



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 19, 2021 – 04:12 PM EDT

PDB ID : 6B7G  
Title : Solution NMR structure of BCoR in complex with AF9 (BCoR-AF9)  
Authors : Schmidt, C.R.; Kuntimaddi, A.; Leach, B.I.; Bushweller, J.H.  
Deposited on : 2017-10-04

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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:

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 : 2.18  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.18

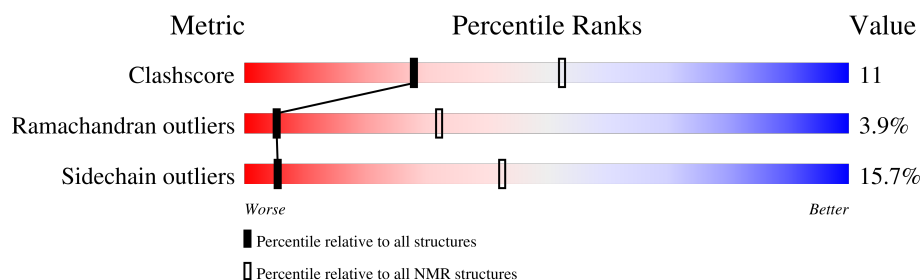
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 87%.

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  $\geq 3$ , 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	70	 66% 19% • 14%
2	B	33	 15% 9% 6% 70%

## 2 Ensemble composition and analysis

This entry contains 10 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: *lowest energy*.

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:502-A:561, B:1193-B:1202 (70)	0.26	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 3 clusters. No single-model clusters were found.

Cluster number	Models
1	3, 5, 6, 10
2	4, 7, 8
3	1, 2, 9

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1680 atoms, of which 840 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein AF-9.

Mol	Chain	Residues	Atoms						Trace
1	A	70	Total	C	H	N	O	S	0
			1164	363	584	101	113	3	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	499	MET	-	initiating methionine	UNP P42568

- Molecule 2 is a protein called BCL-6 corepressor.

Mol	Chain	Residues	Atoms						Trace
2	B	33	Total	C	H	N	O	S	0
			516	160	256	45	54	1	

There is a discrepancy between the modelled and reference sequences:

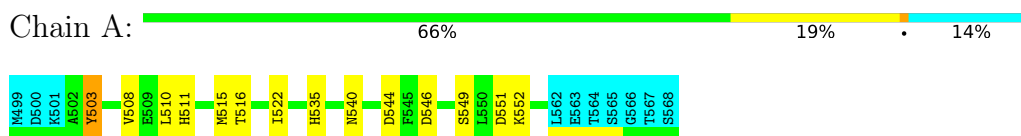
Chain	Residue	Modelled	Actual	Comment	Reference
B	1175	THR	-	expression tag	UNP Q6W2J9

## 4 Residue-property plots [i](#)

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: Protein AF-9



- Molecule 2: BCL-6 corepressor

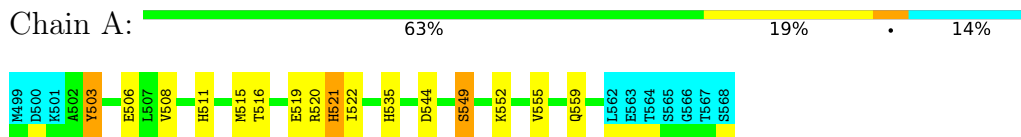


### 4.2 Scores per residue for each member of the ensemble

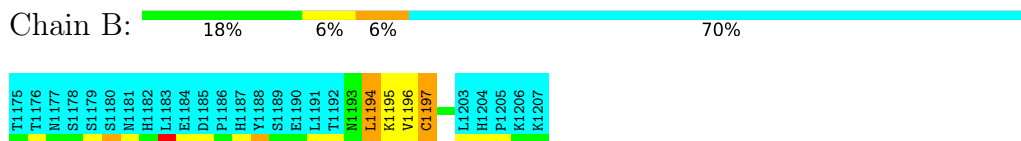
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Protein AF-9

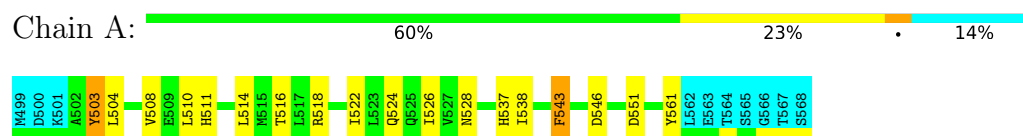


- Molecule 2: BCL-6 corepressor

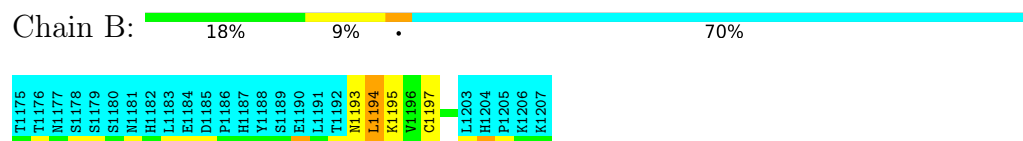


### 4.2.2 Score per residue for model 2

- Molecule 1: Protein AF-9

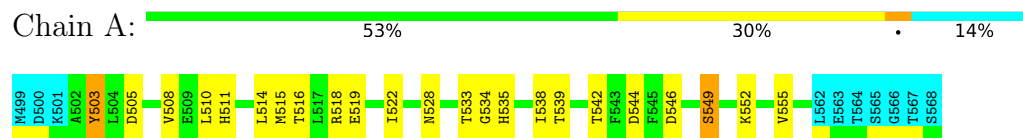


- Molecule 2: BCL-6 corepressor

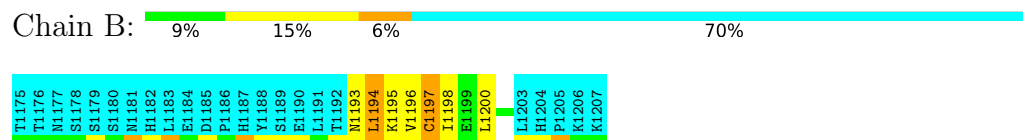


### 4.2.3 Score per residue for model 3

- Molecule 1: Protein AF-9

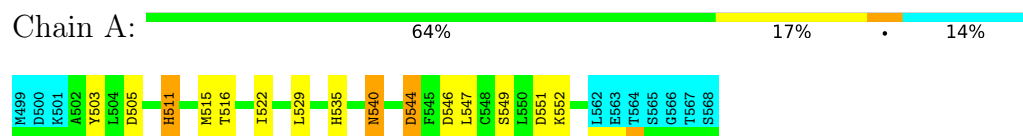


- Molecule 2: BCL-6 corepressor



### 4.2.4 Score per residue for model 4

- Molecule 1: Protein AF-9

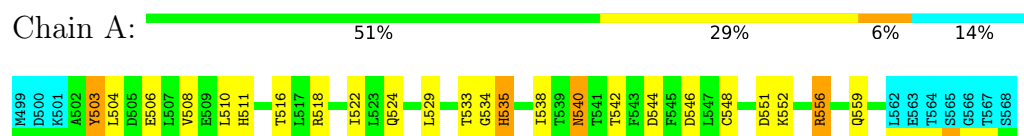


- Molecule 2: BCL-6 corepressor

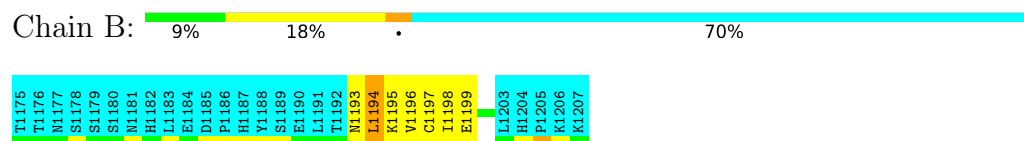


### 4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Protein AF-9

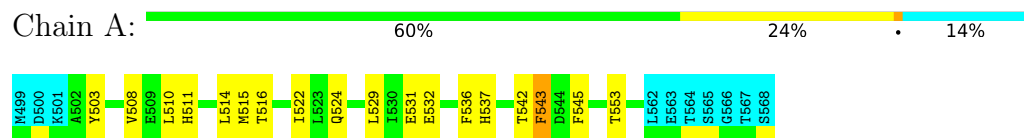


- Molecule 2: BCL-6 corepressor

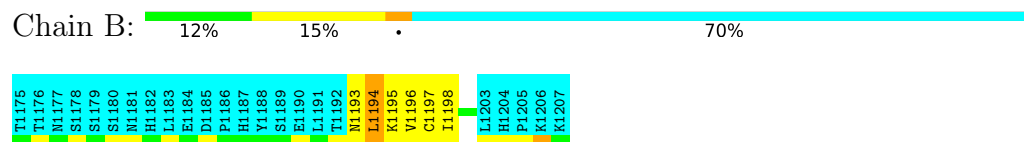


### 4.2.6 Score per residue for model 6

- Molecule 1: Protein AF-9

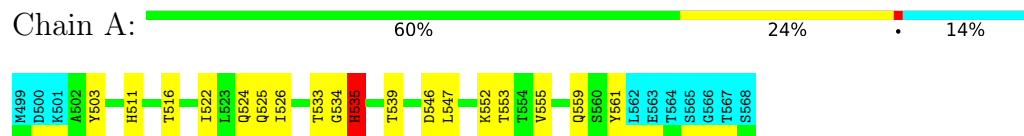


- Molecule 2: BCL-6 corepressor

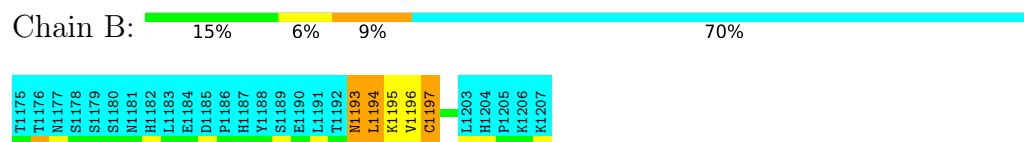


### 4.2.7 Score per residue for model 7

- Molecule 1: Protein AF-9

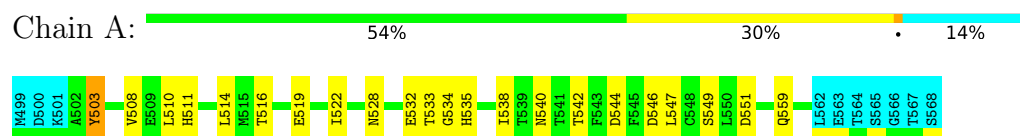


- Molecule 2: BCL-6 corepressor

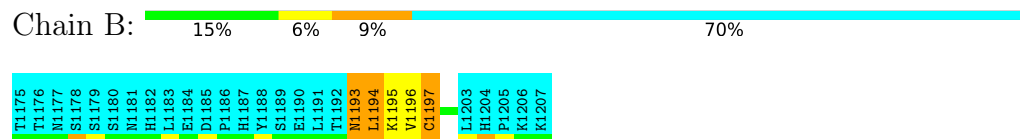


### 4.2.8 Score per residue for model 8

- Molecule 1: Protein AF-9

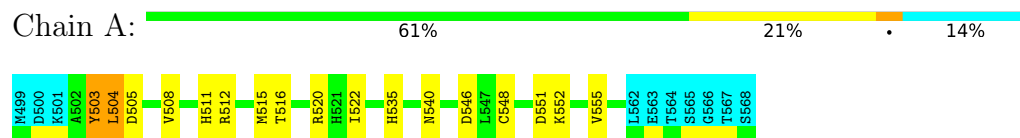


- Molecule 2: BCL-6 corepressor



### 4.2.9 Score per residue for model 9

- Molecule 1: Protein AF-9

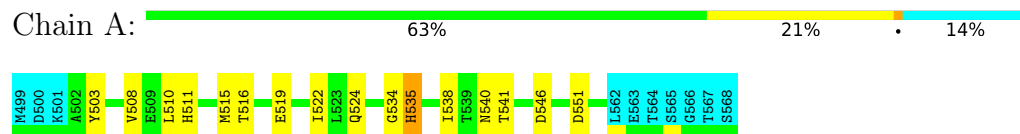


- Molecule 2: BCL-6 corepressor

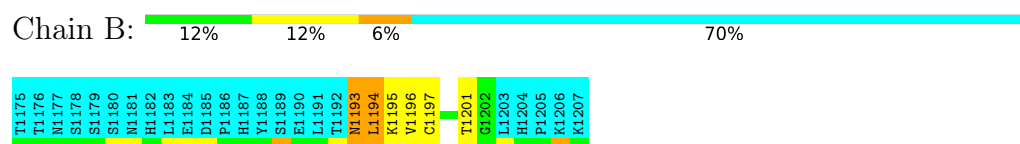


### 4.2.10 Score per residue for model 10

- Molecule 1: Protein AF-9



- Molecule 2: BCL-6 corepressor



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 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
X-PLOR NIH	structure calculation	
X-PLOR NIH	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1247
Number of shifts mapped to atoms	1247
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

## 6 Model quality

### 6.1 Standard geometry

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	507	512	508	11±3
2	B	74	82	82	4±2
All	All	5810	5940	5900	124

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:510:LEU:O	1:A:514:LEU:HD12	0.57	1.98	3	3
1:A:511:HIS:CG	2:B:1194:LEU:HD23	0.55	2.36	1	10
1:A:547:LEU:HD12	2:B:1194:LEU:HD22	0.54	1.80	4	3
1:A:504:LEU:HD21	1:A:548:CYS:SG	0.53	2.43	9	2
1:A:520:ARG:NH2	1:A:521:HIS:CE1	0.52	2.78	1	1
1:A:522:ILE:HD12	1:A:522:ILE:N	0.51	2.20	8	7
1:A:543:PHE:O	1:A:543:PHE:CG	0.49	2.66	6	2
1:A:533:THR:HG23	1:A:534:GLY:N	0.49	2.23	3	4
1:A:522:ILE:N	1:A:522:ILE:HD12	0.46	2.24	5	3
1:A:522:ILE:N	1:A:522:ILE:CD1	0.46	2.79	1	9
2:B:1196:VAL:CG1	2:B:1197:CYS:N	0.46	2.79	5	9
1:A:543:PHE:O	1:A:543:PHE:CD2	0.46	2.69	2	1
1:A:511:HIS:NE2	2:B:1195:LYS:O	0.46	2.49	7	9

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:542:THR:HG23	2:B:1198:ILE:O	0.45	2.12	6	3
1:A:510:LEU:N	1:A:510:LEU:HD12	0.45	2.26	10	2
1:A:522:ILE:CD1	1:A:522:ILE:N	0.45	2.79	7	1
1:A:526:ILE:HD11	1:A:561:TYR:HB2	0.45	1.88	7	2
1:A:520:ARG:NH2	1:A:521:HIS:ND1	0.45	2.65	1	1
1:A:524:GLN:O	1:A:524:GLN:NE2	0.44	2.51	7	2
1:A:503:TYR:O	1:A:503:TYR:CD1	0.43	2.70	9	5
1:A:536:PHE:O	1:A:537:HIS:CG	0.43	2.71	6	1
1:A:543:PHE:CZ	1:A:545:PHE:CD2	0.43	3.06	6	1
1:A:510:LEU:HD12	1:A:510:LEU:N	0.43	2.28	3	2
2:B:1196:VAL:HG12	2:B:1197:CYS:N	0.43	2.27	8	5
1:A:540:ASN:ND2	1:A:541:THR:H	0.43	2.12	10	1
1:A:535:HIS:NE2	1:A:549:SER:OG	0.43	2.52	4	4
1:A:534:GLY:O	1:A:535:HIS:CG	0.43	2.72	7	2
1:A:552:LYS:O	1:A:555:VAL:N	0.43	2.52	7	4
1:A:503:TYR:O	1:A:506:GLU:N	0.43	2.50	1	1
1:A:524:GLN:NE2	1:A:524:GLN:O	0.43	2.52	6	2
1:A:544:ASP:OD1	1:A:544:ASP:N	0.43	2.52	4	1
1:A:556:ARG:NH1	1:A:559:GLN:OE1	0.43	2.51	5	1
1:A:535:HIS:CE1	1:A:549:SER:OG	0.43	2.72	4	2
1:A:534:GLY:O	1:A:535:HIS:ND1	0.43	2.52	10	1
1:A:510:LEU:N	1:A:510:LEU:CD1	0.42	2.82	3	3
1:A:518:ARG:NH1	2:B:1199:GLU:OE1	0.42	2.52	5	1
2:B:1193:ASN:OD1	2:B:1193:ASN:N	0.42	2.52	9	2
1:A:533:THR:CG2	1:A:534:GLY:N	0.42	2.83	7	4
1:A:511:HIS:NE2	2:B:1195:LYS:N	0.42	2.68	7	1
1:A:510:LEU:O	1:A:514:LEU:N	0.41	2.53	2	1
1:A:529:LEU:C	1:A:531:GLU:N	0.41	2.74	6	1
1:A:535:HIS:CD2	1:A:549:SER:OG	0.41	2.74	8	1
1:A:511:HIS:HE2	2:B:1195:LYS:H	0.41	1.59	5	1
1:A:505:ASP:N	1:A:505:ASP:OD1	0.40	2.51	9	1
1:A:552:LYS:CG	1:A:553:THR:N	0.40	2.84	7	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	60/70 (86%)	48±1 (80±2%)	11±1 (19±2%)	1±1 (2±1%)	14	59
2	B	10/33 (30%)	8±1 (77±6%)	0±1 (5±7%)	2±0 (18±4%)	0	3
All	All	700/1030 (68%)	555 (79%)	118 (17%)	27 (4%)	5	32

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	1194	LEU	10
2	B	1193	ASN	8
1	A	540	ASN	4
1	A	519	GLU	3
1	A	535	HIS	2

### 6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	58/67 (87%)	48±2 (84±4%)	10±2 (16±4%)	5	41
2	B	9/32 (28%)	8±1 (89±9%)	1±1 (11±9%)	9	53
All	All	670/990 (68%)	565 (84%)	105 (16%)	5	42

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	503	TYR	10
1	A	516	THR	10
1	A	508	VAL	8
1	A	546	ASP	8
1	A	515	MET	6
2	B	1197	CYS	6
1	A	551	ASP	6
1	A	544	ASP	5
1	A	538	ILE	5
1	A	528	ASN	3
1	A	535	HIS	3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	549	SER	2
1	A	504	LEU	2
1	A	518	ARG	2
1	A	543	PHE	2
1	A	505	ASP	2
1	A	539	THR	2
1	A	529	LEU	2
1	A	540	ASN	2
1	A	552	LYS	2
1	A	532	GLU	2
2	B	1193	ASN	2
2	B	1201	THR	2
1	A	521	HIS	1
1	A	537	HIS	1
1	A	519	GLU	1
1	A	511	HIS	1
1	A	506	GLU	1
1	A	556	ARG	1
1	A	553	THR	1
1	A	525	GLN	1
1	A	542	THR	1
1	A	512	ARG	1
1	A	520	ARG	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 monosaccharides in this entry.

### 6.6 Ligand geometry ⓘ

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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 84% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *BCoRAF9shifts\_NMRSTAR\_reformat2.tab*

#### 7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1247
Number of shifts mapped to atoms	1247
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

#### 7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	102	$2.47 \pm 0.18$	Should be applied
$^{13}\text{C}_\beta$	99	$2.77 \pm 0.08$	Should be applied
$^{13}\text{C}'$	97	$2.59 \pm 0.13$	Should be applied
$^{15}\text{N}$	98	$-0.34 \pm 0.61$	None needed ( $< 0.5$ ppm)

#### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 798 atoms were assigned a chemical shift out of a possible 921. 16 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	350/350 (100%)	140/140 (100%)	140/140 (100%)	70/70 (100%)
Sidechain	405/496 (82%)	247/286 (86%)	152/186 (82%)	6/24 (25%)

*Continued on next page...*

Continued from previous page...

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	43/75 (57%)	22/39 (56%)	21/28 (75%)	0/8 (0%)
Overall	798/921 (87%)	409/465 (88%)	313/354 (88%)	76/102 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 1095 atoms were assigned a chemical shift out of a possible 1305. 20 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	495/511 (97%)	198/204 (97%)	199/206 (97%)	98/101 (97%)
Sidechain	549/690 (80%)	333/401 (83%)	210/260 (81%)	6/29 (21%)
Aromatic	51/104 (49%)	26/55 (47%)	25/38 (66%)	0/11 (0%)
Overall	1095/1305 (84%)	557/660 (84%)	434/504 (86%)	104/141 (74%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

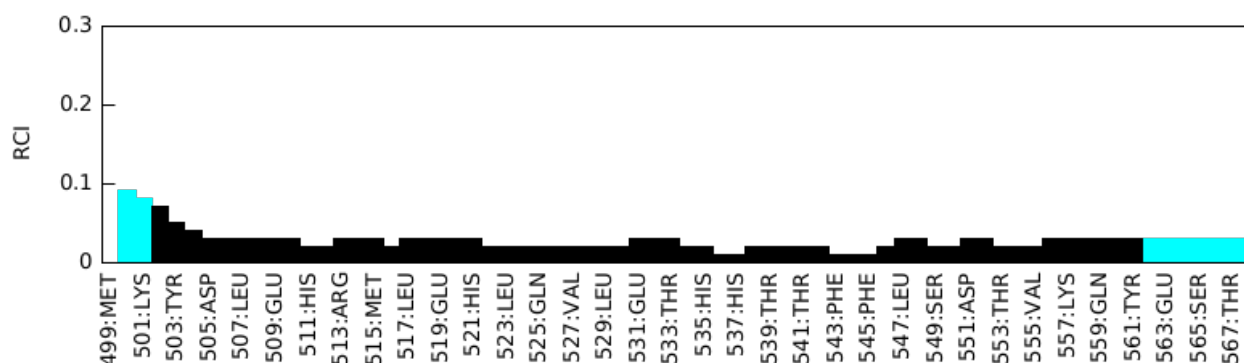
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	544	ASP	HA	6.17	6.15 – 3.05	5.1

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *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:



Random coil index (RCI) for chain B:

