



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 09:34 am BST

PDB ID : 6BF2
Title : Solution structure of a Bcl-xL S62E mutant
Authors : Viacava Follis, A.; Phillips, A.; Kriwacki, R.W.
Deposited on : 2017-10-25

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

<https://www.wwpdb.org/validation/2017/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 : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

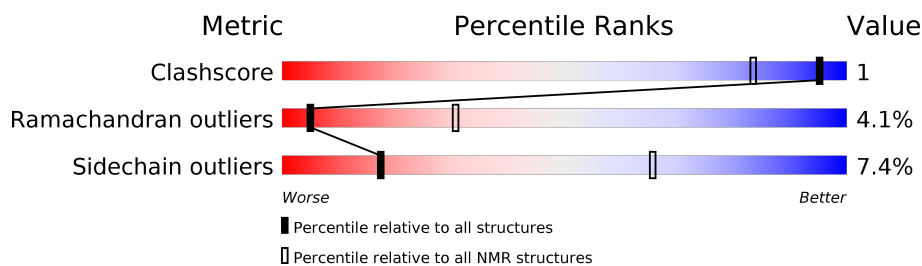
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 76%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	 83% 5% • 12%

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:3-A:32, A:45-A:201 (187)	0.90	9

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 3 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3237 atoms, of which 1566 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Bcl-2-like protein 1.

Mol	Chain	Residues	Atoms						Trace
1	A	212	Total	C	H	N	O	S	0
			3237	1041	1566	290	334	6	

There are 4 discrepancies between the modelled and reference sequences:

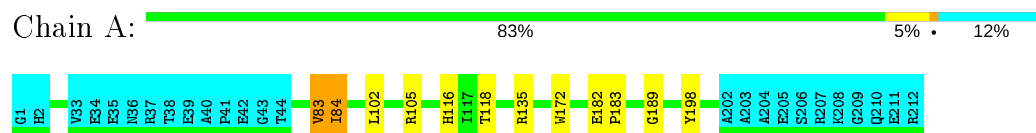
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q07817
A	2	HIS	-	expression tag	UNP Q07817
A	3	SER	-	expression tag	UNP Q07817
A	65	GLU	SER	engineered mutation	UNP Q07817

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: Bcl-2-like protein 1

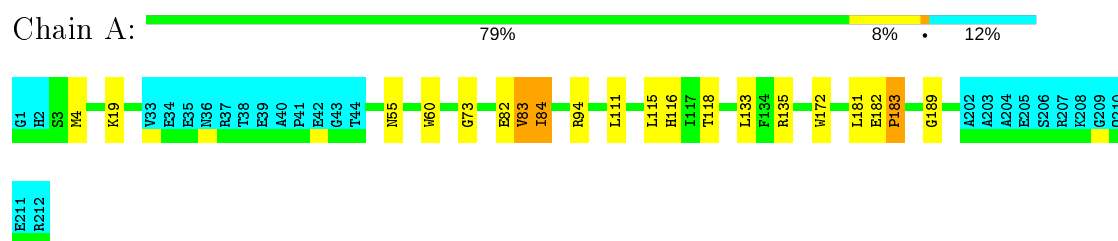


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

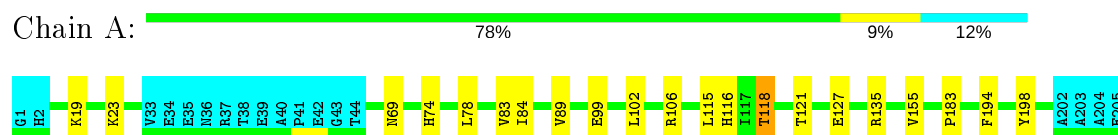
4.2.1 Score per residue for model 1

- Molecule 1: Bcl-2-like protein 1



4.2.2 Score per residue for model 2


- Molecule 1: Bcl-2-like protein 1



S206
R207
R208
G209
Q210
E211
R212

4.2.3 Score per residue for model 3

- Molecule 1: Bcl-2-like protein 1


Chain A:  77% 9% 12%

G1 H2 V33 E34 E35 N36 R37 T38 E39 A40 P41 E42 G43 T44 I54 H61 T72 L78 V83 I84 V89 R90 Q91 D98 L102 R105 T112 L115 H116 E127 R135 D136 Q163 H172 L181 E182 P183 Q186 E187 N188 A202

A203
A204
E205
S206
R207
R208
G209
Q210
E211
R212

4.2.4 Score per residue for model 4


- Molecule 1: Bcl-2-like protein 1

Chain A:  82% 5% 12%

G1 H2 Q22 V33 E34 E35 N36 R37 T38 E39 A40 P41 E42 G43 T44 E45 L62 T72 V83 I84 R105 H116 E127 L133 L165 E182 P183 Y198 A202 A203 A204 E205 S206 R207 G209 Q210 E211 R212

4.2.5 Score per residue for model 5

- Molecule 1: Bcl-2-like protein 1


Chain A:  78% 9% 12%

G1 H2 F15 L16 G24 V33 E34 E35 N36 R37 T38 E39 A40 P41 E42 G43 T44 T50 P51 A71 L78 V83 I84 E99 R103 Y104 R105 E127 L133 F134 R135 R142 F147 P183 M188 G189 F194 Y198 A202 A203 A204 E205

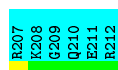
S206
R207
R208
G209
Q210
E211
R212

4.2.6 Score per residue for model 6

- Molecule 1: Bcl-2-like protein 1

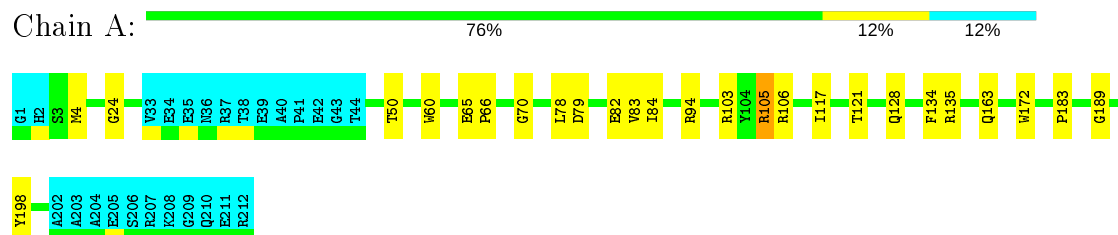
Chain A:  78% 8% 12%

G1 H2 S3 M4 V33 E34 E35 N36 R37 T38 E39 A40 P41 E42 G43 T44 T50 S77 L78 V83 I84 E99 L102 R105 T112 H116 I117 T118 P119 Q124 E127 N131 R135 D159 E182 G189 Y198 A202 A203 A204 E205 S206



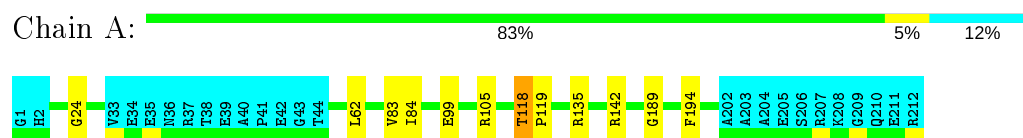
4.2.7 Score per residue for model 7

- Molecule 1: Bcl-2-like protein 1



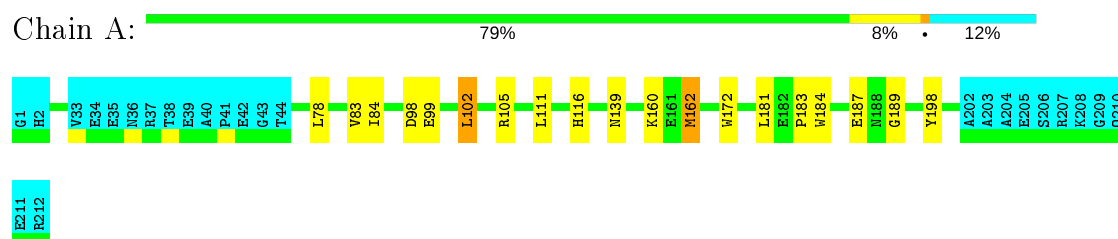
4.2.8 Score per residue for model 8

- Molecule 1: Bcl-2-like protein 1



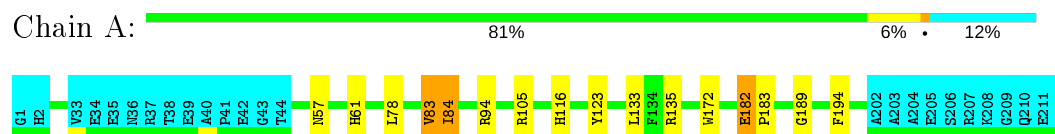
4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Bcl-2-like protein 1



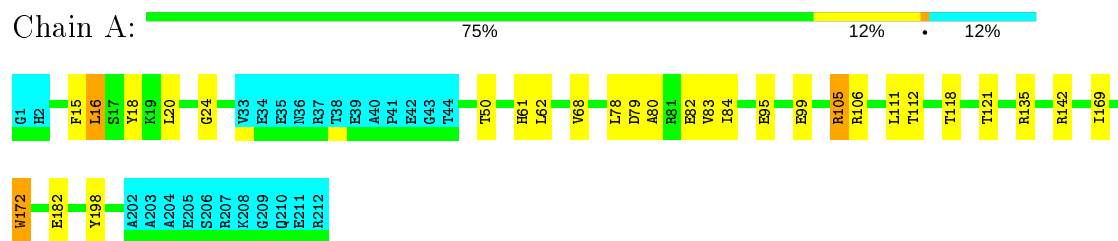
4.2.10 Score per residue for model 10

- Molecule 1: Bcl-2-like protein 1



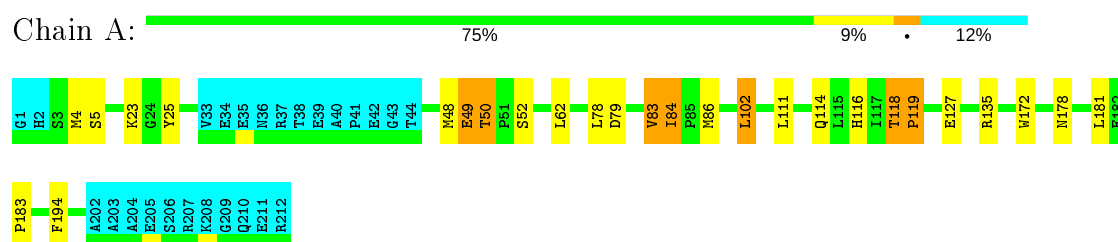
4.2.11 Score per residue for model 11

- Molecule 1: Bcl-2-like protein 1



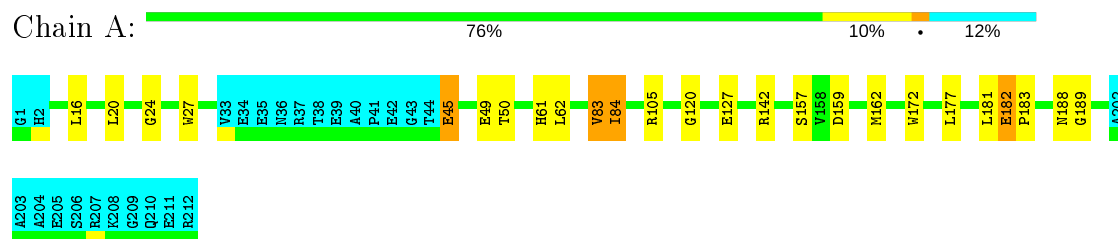
4.2.12 Score per residue for model 12

- Molecule 1: Bcl-2-like protein 1



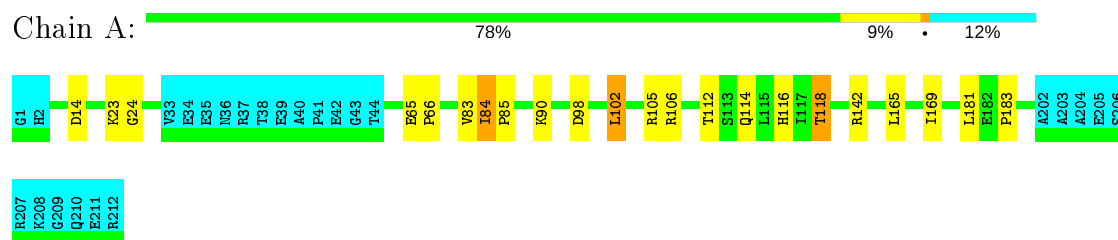
4.2.13 Score per residue for model 13

- Molecule 1: Bcl-2-like protein 1



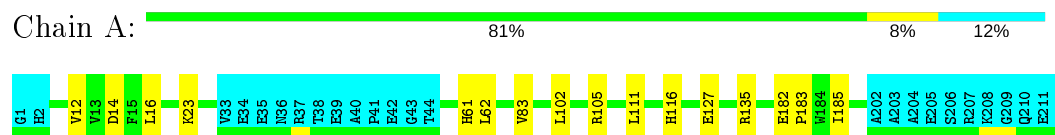
4.2.14 Score per residue for model 14

- Molecule 1: Bcl-2-like protein 1



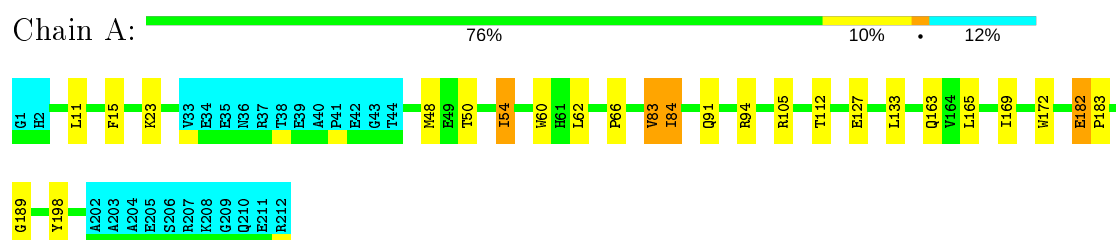
4.2.15 Score per residue for model 15

- Molecule 1: Bcl-2-like protein 1



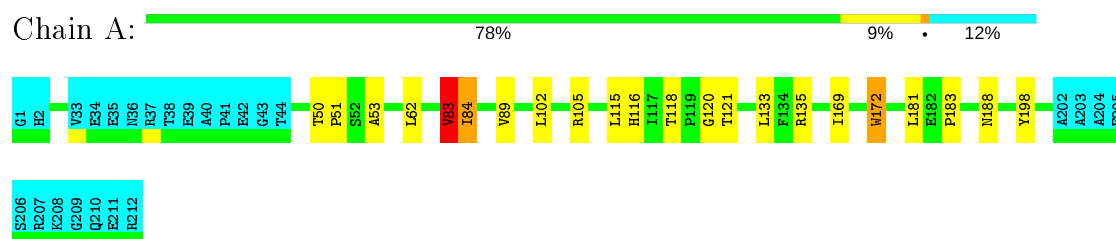
4.2.16 Score per residue for model 16

- Molecule 1: Bcl-2-like protein 1



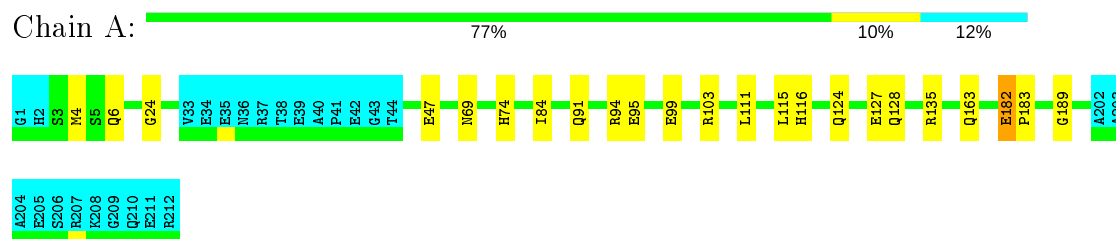
4.2.17 Score per residue for model 17

- Molecule 1: Bcl-2-like protein 1



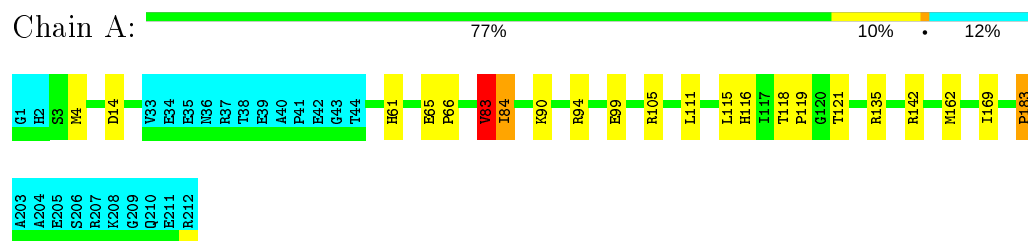
4.2.18 Score per residue for model 18

- Molecule 1: Bcl-2-like protein 1



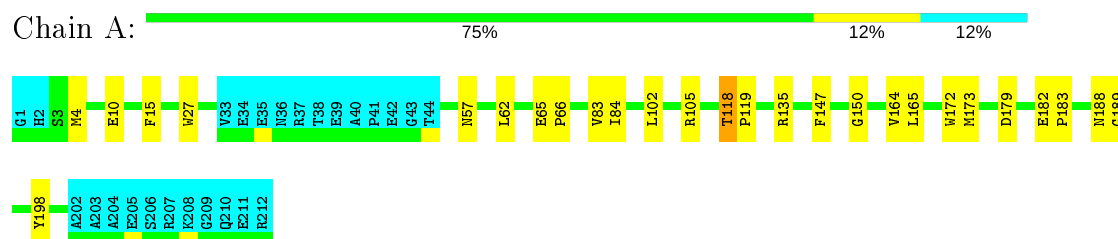
4.2.19 Score per residue for model 19

- Molecule 1: Bcl-2-like protein 1



4.2.20 Score per residue for model 20

- Molecule 1: Bcl-2-like protein 1



5 Refinement protocol and experimental data overview

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

Of the 400 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 calculation	2.1
TALOS	structure calculation	
CNS	refinement	1.3

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	2137
Number of shifts mapped to atoms	2137
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	76%

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](#)

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 [i](#)

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	1481	1390	1386	3±2
All	All	29620	27800	27720	59

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:98:ASP:O	1:A:102:LEU:HB3	0.59	1.98	3	2
1:A:83:VAL:HG12	1:A:84:ILE:H	0.58	1.58	12	2
1:A:83:VAL:O	1:A:84:ILE:HG12	0.55	2.02	6	8
1:A:50:THR:H	1:A:51:PRO:CD	0.51	2.18	5	1
1:A:83:VAL:O	1:A:84:ILE:HB	0.48	2.08	14	3
1:A:5:SER:HA	1:A:178:ASN:ND2	0.48	2.23	12	1
1:A:182:GLU:H	1:A:183:PRO:HD2	0.47	1.68	10	4
1:A:16:LEU:O	1:A:20:LEU:HG	0.47	2.09	13	2
1:A:157:SER:HB2	1:A:162:MET:O	0.47	2.10	13	1
1:A:102:LEU:O	1:A:102:LEU:HG	0.47	2.10	6	2
1:A:160:LYS:HB2	1:A:162:MET:SD	0.46	2.50	9	1
1:A:77:SER:O	1:A:78:LEU:HG	0.46	2.11	6	1
1:A:123:TYR:CD2	1:A:172:TRP:HB2	0.46	2.46	10	1
1:A:165:LEU:O	1:A:169:ILE:HG12	0.46	2.10	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:150:GLY:HA3	1:A:173:MET:SD	0.45	2.52	20	1
1:A:102:LEU:HG	1:A:102:LEU:O	0.45	2.10	12	1
1:A:12:VAL:O	1:A:16:LEU:HB2	0.44	2.12	15	1
1:A:182:GLU:HG2	1:A:185:ILE:HD12	0.44	1.90	15	1
1:A:50:THR:HG23	1:A:51:PRO:HD3	0.43	1.90	5	1
1:A:169:ILE:HA	1:A:172:TRP:CE2	0.43	2.48	11	2
1:A:65:GLU:N	1:A:66:PRO:HD2	0.43	2.28	14	4
1:A:182:GLU:N	1:A:183:PRO:HD3	0.43	2.28	1	2
1:A:15:PHE:CZ	1:A:147:PHE:HB3	0.43	2.49	20	2
1:A:90:LYS:O	1:A:94:ARG:HG2	0.42	2.14	19	1
1:A:95:GLU:O	1:A:99:GLU:HG2	0.42	2.14	11	1
1:A:182:GLU:H	1:A:183:PRO:CD	0.42	2.27	18	1
1:A:74:HIS:O	1:A:91:GLN:HB3	0.41	2.15	18	1
1:A:50:THR:N	1:A:51:PRO:CD	0.41	2.83	5	1
1:A:182:GLU:N	1:A:183:PRO:HD2	0.41	2.29	10	1
1:A:15:PHE:HA	1:A:18:TYR:CD1	0.41	2.50	11	1
1:A:183:PRO:HD2	1:A:184:TRP:CD1	0.41	2.51	9	1
1:A:118:THR:HB	1:A:119:PRO:HD3	0.41	1.93	12	1
1:A:50:THR:H	1:A:51:PRO:HD2	0.41	1.76	5	1
1:A:165:LEU:O	1:A:169:ILE:HG13	0.41	2.15	14	1
1:A:68:VAL:HB	1:A:105:ARG:NH2	0.41	2.31	11	1
1:A:98:ASP:O	1:A:102:LEU:HB2	0.41	2.16	14	1
1:A:83:VAL:HG12	1:A:84:ILE:N	0.40	2.28	12	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	187/212 (88%)	154±5 (82±2%)	26±5 (14±3%)	8±2 (4±1%)	5	31
All	All	3740/4240 (88%)	3075 (82%)	510 (14%)	155 (4%)	5	31

All 30 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	84	ILE	19
1	A	83	VAL	17
1	A	105	ARG	13
1	A	116	HIS	13
1	A	183	PRO	11
1	A	189	GLY	11
1	A	118	THR	8
1	A	24	GLY	7
1	A	62	LEU	7
1	A	50	THR	6
1	A	119	PRO	5
1	A	182	GLU	5
1	A	78	LEU	5
1	A	106	ARG	4
1	A	61	HIS	4
1	A	49	GLU	2
1	A	45	GLU	2
1	A	51	PRO	2
1	A	72	THR	2
1	A	120	GLY	2
1	A	80	ALA	1
1	A	70	GLY	1
1	A	86	MET	1
1	A	66	PRO	1
1	A	54	ILE	1
1	A	73	GLY	1
1	A	71	ALA	1
1	A	52	SER	1
1	A	53	ALA	1
1	A	55	ASN	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	158/176 (90%)	146±4 (93±2%)	12±4 (7±2%)	17	65
All	All	3160/3520 (90%)	2925 (93%)	235 (7%)	17	65

All 73 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	135	ARG	15
1	A	198	TYR	11
1	A	127	GLU	10
1	A	172	TRP	10
1	A	102	LEU	9
1	A	4	MET	7
1	A	99	GLU	7
1	A	118	THR	7
1	A	111	LEU	7
1	A	181	LEU	7
1	A	115	LEU	6
1	A	142	ARG	6
1	A	133	LEU	6
1	A	194	PHE	5
1	A	188	ASN	5
1	A	105	ARG	5
1	A	121	THR	5
1	A	23	LYS	5
1	A	94	ARG	5
1	A	112	THR	5
1	A	78	LEU	4
1	A	89	VAL	3
1	A	60	TRP	3
1	A	103	ARG	3
1	A	82	GLU	3
1	A	79	ASP	3
1	A	83	VAL	3
1	A	50	THR	3
1	A	163	GLN	3
1	A	14	ASP	3
1	A	182	GLU	3
1	A	162	MET	2
1	A	124	GLN	2
1	A	57	ASN	2
1	A	69	ASN	2
1	A	19	LYS	2
1	A	48	MET	2
1	A	61	HIS	2
1	A	159	ASP	2
1	A	128	GLN	2
1	A	114	GLN	2
1	A	54	ILE	2

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Mol	Chain	Res	Type	Models (Total)
1	A	27	TRP	2
1	A	16	LEU	2
1	A	165	LEU	2
1	A	62	LEU	2
1	A	91	GLN	2
1	A	169	ILE	1
1	A	117	ILE	1
1	A	49	GLU	1
1	A	177	LEU	1
1	A	134	PHE	1
1	A	25	TYR	1
1	A	136	ASP	1
1	A	95	GLU	1
1	A	85	PRO	1
1	A	139	ASN	1
1	A	47	GLU	1
1	A	74	HIS	1
1	A	22	GLN	1
1	A	183	PRO	1
1	A	187	GLU	1
1	A	45	GLU	1
1	A	10	GLU	1
1	A	6	GLN	1
1	A	11	LEU	1
1	A	179	ASP	1
1	A	131	ASN	1
1	A	90	LYS	1
1	A	155	VAL	1
1	A	15	PHE	1
1	A	201	ASN	1
1	A	186	GLN	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](#)

There are no ligands in this entry.

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 76% for the well-defined parts and 75% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chemical_shifts_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	2137
Number of shifts mapped to atoms	2137
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	203	0.59 ± 0.16	Should be applied
$^{13}\text{C}_\beta$	187	1.62 ± 0.06	Should be applied
$^{13}\text{C}'$	194	0.04 ± 0.08	None needed (< 0.5 ppm)
^{15}N	203	0.48 ± 0.20	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 76%, i.e. 1719 atoms were assigned a chemical shift out of a possible 2259. 25 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	894/923 (97%)	360/368 (98%)	354/374 (95%)	180/181 (99%)
Sidechain	711/1094 (65%)	484/641 (76%)	227/403 (56%)	0/50 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	114/242 (47%)	108/126 (86%)	0/102 (0%)	6/14 (43%)
Overall	1719/2259 (76%)	952/1135 (84%)	581/879 (66%)	186/245 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 75%, i.e. 1914 atoms were assigned a chemical shift out of a possible 2553. 26 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	1004/1046 (96%)	404/417 (97%)	397/424 (94%)	203/205 (99%)
Sidechain	796/1257 (63%)	546/737 (74%)	250/458 (55%)	0/62 (0%)
Aromatic	114/250 (46%)	108/130 (83%)	0/104 (0%)	6/16 (38%)
Overall	1914/2553 (75%)	1058/1284 (82%)	647/986 (66%)	209/283 (74%)

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	90	LYS	HD3	3.33	2.75 – 0.45	7.5
1	A	90	LYS	HD2	3.33	2.76 – 0.46	7.5
1	A	188	ASN	HB2	0.81	4.36 – 1.26	-6.4
1	A	188	ASN	HB3	0.81	4.41 – 1.11	-5.9
1	A	138	VAL	HG22	-0.75	2.20 – -0.60	-5.5
1	A	138	VAL	HG21	-0.75	2.20 – -0.60	-5.5
1	A	138	VAL	HG23	-0.75	2.20 – -0.60	-5.5
1	A	107	ALA	CB	28.49	28.03 – 9.93	5.3
1	A	140	TRP	HE3	5.26	9.33 – 5.33	-5.2

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:

