



Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 01:07 am GMT

PDB ID : 2ML5
Title : NMR structure of protein ZP_02064002.1 from *Bacteroides ovatus* ATCC 8483
Authors : Dutta, S.K.; Serrano, P.; Geralt, M.; Wuthrich, K.; Joint Center for Structural Genomics (JCSG)
Deposited on : 2014-02-19

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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
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

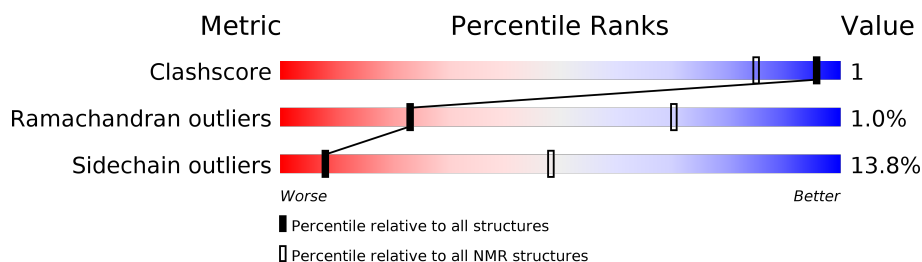
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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	155	 89% 6% 5%

2 Ensemble composition and analysis

This entry contains 20 models. Model 17 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:9-A:155 (147)	0.68	17

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 1 single-model cluster was found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2478 atoms, of which 1209 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms						Trace
1	A	155	Total	C	H	N	O	S	0
			2478	816	1209	195	256	2	

There is a discrepancy between the modelled and reference sequences:

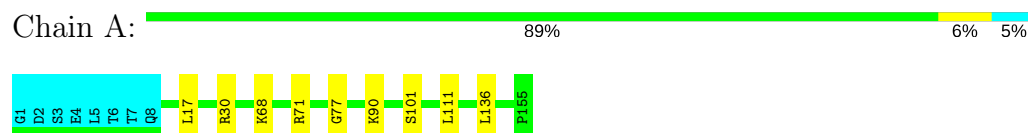
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	leader sequence	UNP A7LT22

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: Uncharacterized protein

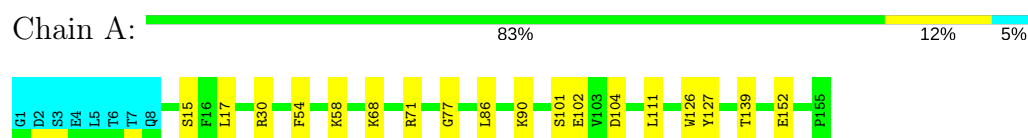


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

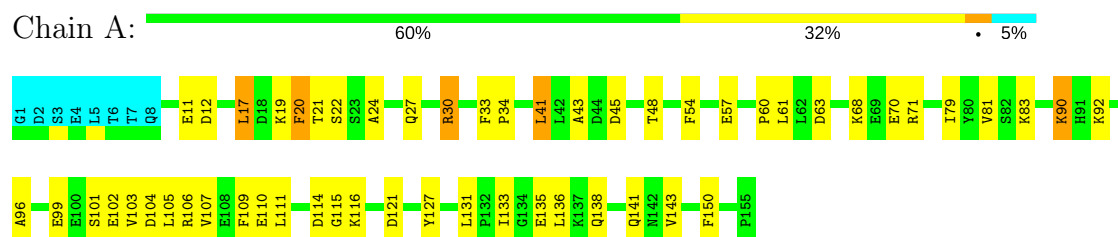
4.2.1 Score per residue for model 1

- Molecule 1: Uncharacterized protein



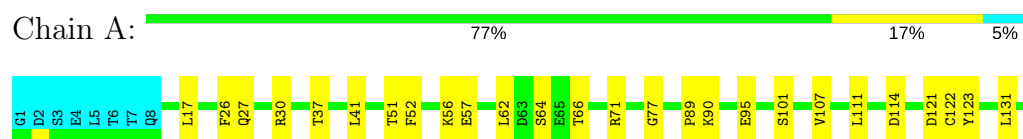
4.2.2 Score per residue for model 2

- Molecule 1: Uncharacterized protein



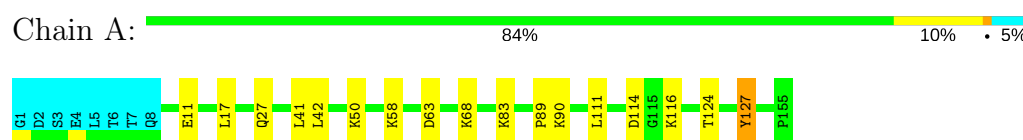
4.2.3 Score per residue for model 3

- Molecule 1: Uncharacterized protein



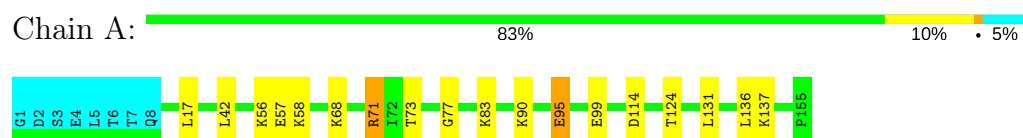
4.2.4 Score per residue for model 4

- Molecule 1: Uncharacterized protein



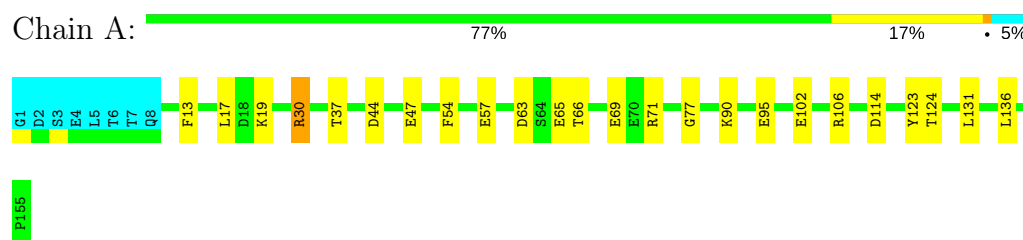
4.2.5 Score per residue for model 5

- Molecule 1: Uncharacterized protein



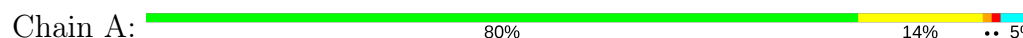
4.2.6 Score per residue for model 6

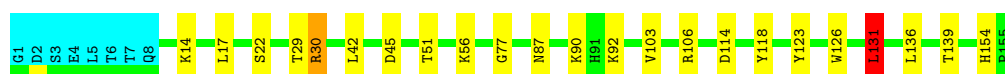
- Molecule 1: Uncharacterized protein



4.2.7 Score per residue for model 7

- Molecule 1: Uncharacterized protein





4.2.8 Score per residue for model 8

- Molecule 1: Uncharacterized protein

Chain A: 81% 14% 5%



4.2.9 Score per residue for model 9

- Molecule 1: Uncharacterized protein

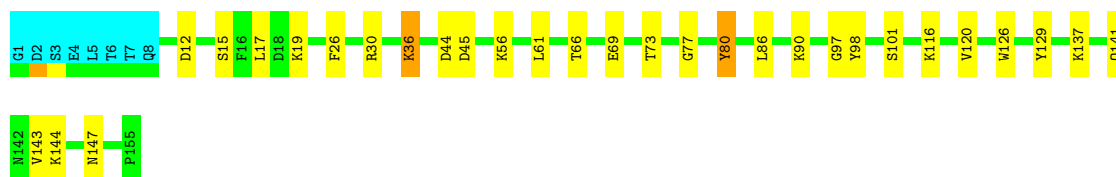
Chain A: 82% 12% 5%



4.2.10 Score per residue for model 10

- Molecule 1: Uncharacterized protein

Chain A: 75% 18% 5%



4.2.11 Score per residue for model 11

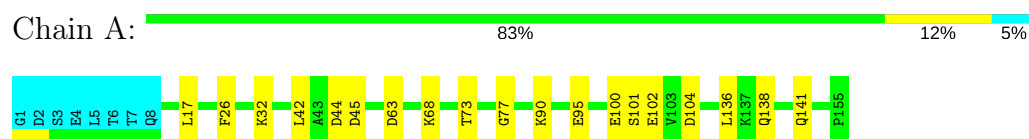
- Molecule 1: Uncharacterized protein

Chain A: 81% 14% 5%



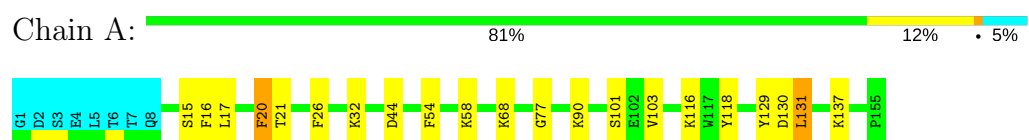
4.2.12 Score per residue for model 12

- Molecule 1: Uncharacterized protein



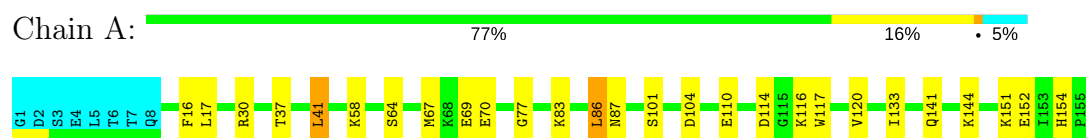
4.2.13 Score per residue for model 13

- Molecule 1: Uncharacterized protein



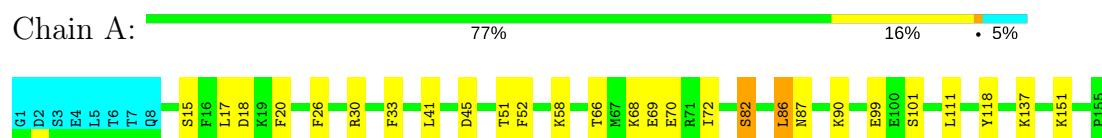
4.2.14 Score per residue for model 14

- Molecule 1: Uncharacterized protein



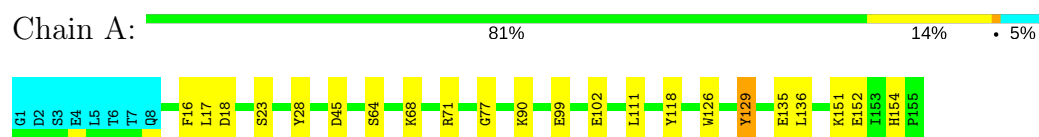
4.2.15 Score per residue for model 15

- Molecule 1: Uncharacterized protein



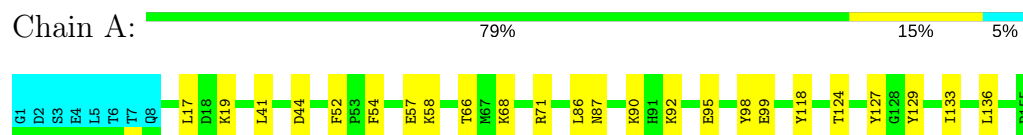
4.2.16 Score per residue for model 16

- Molecule 1: Uncharacterized protein



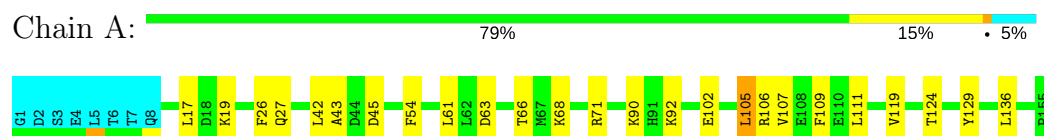
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Uncharacterized protein



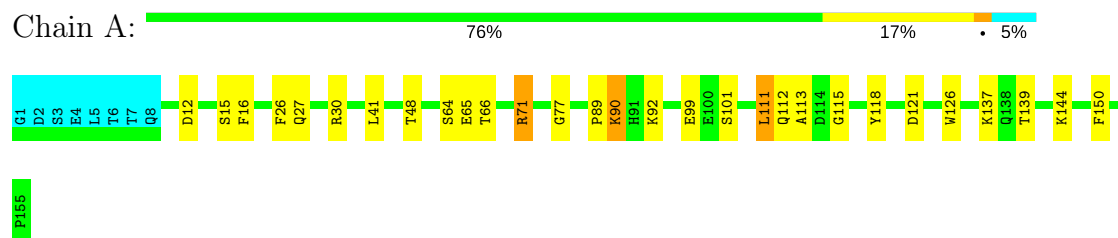
4.2.18 Score per residue for model 18

- Molecule 1: Uncharacterized protein



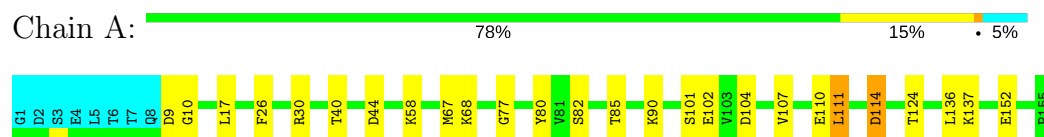
4.2.19 Score per residue for model 19

- Molecule 1: Uncharacterized protein



4.2.20 Score per residue for model 20

- Molecule 1: Uncharacterized protein



5 Refinement protocol and experimental data overview

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

Of the 80 calculated structures, 20 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
CYANA	structure solution	
j-UNIO	structure solution	
OPAL	geometry optimization	
OPAL	refinement	

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)	2ml5_cs.str
Number of chemical shift lists	1
Total number of shifts	1697
Number of shifts mapped to atoms	1697
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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

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	0.65±0.09	0±0/1243 (0.0±0.0%)	0.99±0.15	1±1/1680 (0.1±0.1%)
All	All	0.65	0/24860 (0.0%)	1.00	17/33600 (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	1.4±1.4
All	All	0	29

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	129	TYR	CB-CG-CD2	-7.64	116.42	121.00	16	3
1	A	71	ARG	NE-CZ-NH2	-6.29	117.15	120.30	9	1
1	A	98	TYR	CB-CG-CD1	-5.61	117.63	121.00	9	1
1	A	80	TYR	CB-CG-CD2	-5.54	117.67	121.00	10	1
1	A	111	LEU	CB-CG-CD2	5.54	120.42	111.00	20	1
1	A	27	GLN	CA-CB-CG	5.50	125.51	113.40	19	1
1	A	71	ARG	NE-CZ-NH1	5.33	122.96	120.30	19	1
1	A	54	PHE	CB-CG-CD1	-5.32	117.08	120.80	11	1
1	A	27	GLN	CB-CA-C	5.27	120.95	110.40	19	1
1	A	113	ALA	CB-CA-C	5.24	117.95	110.10	19	1
1	A	95	GLU	CA-CB-CG	5.11	124.64	113.40	5	1
1	A	118	TYR	CB-CG-CD2	-5.08	117.95	121.00	15	1
1	A	131	LEU	CB-CA-C	5.04	119.79	110.20	7	1
1	A	107	VAL	CA-CB-CG1	5.04	118.47	110.90	8	1
1	A	80	TYR	CB-CG-CD1	-5.02	117.99	121.00	11	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	30	ARG	Sidechain	5
1	A	118	TYR	Sidechain	4
1	A	127	TYR	Sidechain	3
1	A	71	ARG	Sidechain	3
1	A	98	TYR	Sidechain	2
1	A	106	ARG	Sidechain	2
1	A	129	TYR	Sidechain	2
1	A	114	ASP	Peptide	1
1	A	130	ASP	Peptide	1
1	A	82	SER	Peptide	1
1	A	123	TYR	Sidechain	1
1	A	10	GLY	Peptide	1
1	A	44	ASP	Peptide	1
1	A	22	SER	Peptide	1
1	A	28	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	1211	1158	1158	2±4
All	All	24220	23160	23160	50

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LEU:HD23	1:A:150:PHE:CD1	0.68	2.24	2	1
1:A:17:LEU:O	1:A:21:THR:HG23	0.65	1.91	2	1
1:A:111:LEU:HD13	1:A:114:ASP:HA	0.64	1.70	2	1
1:A:131:LEU:C	1:A:131:LEU:HD22	0.61	2.16	7	2
1:A:41:LEU:CD2	1:A:136:LEU:HD22	0.58	2.28	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:41:LEU:HD21	1:A:136:LEU:HD22	0.57	1.75	2	1
1:A:41:LEU:HD22	1:A:133:ILE:HA	0.56	1.77	2	2
1:A:127:TYR:OH	1:A:143:VAL:HG21	0.55	2.01	2	1
1:A:41:LEU:HD13	1:A:133:ILE:HA	0.55	1.78	17	2
1:A:90:LYS:HG3	1:A:111:LEU:HD12	0.50	1.83	2	1
1:A:90:LYS:CD	1:A:111:LEU:HD12	0.50	2.37	19	1
1:A:17:LEU:HD11	1:A:67:MET:HG2	0.49	1.85	20	1
1:A:107:VAL:HG12	1:A:109:PHE:CE1	0.49	2.43	2	1
1:A:41:LEU:HD12	1:A:52:PHE:CE1	0.48	2.42	17	2
1:A:71:ARG:HD3	1:A:79:ILE:HG21	0.48	1.86	2	1
1:A:24:ALA:HB1	1:A:61:LEU:HD21	0.48	1.86	2	1
1:A:141:GLN:HA	1:A:144:LYS:HE3	0.47	1.86	8	2
1:A:37:THR:HG22	1:A:121:ASP:OD1	0.47	2.10	3	1
1:A:148:ALA:HA	1:A:151:LYS:HD2	0.46	1.88	9	1
1:A:126:TRP:CE3	1:A:139:THR:HG23	0.46	2.46	7	2
1:A:109:PHE:CZ	1:A:119:VAL:HG22	0.46	2.46	18	1
1:A:35:LEU:HD22	1:A:120:VAL:C	0.46	2.32	11	1
1:A:141:GLN:HA	1:A:144:LYS:CE	0.45	2.41	14	1
1:A:16:PHE:CD2	1:A:117:TRP:HB2	0.45	2.47	9	1
1:A:86:LEU:HD22	1:A:87:ASN:H	0.45	1.72	17	3
1:A:37:THR:HG21	1:A:123:TYR:HB2	0.44	1.88	3	1
1:A:105:LEU:HD11	1:A:107:VAL:HG12	0.44	1.89	18	1
1:A:20:PHE:CE1	1:A:21:THR:HG23	0.44	2.48	13	1
1:A:20:PHE:C	1:A:20:PHE:CD1	0.43	2.92	2	1
1:A:43:ALA:HB3	1:A:48:THR:HB	0.43	1.90	2	1
1:A:12:ASP:HB3	1:A:15:SER:HB2	0.42	1.90	10	2
1:A:33:PHE:HA	1:A:34:PRO:C	0.42	2.33	2	1
1:A:70:GLU:O	1:A:81:VAL:HG23	0.42	2.14	2	1
1:A:96:ALA:O	1:A:103:VAL:HG12	0.41	2.15	2	1
1:A:70:GLU:HG3	1:A:72:ILE:HD11	0.41	1.91	15	1
1:A:103:VAL:HG23	1:A:123:TYR:CE2	0.41	2.49	7	1
1:A:36:LYS:HE3	1:A:120:VAL:CG1	0.41	2.45	10	1
1:A:16:PHE:CD2	1:A:117:TRP:CD1	0.41	3.09	14	1
1:A:112:GLN:HG3	1:A:118:TYR:CD1	0.40	2.51	19	1
1:A:60:PRO:HB3	1:A:143:VAL:HG13	0.40	1.92	2	1
1:A:126:TRP:CD2	1:A:143:VAL:HG22	0.40	2.52	10	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	146/155 (94%)	129±3 (88±2%)	16±3 (11±2%)	1±1 (1±1%)	23	70
All	All	2920/3100 (94%)	2572 (88%)	319 (11%)	29 (1%)	23	70

All 12 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	GLY	14
1	A	89	PRO	3
1	A	40	THR	2
1	A	115	GLY	2
1	A	97	GLY	1
1	A	98	TYR	1
1	A	43	ALA	1
1	A	30	ARG	1
1	A	114	ASP	1
1	A	107	VAL	1
1	A	69	GLU	1
1	A	129	TYR	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	131/138 (95%)	113±4 (86±3%)	18±4 (14±3%)	8	48
All	All	2620/2760 (95%)	2258 (86%)	362 (14%)	8	48

All 92 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	17	LEU	18
1	A	90	LYS	17
1	A	101	SER	13
1	A	68	LYS	12
1	A	136	LEU	11
1	A	111	LEU	10
1	A	26	PHE	9
1	A	30	ARG	9
1	A	45	ASP	8
1	A	124	THR	8
1	A	66	THR	8
1	A	102	GLU	8
1	A	58	LYS	8
1	A	99	GLU	7
1	A	44	ASP	6
1	A	42	LEU	6
1	A	92	LYS	6
1	A	71	ARG	6
1	A	137	LYS	6
1	A	131	LEU	6
1	A	95	GLU	6
1	A	114	ASP	6
1	A	54	PHE	6
1	A	116	LYS	5
1	A	57	GLU	5
1	A	104	ASP	5
1	A	15	SER	5
1	A	63	ASP	5
1	A	19	LYS	5
1	A	152	GLU	5
1	A	41	LEU	5
1	A	16	PHE	5
1	A	51	THR	4
1	A	20	PHE	4
1	A	83	LYS	4
1	A	151	LYS	4
1	A	27	GLN	4
1	A	56	LYS	4
1	A	64	SER	4
1	A	86	LEU	4
1	A	69	GLU	4
1	A	110	GLU	3
1	A	80	TYR	3

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Mol	Chain	Res	Type	Models (Total)
1	A	154	HIS	3
1	A	73	THR	3
1	A	121	ASP	3
1	A	32	LYS	2
1	A	47	GLU	2
1	A	146	GLU	2
1	A	12	ASP	2
1	A	105	LEU	2
1	A	37	THR	2
1	A	122	CYS	2
1	A	138	GLN	2
1	A	135	GLU	2
1	A	48	THR	2
1	A	52	PHE	2
1	A	33	PHE	2
1	A	18	ASP	2
1	A	141	GLN	2
1	A	61	LEU	2
1	A	106	ARG	2
1	A	126	TRP	2
1	A	65	GLU	2
1	A	11	GLU	2
1	A	82	SER	2
1	A	107	VAL	1
1	A	144	LYS	1
1	A	103	VAL	1
1	A	23	SER	1
1	A	70	GLU	1
1	A	75	GLU	1
1	A	36	LYS	1
1	A	142	ASN	1
1	A	85	THR	1
1	A	67	MET	1
1	A	14	LYS	1
1	A	9	ASP	1
1	A	50	LYS	1
1	A	118	TYR	1
1	A	13	PHE	1
1	A	150	PHE	1
1	A	100	GLU	1
1	A	62	LEU	1
1	A	120	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	22	SER	1
1	A	127	TYR	1
1	A	129	TYR	1
1	A	147	ASN	1
1	A	139	THR	1
1	A	87	ASN	1
1	A	29	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 ⓘ

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 81% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: 2ml5_cs.str

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	1697
Number of shifts mapped to atoms	1697
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	152	-0.03 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	137	0.25 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	146	0.45 ± 0.28	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 81%, i.e. 1504 atoms were assigned a chemical shift out of a possible 1853. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	572/721 (79%)	286/287 (100%)	146/294 (50%)	140/140 (100%)
Sidechain	779/927 (84%)	489/544 (90%)	282/351 (80%)	8/32 (25%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	153/205 (75%)	78/109 (72%)	72/91 (79%)	3/5 (60%)
Overall	1504/1853 (81%)	853/940 (91%)	500/736 (68%)	151/177 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1547 atoms were assigned a chemical shift out of a possible 1934. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	595/761 (78%)	297/303 (98%)	152/310 (49%)	146/148 (99%)
Sidechain	799/968 (83%)	501/567 (88%)	289/368 (79%)	9/33 (27%)
Aromatic	153/205 (75%)	78/109 (72%)	72/91 (79%)	3/5 (60%)
Overall	1547/1934 (80%)	876/979 (89%)	513/769 (67%)	158/186 (85%)

7.1.4 Statistically unusual chemical shifts [i](#)

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	111	LEU	HB2	-0.99	3.32 – -0.08	-7.7
1	A	31	VAL	HG13	-1.02	2.13 – -0.47	-7.1
1	A	31	VAL	HG12	-1.02	2.13 – -0.47	-7.1
1	A	31	VAL	HG11	-1.02	2.13 – -0.47	-7.1
1	A	61	LEU	HB3	-0.44	3.34 – -0.26	-5.5

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:

