



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 2N83
Title : p75NTR DD:RIP2 CARD
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Deposited on : 2015-10-02

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

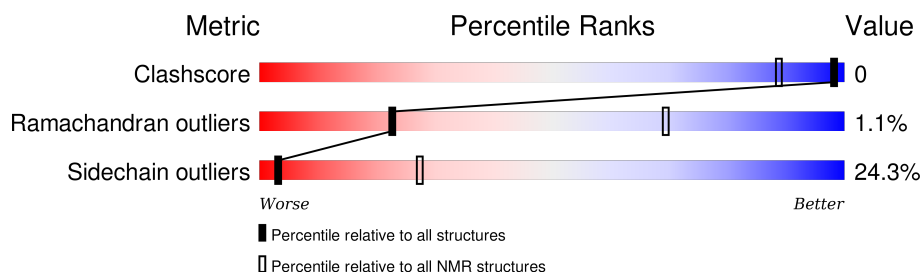
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	98	 68% 15% 12% •
2	B	106	 66% 21% 12% •

2 Ensemble composition and analysis

This entry contains 10 models. Model 2 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:335-A:351, A:357-A:421, B:435-B:526 (174)	0.40	2

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3129 atoms, of which 1573 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	94	Total	C	H	N	O	S	0
			1413	444	699	126	142	2	

- Molecule 2 is a protein called Receptor-interacting serine/threonine-protein kinase 2.

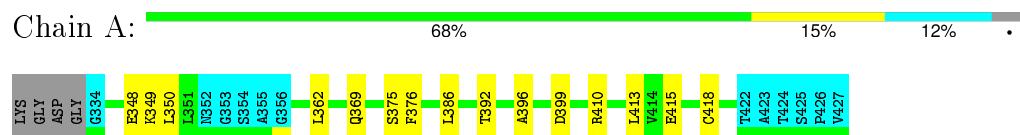
Mol	Chain	Residues	Atoms						Trace
2	B	105	Total	C	H	N	O	S	0
			1716	526	874	146	166	4	

4 Residue-property plots

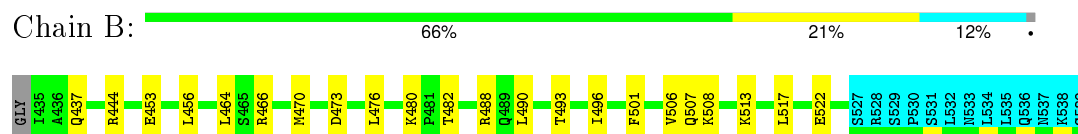
4.1 Average score per residue in the NMR ensemble

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: Tumor necrosis factor receptor superfamily member 16



- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

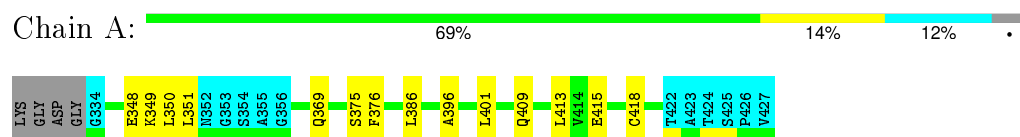


4.2 Scores per residue for each member of the ensemble

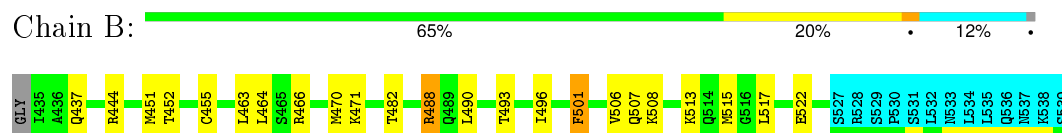
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

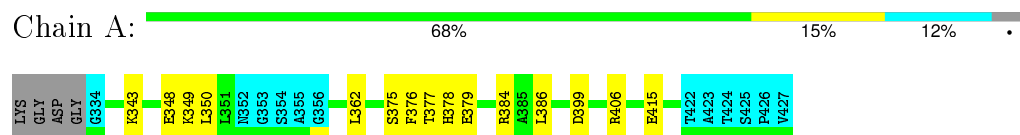


- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

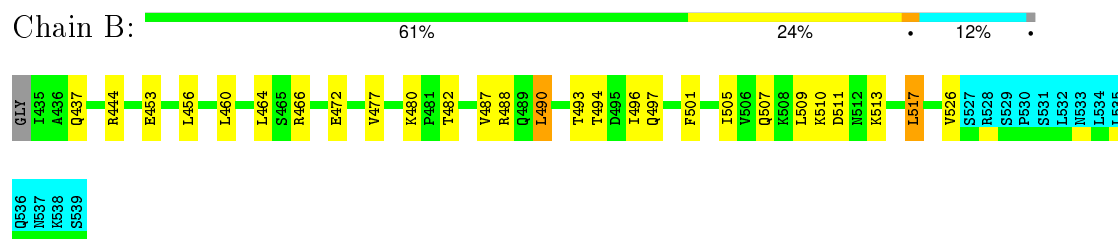


4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

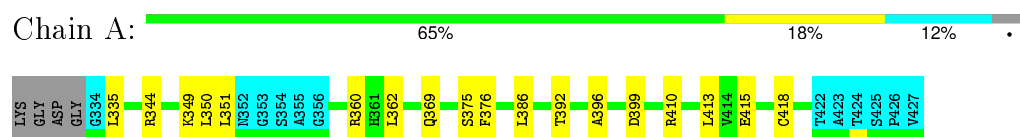


- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

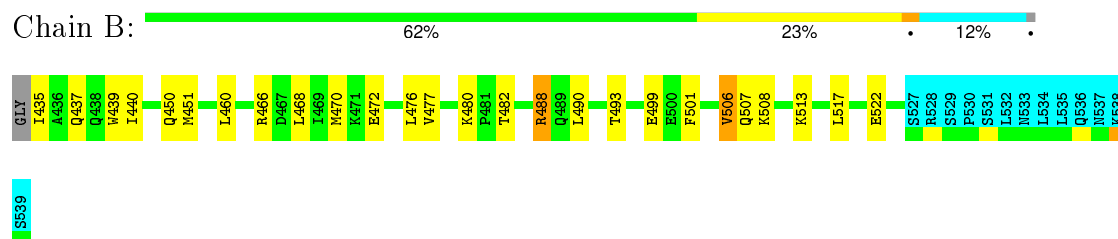


4.2.3 Score per residue for model 3

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

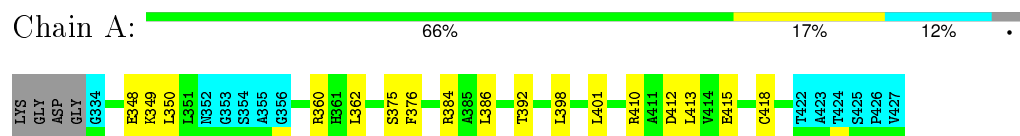


- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

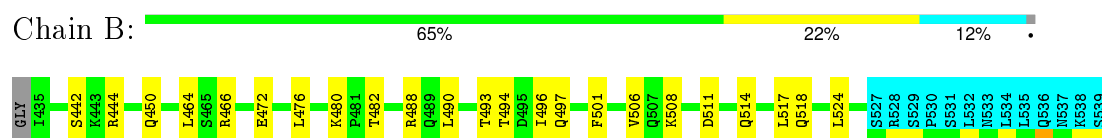


4.2.4 Score per residue for model 4

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

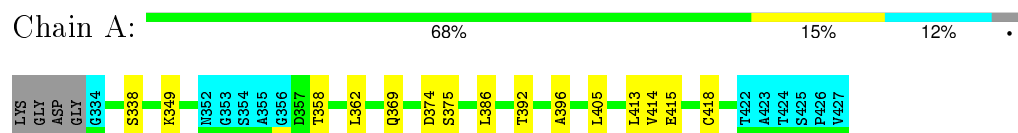


- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

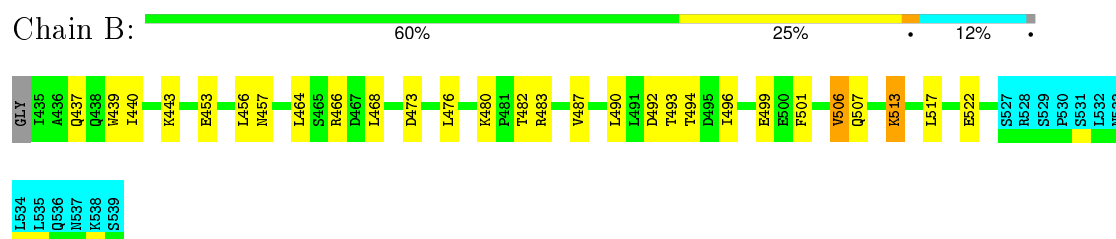


4.2.5 Score per residue for model 5

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

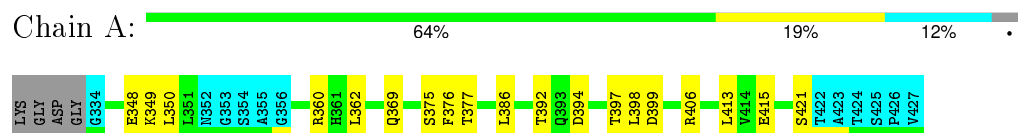


- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

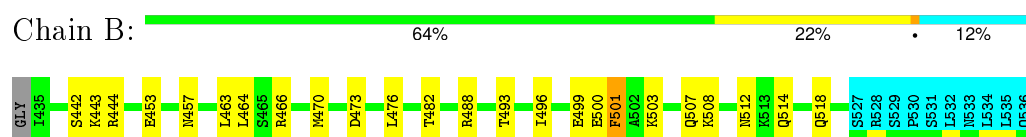


4.2.6 Score per residue for model 6

- Molecule 1: Tumor necrosis factor receptor superfamily member 16



- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2



4.2.7 Score per residue for model 7

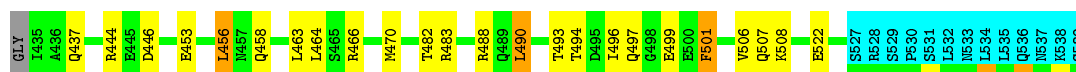
- Molecule 1: Tumor necrosis factor receptor superfamily member 16





- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

Chain B: 64% 20% 12%



4.2.8 Score per residue for model 8

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

Chain A: 65% 17% 12%



- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

Chain B: 63% 23% 12%



4.2.9 Score per residue for model 9

- Molecule 1: Tumor necrosis factor receptor superfamily member 16

Chain A: 61% 21% 12%



- Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

Chain B: 65% 22% 12%



4.2.10 Score per residue for model 10

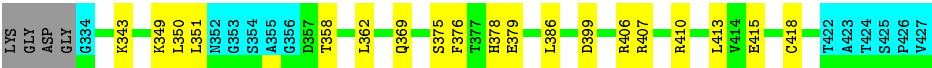
- Molecule 1: Tumor necrosis factor receptor superfamily member 16

Chain A:

64%

19%

12%



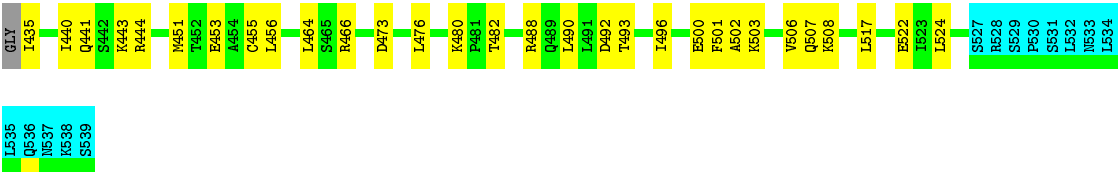
● Molecule 2: Receptor-interacting serine/threonine-protein kinase 2

Chain B:

58%

28%

12%



5 Refinement protocol and experimental data overview

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

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
CYANA	structure solution	
AMBER	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)	2n83_cs.str
Number of chemical shift lists	2
Total number of shifts	2315
Number of shifts mapped to atoms	2315
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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	0.69±0.01	0±0/658 (0.0±0.0%)	0.99±0.02	1±1/897 (0.1±0.1%)
2	B	0.64±0.01	0±0/750 (0.0±0.0%)	0.96±0.02	0±0/1013 (0.0±0.0%)
All	All	0.67	0/14080 (0.0%)	0.98	16/19100 (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	0.2±0.4
2	B	0.0±0.0	0.1±0.3
All	All	0	3

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	360	ARG	NE-CZ-NH1	6.40	123.50	120.30	4	4
1	A	410	ARG	NE-CZ-NH1	5.51	123.06	120.30	8	3
1	A	406	ARG	NE-CZ-NH1	5.48	123.04	120.30	6	3
2	B	444	ARG	NE-CZ-NH1	5.46	123.03	120.30	10	1
1	A	407	ARG	NE-CZ-NH1	5.43	123.02	120.30	10	1
2	B	488	ARG	NE-CZ-NH1	5.19	122.90	120.30	3	3
1	A	344	ARG	NE-CZ-NH1	5.14	122.87	120.30	3	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	336	TYR	Sidechain	2
2	B	466	ARG	Sidechain	1

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	644	634	634	0±0
2	B	742	768	767	1±1
All	All	13860	14020	14010	14

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:363:ALA:HB2	1:A:386:LEU:HD11	0.66	1.68	9	2
2:B:440:ILE:HG13	2:B:502:ALA:HB1	0.55	1.77	10	1
1:A:405:LEU:HD13	1:A:414:VAL:HG22	0.55	1.79	5	1
2:B:460:LEU:HD21	2:B:477:VAL:HG11	0.54	1.77	3	2
2:B:439:TRP:CZ3	2:B:506:VAL:HG12	0.53	2.38	3	2
2:B:509:LEU:HD13	2:B:517:LEU:HD22	0.43	1.91	2	1
2:B:463:LEU:HD13	2:B:501:PHE:CZ	0.41	2.50	7	3
2:B:490:LEU:HD11	2:B:505:ILE:CD1	0.41	2.46	2	1
2:B:456:LEU:CD2	2:B:490:LEU:HD13	0.40	2.46	7	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	82/98 (84%)	79±1 (96±1%)	3±1 (3±1%)	1±1 (1±1%)	26	73
2	B	91/106 (86%)	82±2 (90±2%)	8±2 (9±2%)	1±1 (1±1%)	20	66
All	All	1730/2040 (85%)	1604 (93%)	107 (6%)	19 (1%)	23	69

All 9 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	396	ALA	5
2	B	513	LYS	4
2	B	441	GLN	2
2	B	518	GLN	2
2	B	524	LEU	2
2	B	526	VAL	1
1	A	409	GLN	1
2	B	452	THR	1
1	A	394	ASP	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	69/78 (88%)	54±2 (78±3%)	15±2 (22±3%)	4	32
2	B	86/99 (87%)	63±2 (74±2%)	23±2 (26±2%)	3	23
All	All	1550/1770 (88%)	1173 (76%)	377 (24%)	3	27

All 83 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	415	GLU	10
1	A	386	LEU	10
2	B	493	THR	10
2	B	501	PHE	10
2	B	482	THR	10
1	A	349	LYS	10
1	A	350	LEU	9

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Mol	Chain	Res	Type	Models (Total)
2	B	464	LEU	9
2	B	507	GLN	9
1	A	375	SER	9
1	A	362	LEU	9
2	B	490	LEU	9
1	A	418	CYS	8
2	B	466	ARG	8
2	B	488	ARG	8
2	B	496	ILE	8
1	A	376	PHE	7
1	A	348	GLU	7
1	A	369	GLN	7
2	B	508	LYS	7
2	B	517	LEU	7
2	B	444	ARG	6
2	B	437	GLN	6
1	A	392	THR	6
2	B	506	VAL	6
1	A	413	LEU	6
2	B	453	GLU	6
2	B	522	GLU	6
2	B	456	LEU	6
2	B	476	LEU	6
2	B	470	MET	5
1	A	399	ASP	5
2	B	480	LYS	5
2	B	473	ASP	5
1	A	378	HIS	4
2	B	443	LYS	4
2	B	435	ILE	4
2	B	472	GLU	4
1	A	335	LEU	4
2	B	494	THR	4
1	A	384	ARG	4
2	B	451	MET	4
2	B	492	ASP	4
1	A	377	THR	4
2	B	499	GLU	4
2	B	450	GLN	3
2	B	511	ASP	3
2	B	487	VAL	3
2	B	497	GLN	3

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Mol	Chain	Res	Type	Models (Total)
2	B	500	GLU	3
1	A	343	LYS	3
2	B	513	LYS	3
1	A	358	THR	3
1	A	379	GLU	3
1	A	351	LEU	3
1	A	410	ARG	2
2	B	457	ASN	2
2	B	442	SER	2
1	A	374	ASP	2
2	B	468	LEU	2
1	A	398	LEU	2
2	B	514	GLN	2
2	B	440	ILE	2
1	A	401	LEU	2
2	B	446	ASP	2
2	B	503	LYS	2
2	B	510	LYS	2
1	A	338	SER	2
2	B	458	GLN	2
2	B	471	LYS	2
2	B	455	CYS	2
2	B	483	ARG	2
1	A	412	ASP	2
2	B	512	ASN	2
2	B	515	MET	2
1	A	345	GLU	1
1	A	421	SER	1
1	A	406	ARG	1
1	A	397	THR	1
1	A	395	SER	1
1	A	405	LEU	1
1	A	346	GLU	1
2	B	489	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 83% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: 2n83_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	1041
Number of shifts mapped to atoms	1041
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	97	2.36 ± 0.16	Should be applied
$^{13}\text{C}_\beta$	90	3.19 ± 0.09	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	93	0.69 ± 0.37	None needed (imprecise)

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 37%, i.e. 816 atoms were assigned a chemical shift out of a possible 2184. 17 out of 35 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	314/856 (37%)	155/341 (45%)	81/348 (23%)	78/167 (47%)
Sidechain	444/1221 (36%)	270/712 (38%)	168/453 (37%)	6/56 (11%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	58/107 (54%)	31/56 (55%)	25/45 (56%)	2/6 (33%)
Overall	816/2184 (37%)	456/1109 (41%)	274/846 (32%)	86/229 (38%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 37%, i.e. 895 atoms were assigned a chemical shift out of a possible 2448. 18 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	358/977 (37%)	176/389 (45%)	93/398 (23%)	89/190 (47%)
Sidechain	479/1364 (35%)	291/797 (37%)	181/503 (36%)	7/64 (11%)
Aromatic	58/107 (54%)	31/56 (55%)	25/45 (56%)	2/6 (33%)
Overall	895/2448 (37%)	498/1242 (40%)	299/946 (32%)	98/260 (38%)

7.1.4 Statistically unusual chemical shifts ⓘ

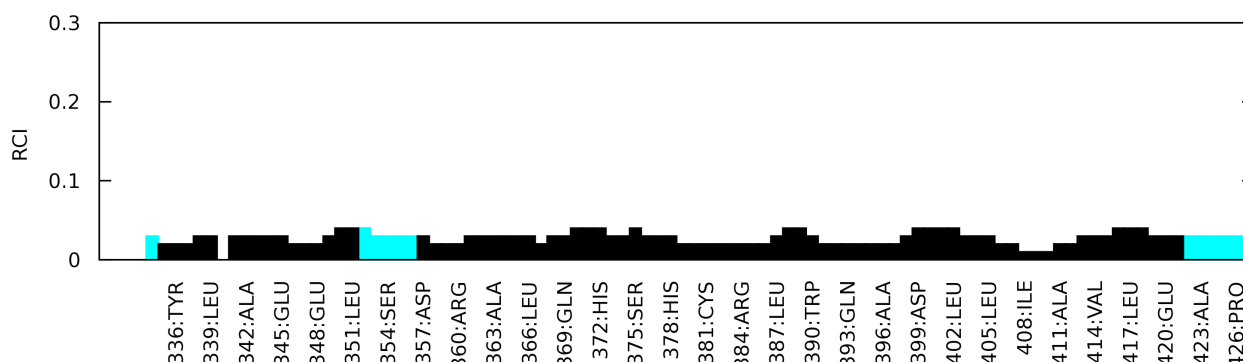
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	396	ALA	HB3	-0.22	2.61 – 0.11	-6.3
1	A	396	ALA	HB1	-0.22	2.61 – 0.11	-6.3
1	A	396	ALA	HB2	-0.22	2.61 – 0.11	-6.3
1	A	410	ARG	CD	37.73	47.57 – 38.77	-6.2
1	A	382	PRO	HB2	-0.08	3.82 – 0.32	-6.1
1	A	360	ARG	HG2	-0.03	2.92 – 0.22	-5.9

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:



7.2 Chemical shift list 2

File name: 2n83_cs.str

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	1274
Number of shifts mapped to atoms	1274
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	106	2.07 ± 0.07	Should be applied
$^{13}\text{C}_\beta$	103	2.92 ± 0.10	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	102	-0.03 ± 0.36	None needed (< 0.5 ppm)

7.2.3 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 46%, i.e. 999 atoms were assigned a chemical shift out of a possible 2184. 18 out of 35 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	362/856 (42%)	181/341 (53%)	92/348 (26%)	89/167 (53%)
Sidechain	614/1221 (50%)	378/712 (53%)	219/453 (48%)	17/56 (30%)
Aromatic	23/107 (21%)	12/56 (21%)	10/45 (22%)	1/6 (17%)
Overall	999/2184 (46%)	571/1109 (51%)	321/846 (38%)	107/229 (47%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 46%, i.e. 1133 atoms were assigned a chemical shift out of a possible 2448. 21 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	412/977 (42%)	206/389 (53%)	105/398 (26%)	101/190 (53%)
Sidechain	698/1364 (51%)	429/797 (54%)	249/503 (50%)	20/64 (31%)
Aromatic	23/107 (21%)	12/56 (21%)	10/45 (22%)	1/6 (17%)
Overall	1133/2448 (46%)	647/1242 (52%)	364/946 (38%)	122/260 (47%)

7.2.4 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
2	B	471	LYS	HE2	4.20	3.87 – 1.97	6.7
2	B	521	PRO	HD2	1.43	5.45 – 1.85	-6.2
2	B	436	ALA	H	11.72	11.19 – 5.19	5.9
2	B	521	PRO	CD	45.20	55.31 – 45.41	-5.2

7.2.5 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 B:

