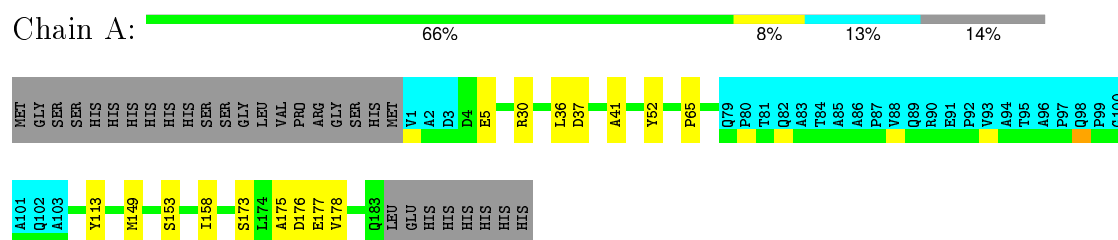
4.2.14 Score per residue for model 14

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



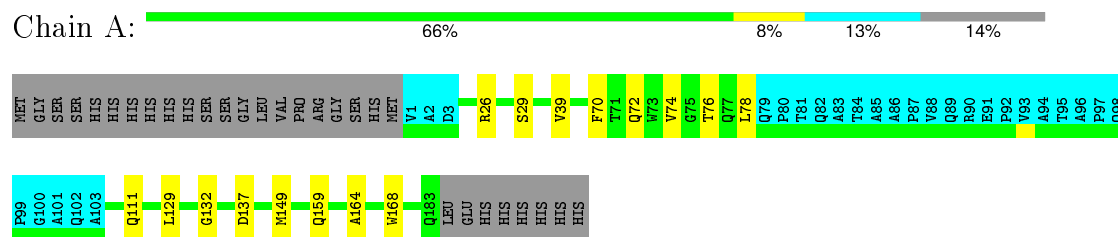
4.2.15 Score per residue for model 15

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



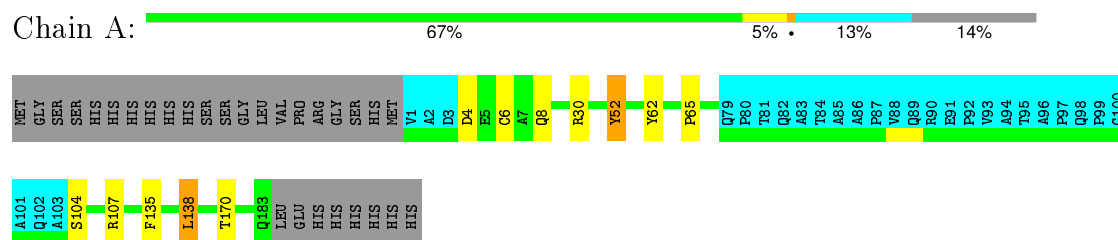
4.2.16 Score per residue for model 16

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



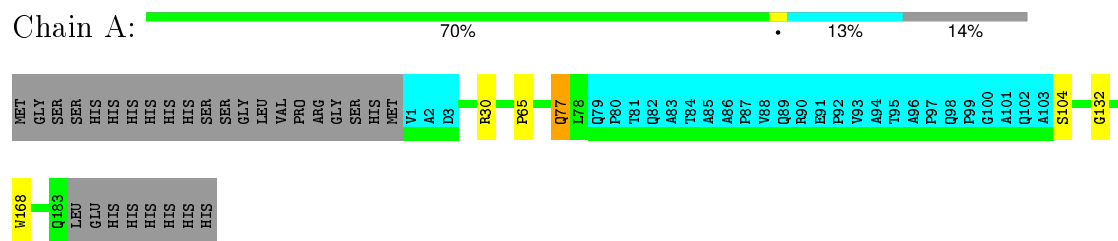
4.2.17 Score per residue for model 17

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



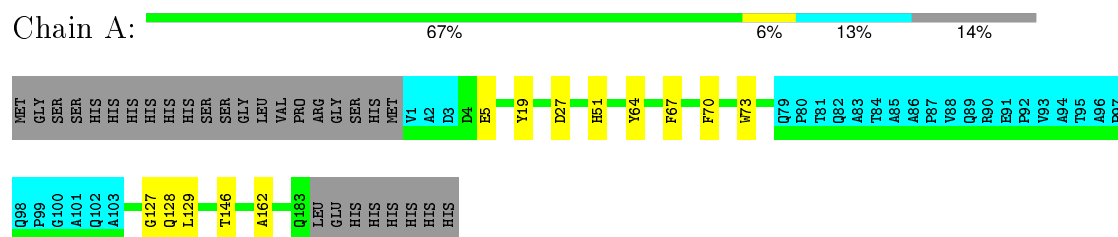
4.2.18 Score per residue for model 18

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



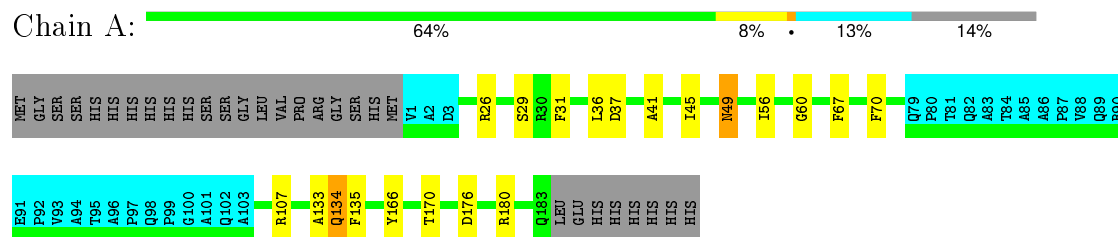
4.2.19 Score per residue for model 19

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



4.2.20 Score per residue for model 20

- Molecule 1: Mupirocin didomain Acyl Carrier Protein



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
ARIA	refinement	2.2

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 17111
Number of chemical shift lists	1
Total number of shifts	2061
Number of shifts mapped to atoms	2061
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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

6 Model quality

6.1 Standard geometry

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	0.69±0.05	2±2/1269 (0.1±0.1%)	0.63±0.02	0±0/1718 (0.0±0.0%)
All	All	0.69	32/25380 (0.1%)	0.63	0/34360 (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	0.2±0.4
All	All	0	5

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	52	TYR	CE1-CZ	-10.73	1.24	1.38	5	7
1	A	52	TYR	CE2-CZ	9.94	1.51	1.38	5	6
1	A	70	PHE	CE1-CZ	9.32	1.55	1.37	1	2
1	A	62	TYR	CE1-CZ	-8.26	1.27	1.38	17	3
1	A	62	TYR	CE2-CZ	8.23	1.49	1.38	17	2
1	A	70	PHE	CE2-CZ	-7.10	1.23	1.37	1	2
1	A	166	TYR	CE1-CZ	-6.94	1.29	1.38	2	1
1	A	166	TYR	CE2-CZ	6.30	1.46	1.38	2	2
1	A	113	TYR	CE2-CZ	-6.26	1.30	1.38	15	1
1	A	64	TYR	CE2-CZ	-6.01	1.30	1.38	6	1
1	A	31	PHE	CE1-CZ	5.87	1.48	1.37	5	1
1	A	64	TYR	CE1-CZ	-5.71	1.31	1.38	19	1
1	A	113	TYR	CE1-CZ	5.69	1.46	1.38	15	1
1	A	19	TYR	CE1-CZ	-5.57	1.31	1.38	19	1
1	A	19	TYR	CE2-CZ	5.01	1.45	1.38	19	1

There are no bond-angle outliers.

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	64	TYR	Sidechain	1
1	A	180	ARG	Sidechain	1
1	A	52	TYR	Sidechain	1
1	A	62	TYR	Sidechain	1
1	A	166	TYR	Sidechain	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	1242	1225	1223	5±2
All	All	24840	24500	24460	103

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:164:ALA:HA	1:A:168:TRP:CZ3	0.62	2.29	16	1
1:A:110:ILE:HG21	1:A:178:VAL:HG11	0.60	1.73	3	6
1:A:60:GLY:HA2	1:A:73:TRP:CZ3	0.60	2.32	7	1
1:A:30:ARG:HA	1:A:65:PRO:O	0.59	1.97	8	12
1:A:27:ASP:HA	1:A:67:PHE:CZ	0.56	2.36	13	2
1:A:150:ARG:HA	1:A:150:ARG:NE	0.56	2.16	11	1
1:A:15:ALA:HA	1:A:20:CYS:SG	0.55	2.41	10	3
1:A:73:TRP:O	1:A:77:GLN:HG2	0.53	2.04	12	2
1:A:7:ALA:O	1:A:11:ARG:HG3	0.53	2.03	8	1
1:A:49:ASN:OD1	1:A:56:ILE:HB	0.51	2.04	6	1
1:A:164:ALA:HA	1:A:168:TRP:CE3	0.49	2.42	16	1
1:A:134:GLN:NE2	1:A:135:PHE:H	0.48	2.06	20	1
1:A:36:LEU:HD21	1:A:41:ALA:HB2	0.48	1.85	15	3
1:A:168:TRP:CZ2	1:A:177:GLU:HG2	0.48	2.44	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:VAL:O	1:A:78:LEU:HG	0.48	2.08	16	2
1:A:173:SER:HA	1:A:176:ASP:OD2	0.47	2.09	15	1
1:A:49:ASN:O	1:A:53:GLN:HA	0.47	2.09	11	1
1:A:176:ASP:O	1:A:180:ARG:HG2	0.47	2.08	7	2
1:A:148:TRP:O	1:A:152:VAL:HG23	0.47	2.10	1	1
1:A:135:PHE:CD1	1:A:169:PRO:HA	0.47	2.45	13	2
1:A:175:ALA:O	1:A:178:VAL:HG12	0.46	2.10	15	1
1:A:8:GLN:O	1:A:12:GLN:HG3	0.46	2.11	2	1
1:A:141:ASP:OD2	1:A:143:VAL:HG12	0.46	2.11	4	1
1:A:133:ALA:O	1:A:170:THR:HA	0.46	2.11	20	2
1:A:46:ARG:HA	1:A:46:ARG:NE	0.46	2.25	14	1
1:A:4:ASP:O	1:A:8:GLN:HG3	0.45	2.11	5	2
1:A:135:PHE:HB3	1:A:168:TRP:O	0.45	2.12	4	1
1:A:6:CYS:HA	1:A:52:TYR:OH	0.45	2.11	17	2
1:A:176:ASP:O	1:A:180:ARG:HG3	0.45	2.11	8	1
1:A:70:PHE:O	1:A:73:TRP:HB3	0.45	2.12	19	4
1:A:118:LEU:HD12	1:A:119:GLY:N	0.44	2.27	8	2
1:A:110:ILE:HG12	1:A:156:PHE:CZ	0.44	2.47	6	1
1:A:181:ARG:HA	1:A:181:ARG:NE	0.44	2.27	1	1
1:A:42:ALA:O	1:A:46:ARG:HG2	0.44	2.12	1	1
1:A:164:ALA:HA	1:A:167:THR:OG1	0.44	2.12	5	1
1:A:140:MET:SD	1:A:165:ILE:HD12	0.44	2.52	7	1
1:A:74:VAL:O	1:A:77:GLN:HG2	0.44	2.12	13	1
1:A:168:TRP:CZ3	1:A:174:LEU:HD13	0.44	2.48	7	1
1:A:49:ASN:ND2	1:A:56:ILE:HG22	0.44	2.28	20	1
1:A:26:ARG:HD2	1:A:26:ARG:N	0.44	2.28	13	1
1:A:153:SER:OG	1:A:160:LEU:HB2	0.44	2.12	7	1
1:A:68:LYS:O	1:A:72:GLN:HG2	0.43	2.13	12	1
1:A:49:ASN:ND2	1:A:56:ILE:HB	0.43	2.29	3	1
1:A:135:PHE:HA	1:A:169:PRO:O	0.43	2.14	2	1
1:A:73:TRP:CZ3	1:A:77:GLN:HG3	0.43	2.48	3	1
1:A:44:TRP:O	1:A:47:GLU:HG3	0.43	2.13	12	1
1:A:164:ALA:HB1	1:A:168:TRP:CD1	0.43	2.48	9	1
1:A:121:LEU:HD21	1:A:144:THR:HB	0.42	1.90	1	1
1:A:26:ARG:HB3	1:A:29:SER:OG	0.42	2.14	20	1
1:A:107:ARG:O	1:A:111:GLN:HG2	0.42	2.14	14	1
1:A:42:ALA:O	1:A:46:ARG:HG3	0.42	2.14	9	1
1:A:27:ASP:HA	1:A:67:PHE:CE2	0.41	2.49	9	1
1:A:72:GLN:O	1:A:76:THR:HG22	0.41	2.16	16	1
1:A:26:ARG:HG2	1:A:29:SER:OG	0.41	2.15	16	1
1:A:60:GLY:HA3	1:A:70:PHE:CE1	0.41	2.51	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:104:SER:O	1:A:107:ARG:HB3	0.41	2.16	17	1
1:A:63:THR:HG23	1:A:64:TYR:CD2	0.41	2.50	3	1
1:A:31:PHE:CZ	1:A:67:PHE:HA	0.41	2.51	20	1
1:A:153:SER:HB2	1:A:158:ILE:O	0.41	2.16	15	1
1:A:77:GLN:HA	1:A:77:GLN:HE21	0.41	1.76	18	1
1:A:68:LYS:O	1:A:72:GLN:HG3	0.41	2.16	5	1
1:A:27:ASP:O	1:A:68:LYS:HB2	0.41	2.16	4	1
1:A:21:GLU:O	1:A:24:GLN:HG2	0.40	2.16	12	1
1:A:41:ALA:O	1:A:45:ILE:HG12	0.40	2.16	20	1
1:A:146:THR:HB	1:A:162:ALA:HB1	0.40	1.92	19	1
1:A:37:ASP:OD2	1:A:39:VAL:HG22	0.40	2.17	10	1
1:A:26:ARG:HB2	1:A:29:SER:OG	0.40	2.16	14	1
1:A:135:PHE:O	1:A:138:LEU:HD22	0.40	2.17	17	1
1:A:36:LEU:N	1:A:36:LEU:HD23	0.40	2.32	5	1
1:A:59:ASP:HA	1:A:62:TYR:CD2	0.40	2.52	13	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	154/212 (73%)	146±2 (95±1%)	7±2 (5±1%)	1±1 (1±1%)	31	76
All	All	3080/4240 (73%)	2914 (95%)	144 (5%)	22 (1%)	31	76

All 14 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	PHE	4
1	A	129	LEU	3
1	A	130	ARG	2
1	A	157	SER	2
1	A	132	GLY	2
1	A	128	GLN	1
1	A	139	GLY	1

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Mol	Chain	Res	Type	Models (Total)
1	A	127	GLY	1
1	A	25	ILE	1
1	A	104	SER	1
1	A	23	GLY	1
1	A	26	ARG	1
1	A	133	ALA	1
1	A	140	MET	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	131/176 (74%)	129±1 (98±1%)	2±1 (2±1%)	67	95
All	All	2620/3520 (74%)	2571 (98%)	49 (2%)	67	95

All 34 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	149	MET	4
1	A	5	GLU	3
1	A	134	GLN	3
1	A	177	GLU	3
1	A	47	GLU	2
1	A	168	TRP	2
1	A	49	ASN	2
1	A	36	LEU	2
1	A	37	ASP	2
1	A	144	THR	2
1	A	39	VAL	1
1	A	159	GLN	1
1	A	26	ARG	1
1	A	73	TRP	1
1	A	54	LEU	1
1	A	150	ARG	1
1	A	138	LEU	1
1	A	128	GLN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	51	HIS	1
1	A	137	ASP	1
1	A	183	GLN	1
1	A	108	GLU	1
1	A	50	LYS	1
1	A	125	ASP	1
1	A	141	ASP	1
1	A	107	ARG	1
1	A	170	THR	1
1	A	46	ARG	1
1	A	129	LEU	1
1	A	172	LYS	1
1	A	111	GLN	1
1	A	8	GLN	1
1	A	77	GLN	1
1	A	57	PRO	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 ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 80% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 17111

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	2061
Number of shifts mapped to atoms	2061
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	181	-0.22 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	168	0.24 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}'$	152	-0.39 ± 0.14	None needed (< 0.5 ppm)
^{15}N	172	0.19 ± 0.32	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 80%, i.e. 1559 atoms were assigned a chemical shift out of a possible 1948. 21 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	737/765 (96%)	303/305 (99%)	285/310 (92%)	149/150 (99%)
Sidechain	758/1008 (75%)	484/591 (82%)	271/366 (74%)	3/51 (6%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	64/175 (37%)	60/91 (66%)	0/76 (0%)	4/8 (50%)
Overall	1559/1948 (80%)	847/987 (86%)	556/752 (74%)	156/209 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1809 atoms were assigned a chemical shift out of a possible 2248. 23 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	859/895 (96%)	354/356 (99%)	333/366 (91%)	172/173 (99%)
Sidechain	886/1178 (75%)	565/691 (82%)	317/428 (74%)	4/59 (7%)
Aromatic	64/175 (37%)	60/91 (66%)	0/76 (0%)	4/8 (50%)
Overall	1809/2248 (80%)	979/1138 (86%)	650/870 (75%)	180/240 (75%)

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	167	THR	HG21	-0.17	2.29 – -0.01	-5.7
1	A	167	THR	HG22	-0.17	2.29 – -0.01	-5.7
1	A	167	THR	HG23	-0.17	2.29 – -0.01	-5.7

7.1.5 Random Coil Index (RCI) plots ⓘ

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:

