



Full wwPDB NMR Structure Validation Report ⓘ

Mar 1, 2026 – 08:43 AM UTC

PDB ID : 7CSQ / pdb_00007csq
BMRB ID : 36370
Title : Solution structure of the complex between p75NTR-DD and TRADD-DD
Authors : Lin, Z.; Zhang, N.
Deposited on : 2020-08-16

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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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

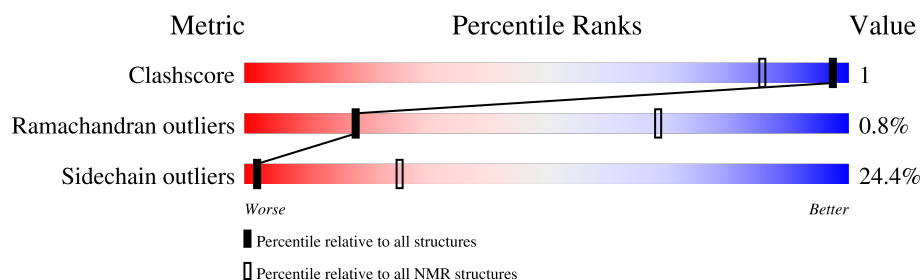
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 82%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	98	
2	B	114	

2 Ensemble composition and analysis

This entry contains 10 models. Model 10 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:334-A:420, B:199-B:306 (195)	0.40	10

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	3, 4, 5, 6, 7, 8, 10
2	1, 2, 9

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3289 atoms, of which 1639 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Tumor necrosis factor receptor superfamily member 16.

Mol	Chain	Residues	Atoms						Trace
1	A	98	Total	C	H	N	O	S	0
			1461	458	722	131	148	2	

- Molecule 2 is a protein called Tumor necrosis factor receptor type 1-associated DEATH domain protein.

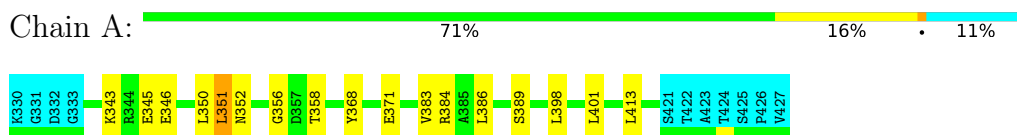
Mol	Chain	Residues	Atoms						Trace
2	B	114	Total	C	H	N	O	S	0
			1828	570	917	170	170	1	

4 Residue-property plots

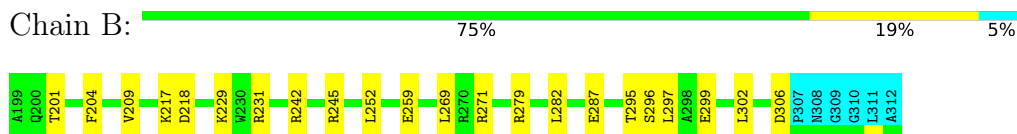
4.1 Average score per residue in the NMR ensemble

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: Tumor necrosis factor receptor superfamily member 16



- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

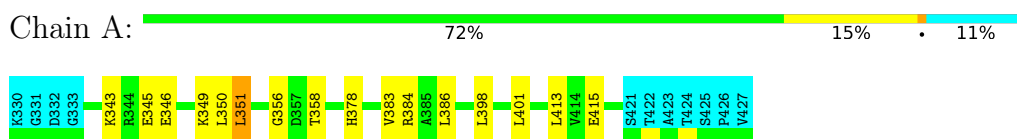


4.2 Scores per residue for each member of the ensemble

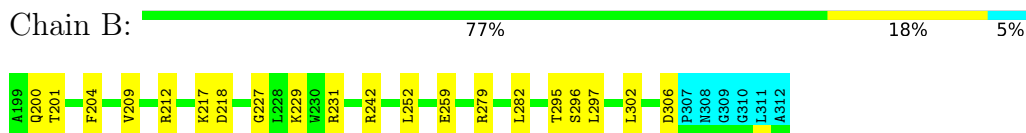
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

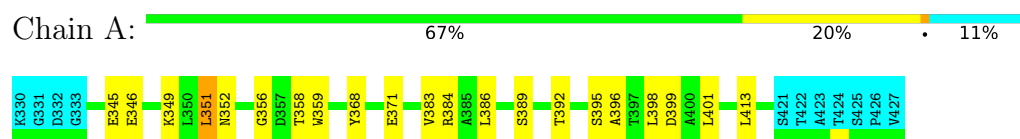


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

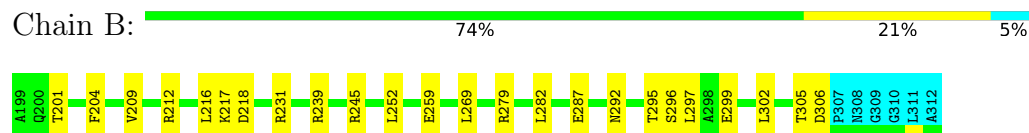


4.2.2 Score per residue for model 2

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

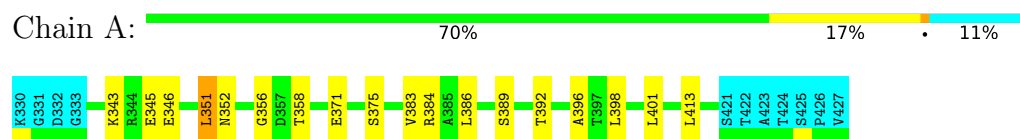


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

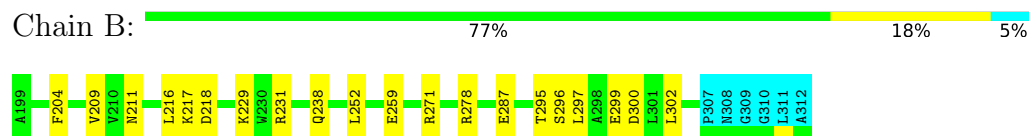


4.2.3 Score per residue for model 3

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

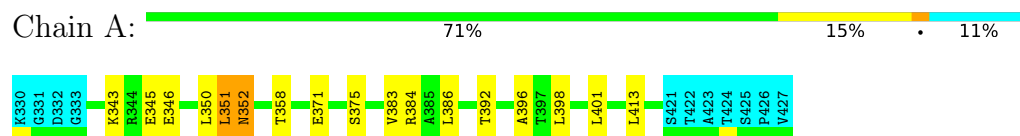


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

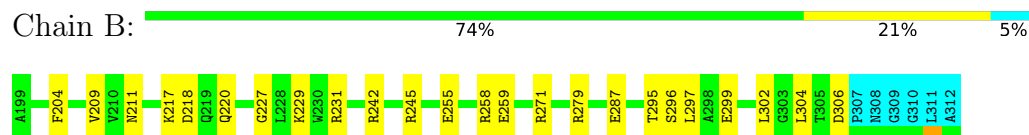


4.2.4 Score per residue for model 4

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

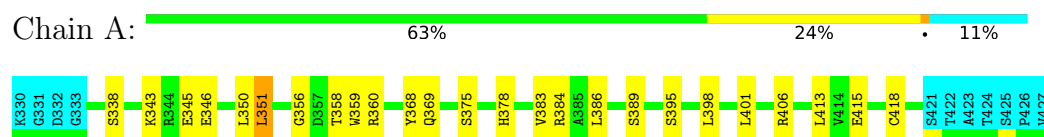


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

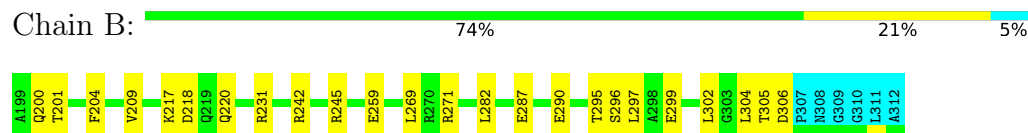


4.2.5 Score per residue for model 5

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

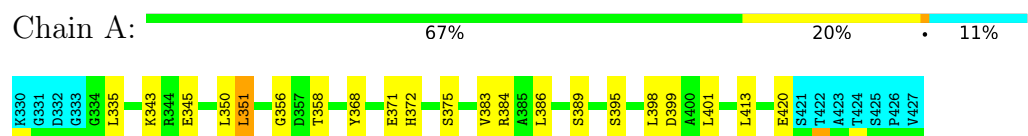


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

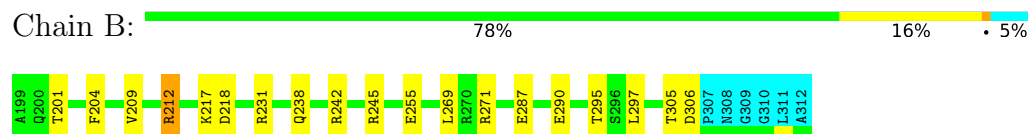


4.2.6 Score per residue for model 6

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

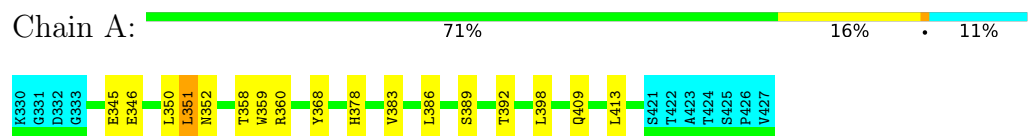


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

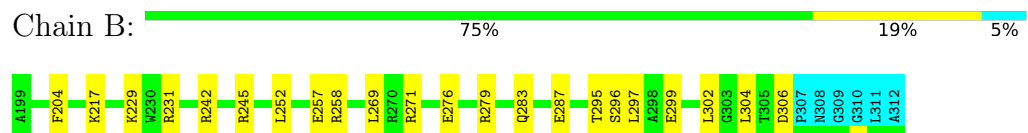


4.2.7 Score per residue for model 7

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

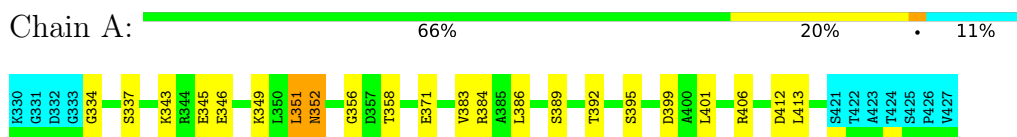


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

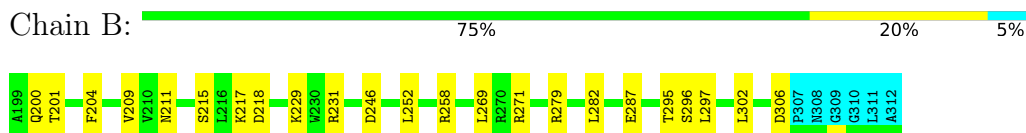


4.2.8 Score per residue for model 8

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

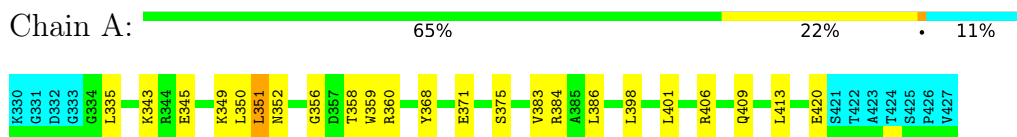


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

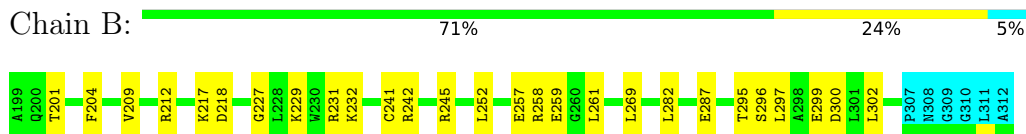


4.2.9 Score per residue for model 9

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

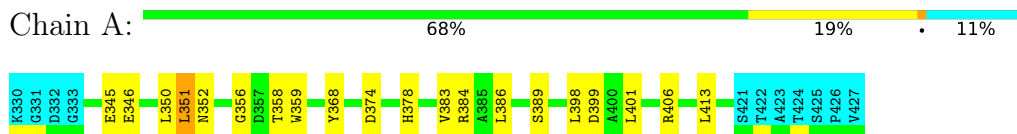


- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein

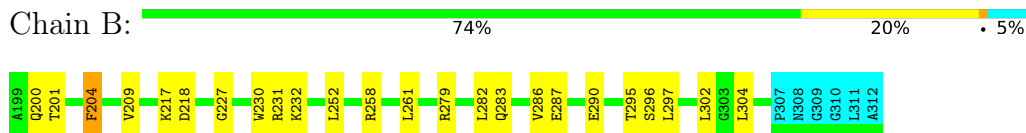


4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Tumor necrosis factor receptor superfamily member 16



- Molecule 2: Tumor necrosis factor receptor type 1-associated DEATH domain protein



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 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
Amber	refinement	
CYANA	structure calculation	

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	2363
Number of shifts mapped to atoms	2361
Number of unparsed shifts	0
Number of shifts with mapping errors	2
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

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	0.89±0.03	0±0/683 (0.0± 0.0%)	1.39±0.02	0±0/930 (0.0± 0.0%)
2	B	0.86±0.03	0±0/888 (0.0± 0.0%)	1.44±0.02	0±0/1198 (0.0± 0.0%)
All	All	0.87	0/15710 (0.0%)	1.42	3/21280 (0.0%)

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
2	B	283	GLN	OE1-CD-NE2	-5.17	117.42	122.60	10	2
2	B	212	ARG	N-CA-C	5.04	112.76	108.22	6	1

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	669	654	654	2±0
2	B	875	882	881	0±0
All	All	15440	15360	15350	18

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:351:LEU:HD11	1:A:383:VAL:HG11	0.61	1.72	9	10
1:A:351:LEU:HD13	1:A:352:ASN:N	0.45	2.27	10	7
2:B:204:PHE:CD2	2:B:286:VAL:CG1	0.40	3.05	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	87/98 (89%)	82±1 (94±1%)	4±1 (4±1%)	1±1 (1±1%)	11	58
2	B	107/114 (94%)	97±1 (90±1%)	10±1 (9±1%)	0±0 (0±0%)	31	76
All	All	1940/2120 (92%)	1789 (92%)	135 (7%)	16 (1%)	18	68

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	356	GLY	8
2	B	227	GLY	4
1	A	396	ALA	3
1	A	334	GLY	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	70/78 (90%)	53±3 (75±4%)	17±3 (25±4%)	2	25
2	B	91/94 (97%)	69±2 (76±2%)	22±2 (24±2%)	2	26
All	All	1610/1720 (94%)	1217 (76%)	393 (24%)	2	26

All 80 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	345	GLU	10
1	A	351	LEU	10
1	A	358	THR	10
1	A	386	LEU	10
1	A	413	LEU	10
2	B	204	PHE	10
2	B	217	LYS	10
2	B	231	ARG	10
2	B	295	THR	10
2	B	297	LEU	10
1	A	384	ARG	9
1	A	398	LEU	9
1	A	401	LEU	9
2	B	209	VAL	9
2	B	218	ASP	9
2	B	296	SER	9
2	B	302	LEU	9
2	B	287	GLU	9
1	A	346	GLU	8
1	A	343	LYS	7
1	A	350	LEU	7
2	B	201	THR	7
2	B	252	LEU	7
2	B	306	ASP	7
1	A	389	SER	7
2	B	229	LYS	6
2	B	242	ARG	6
2	B	259	GLU	6
2	B	279	ARG	6
2	B	282	LEU	6
1	A	368	TYR	6
1	A	371	GLU	6
2	B	245	ARG	6
2	B	269	LEU	6
2	B	299	GLU	6
2	B	271	ARG	6
1	A	359	TRP	5
1	A	392	THR	5
1	A	375	SER	5
2	B	258	ARG	5
1	A	349	LYS	4

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Mol	Chain	Res	Type	Models (Total)
1	A	378	HIS	4
2	B	200	GLN	4
2	B	212	ARG	4
1	A	395	SER	4
1	A	399	ASP	4
2	B	304	LEU	4
1	A	406	ARG	4
2	B	305	THR	3
2	B	211	ASN	3
1	A	360	ARG	3
2	B	290	GLU	3
1	A	415	GLU	2
2	B	216	LEU	2
2	B	238	GLN	2
2	B	300	ASP	2
1	A	352	ASN	2
2	B	220	GLN	2
2	B	255	GLU	2
1	A	335	LEU	2
1	A	420	GLU	2
1	A	409	GLN	2
2	B	257	GLU	2
2	B	232	LYS	2
2	B	261	LEU	2
2	B	239	ARG	1
2	B	292	ASN	1
2	B	278	ARG	1
1	A	338	SER	1
1	A	369	GLN	1
1	A	418	CYS	1
1	A	372	HIS	1
2	B	276	GLU	1
1	A	337	SER	1
1	A	412	ASP	1
2	B	215	SER	1
2	B	246	ASP	1
2	B	241	CYS	1
1	A	374	ASP	1
2	B	230	TRP	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 oligosaccharides 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 82% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *ChemicalShift.txt*

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	2363
Number of shifts mapped to atoms	2361
Number of unparsed shifts	0
Number of shifts with mapping errors	2
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

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

- No matching atom found in the structure. All 2 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	330	LYS	H	8.417	0.02	1
1	B	199	ALA	H	8.303	0.02	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	211	0.46 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	195	0.97 ± 0.06	Should be checked
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	203	0.55 ± 0.30	None needed (imprecise)

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 82%, i.e. 2212 atoms were assigned a chemical shift out of a possible 2708. 0 out of 42 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	768/973 (79%)	386/395 (98%)	194/390 (50%)	188/188 (100%)
Sidechain	1346/1573 (86%)	915/1019 (90%)	410/476 (86%)	21/78 (27%)
Aromatic	98/162 (60%)	49/80 (61%)	46/76 (61%)	3/6 (50%)
Overall	2212/2708 (82%)	1350/1494 (90%)	650/942 (69%)	212/272 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 82%, i.e. 2363 atoms were assigned a chemical shift out of a possible 2884. 0 out of 44 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	834/1058 (79%)	420/431 (97%)	211/424 (50%)	203/203 (100%)
Sidechain	1431/1664 (86%)	973/1079 (90%)	436/505 (86%)	22/80 (28%)
Aromatic	98/162 (60%)	49/80 (61%)	46/76 (61%)	3/6 (50%)
Overall	2363/2884 (82%)	1442/1590 (91%)	693/1005 (69%)	228/289 (79%)

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.

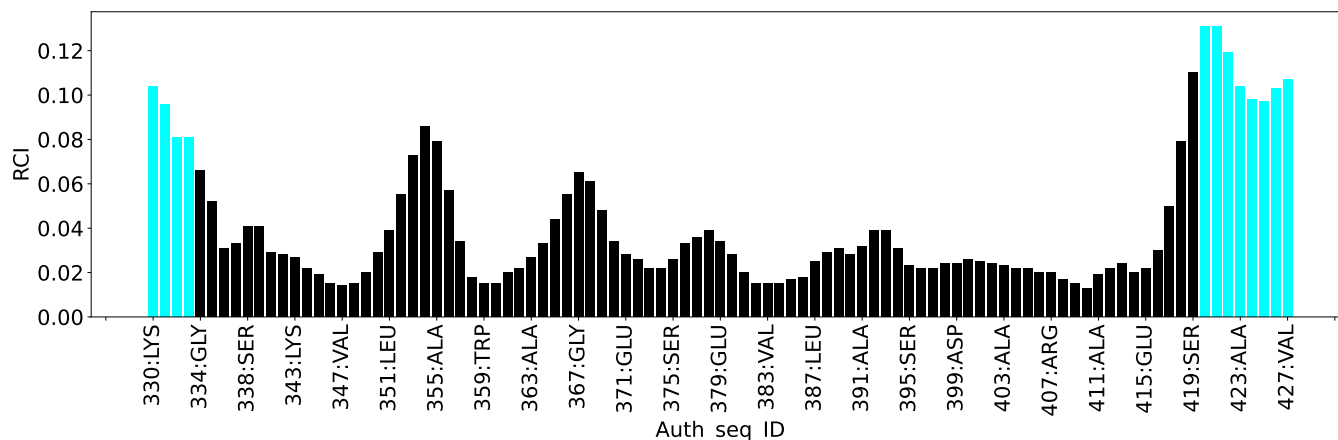
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	B	264	GLN	HB2	0.30	0.80 – 3.29	-7.0
1	B	267	GLN	HG3	0.43	0.91 – 3.68	-6.7
1	A	396	ALA	HB1	-0.22	0.14 – 2.58	-6.5
1	A	396	ALA	HB2	-0.22	0.14 – 2.58	-6.5
1	A	396	ALA	HB3	-0.22	0.14 – 2.58	-6.5
1	A	360	ARG	HG2	-0.03	0.26 – 2.87	-6.1
1	A	382	PRO	HB3	-0.08	0.25 – 3.76	-5.9

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

