



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 06:10 pm GMT

PDB ID : 1GEA
Title : RECEPTOR-BOUND CONFORMATION OF PACAP21
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Deposited on : 2000-10-20

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	:	1.7.2 (RC1), CSD as538be (2017)
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

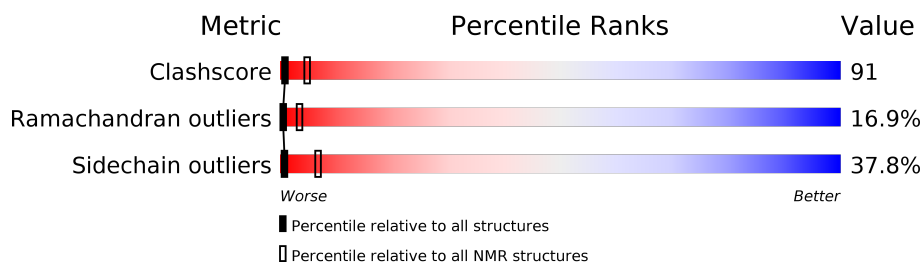
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 47%.

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	21	

2 Ensemble composition and analysis

This entry contains 25 models. Model 12 is the overall representative, medoid model (most similar to other models).

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:20 (18)	0.22	12

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 6 clusters and 2 single-model clusters were found.

Cluster number	Models
1	2, 6, 10, 11, 12, 16, 18, 20
2	3, 7, 9, 13, 14, 17
3	8, 21, 22
4	23, 25
5	1, 15
6	4, 19
Single-model clusters	5; 24

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 355 atoms, of which 178 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE.

Mol	Chain	Residues	Atoms						Trace
1	A	21	Total	C	H	N	O	S	0
			355	110	178	34	32	1	

There is a discrepancy between the modelled and reference sequences:

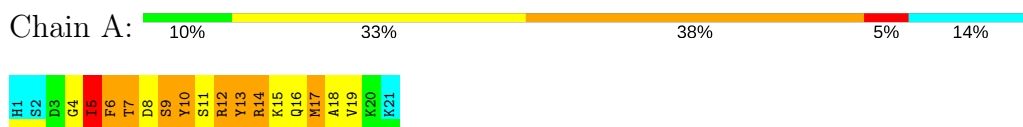
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	LYN	LYS	MODIFIED RESIDUE	UNP P18509

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: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

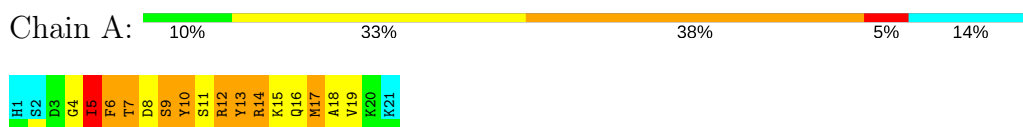


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



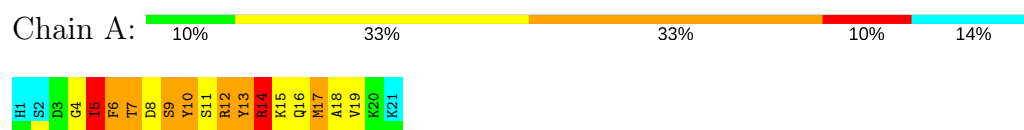
4.2.2 Score per residue for model 2

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



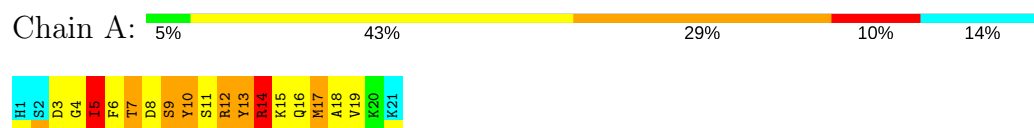
4.2.3 Score per residue for model 3

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



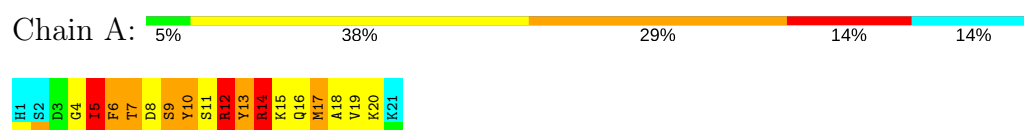
4.2.4 Score per residue for model 4

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



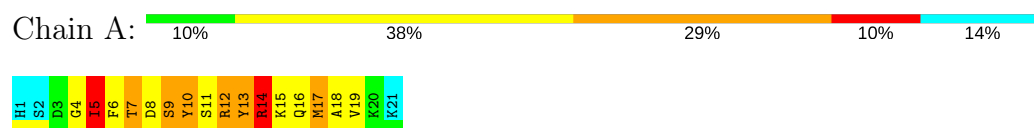
4.2.5 Score per residue for model 5

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



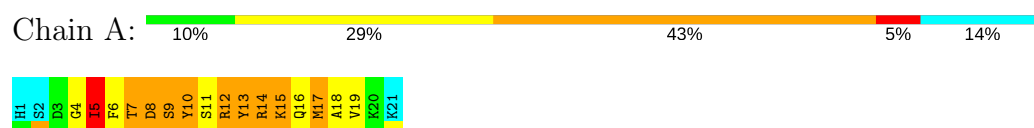
4.2.6 Score per residue for model 6

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.7 Score per residue for model 7

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.8 Score per residue for model 8


- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

Chain A: 



4.2.9 Score per residue for model 9

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

Chain A: 



4.2.10 Score per residue for model 10

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

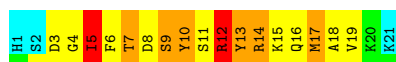
Chain A: 



4.2.11 Score per residue for model 11

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

Chain A: 



4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE

Chain A: 



4.2.13 Score per residue for model 13

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



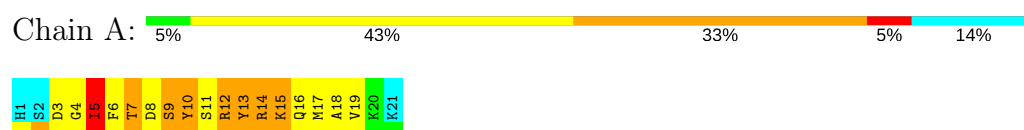
4.2.14 Score per residue for model 14

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



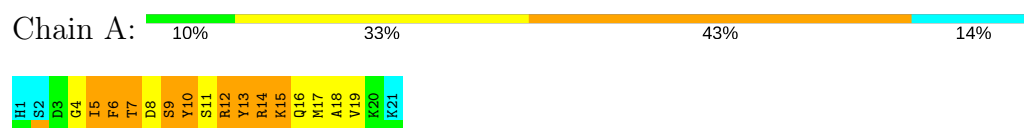
4.2.15 Score per residue for model 15

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



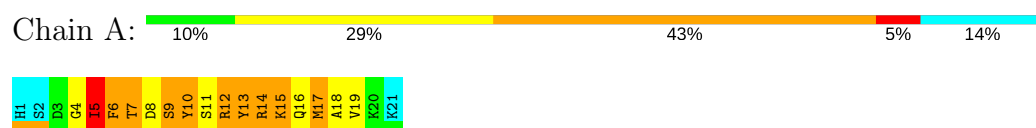
4.2.16 Score per residue for model 16

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.17 Score per residue for model 17

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



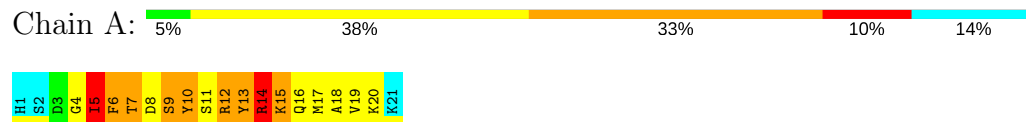
4.2.18 Score per residue for model 18

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



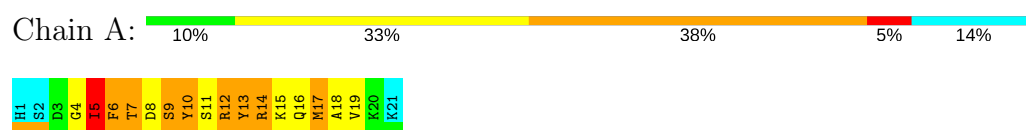
4.2.19 Score per residue for model 19

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



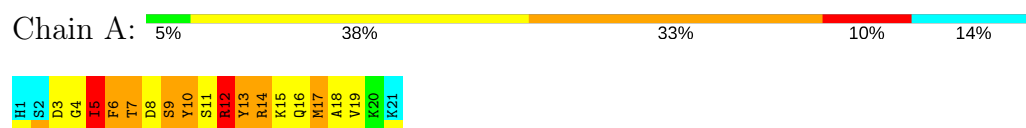
4.2.20 Score per residue for model 20

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



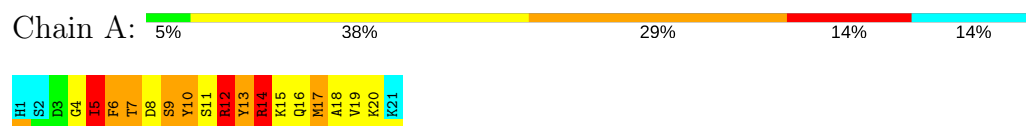
4.2.21 Score per residue for model 21

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.22 Score per residue for model 22

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.23 Score per residue for model 23

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



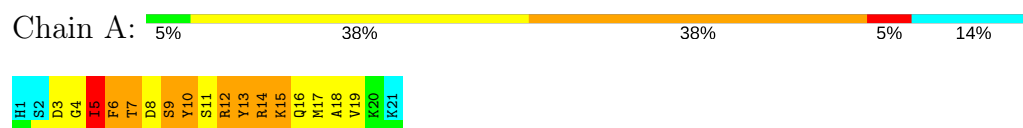
4.2.24 Score per residue for model 24

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



4.2.25 Score per residue for model 25

- Molecule 1: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Iterative relaxation matrix analysis (IRMA) and simulated annealing (SA)*.

Of the 200 calculated structures, 25 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	structure solution	3.1
X-PLOR	refinement	3.1

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)	BMRB entry 4916
Number of chemical shift lists	1
Total number of shifts	148
Number of shifts mapped to atoms	136
Number of unparsed shifts	0
Number of shifts with mapping errors	12
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	47%

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LYN

There are no covalent bond-length or bond-angle outliers.

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	2.0±0.0
All	All	0	50

There are no bond-length outliers.

There are no bond-angle outliers.

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	12	ARG	Sidechain	25
1	A	14	ARG	Sidechain	25

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	151	149	149	27±3
All	All	3775	3725	3725	682

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 91.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:GLY:O	1:A:7:THR:HG22	0.98	1.59	10	25
1:A:5:ILE:HD13	1:A:5:ILE:O	0.77	1.79	24	1
1:A:5:ILE:HD13	1:A:5:ILE:C	0.67	2.10	5	7
1:A:5:ILE:C	1:A:5:ILE:HD13	0.67	2.10	1	5
1:A:13:TYR:CD1	1:A:14:ARG:N	0.63	2.67	15	1
1:A:10:TYR:CD1	1:A:11:SER:N	0.62	2.67	22	16
1:A:5:ILE:O	1:A:10:TYR:CG	0.62	2.53	24	25
1:A:13:TYR:C	1:A:13:TYR:CD1	0.61	2.72	8	15
1:A:13:TYR:CD1	1:A:13:TYR:C	0.61	2.74	5	10
1:A:5:ILE:O	1:A:10:TYR:CD1	0.60	2.55	2	15
1:A:5:ILE:O	1:A:10:TYR:CD2	0.59	2.55	15	10
1:A:13:TYR:O	1:A:13:TYR:CG	0.59	2.55	7	8
1:A:10:TYR:O	1:A:14:ARG:N	0.59	2.35	24	22
1:A:13:TYR:O	1:A:13:TYR:CD1	0.59	2.56	16	3
1:A:13:TYR:CG	1:A:13:TYR:O	0.58	2.57	19	9
1:A:10:TYR:CG	1:A:11:SER:N	0.56	2.74	21	25
1:A:9:SER:O	1:A:12:ARG:CG	0.55	2.55	5	8
1:A:9:SER:O	1:A:13:TYR:N	0.54	2.39	7	19
1:A:10:TYR:CD2	1:A:11:SER:N	0.54	2.76	12	9
1:A:7:THR:OG1	1:A:8:ASP:N	0.53	2.41	24	2
1:A:10:TYR:CD2	1:A:14:ARG:HG3	0.53	2.38	9	1
1:A:11:SER:O	1:A:15:LYS:CE	0.53	2.57	1	1
1:A:4:GLY:O	1:A:6:PHE:N	0.53	2.42	5	24
1:A:11:SER:O	1:A:15:LYS:CD	0.53	2.57	16	3
1:A:7:THR:HG23	1:A:8:ASP:N	0.52	2.20	5	20
1:A:11:SER:O	1:A:15:LYS:CG	0.52	2.57	19	3
1:A:4:GLY:O	1:A:7:THR:CG2	0.52	2.56	24	1
1:A:10:TYR:HA	1:A:13:TYR:CD1	0.51	2.40	10	18
1:A:12:ARG:O	1:A:16:GLN:NE2	0.51	2.43	10	2
1:A:5:ILE:CD1	1:A:5:ILE:O	0.51	2.56	24	1
1:A:13:TYR:CG	1:A:14:ARG:N	0.50	2.79	22	2
1:A:13:TYR:CD1	1:A:13:TYR:O	0.50	2.64	9	5
1:A:3:ASP:O	1:A:5:ILE:N	0.50	2.45	10	1
1:A:4:GLY:O	1:A:5:ILE:C	0.50	2.50	22	24
1:A:9:SER:O	1:A:12:ARG:HG2	0.49	2.08	3	25
1:A:5:ILE:HA	1:A:10:TYR:HB2	0.49	1.83	16	25
1:A:5:ILE:O	1:A:10:TYR:CE1	0.49	2.65	9	8
1:A:12:ARG:O	1:A:16:GLN:CG	0.49	2.61	13	2
1:A:8:ASP:O	1:A:9:SER:C	0.49	2.51	25	25
1:A:10:TYR:O	1:A:14:ARG:CG	0.49	2.61	9	1
1:A:5:ILE:HA	1:A:10:TYR:CG	0.48	2.44	9	2
1:A:5:ILE:HA	1:A:10:TYR:CB	0.48	2.39	16	25

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:GLN:HG3	1:A:17:MET:N	0.48	2.22	7	3
1:A:5:ILE:CD1	1:A:5:ILE:C	0.48	2.80	8	7
1:A:9:SER:O	1:A:12:ARG:N	0.48	2.47	5	3
1:A:12:ARG:HG3	1:A:13:TYR:N	0.47	2.24	5	6
1:A:18:ALA:O	1:A:19:VAL:C	0.47	2.53	11	25
1:A:8:ASP:CG	1:A:9:SER:N	0.47	2.67	7	1
1:A:10:TYR:HA	1:A:13:TYR:CD2	0.47	2.44	22	2
1:A:17:MET:O	1:A:18:ALA:C	0.47	2.54	14	24
1:A:13:TYR:O	1:A:17:MET:SD	0.46	2.73	7	1
1:A:13:TYR:CZ	1:A:17:MET:CE	0.46	2.98	6	1
1:A:5:ILE:C	1:A:5:ILE:CD1	0.46	2.80	2	2
1:A:14:ARG:O	1:A:15:LYS:C	0.46	2.53	4	17
1:A:4:GLY:O	1:A:10:TYR:HB3	0.46	2.10	10	19
1:A:16:GLN:CG	1:A:17:MET:N	0.46	2.78	7	1
1:A:15:LYS:O	1:A:16:GLN:C	0.46	2.54	1	22
1:A:11:SER:O	1:A:15:LYS:HD3	0.46	2.11	16	2
1:A:11:SER:O	1:A:15:LYS:HG2	0.45	2.12	5	3
1:A:14:ARG:O	1:A:17:MET:N	0.45	2.48	20	2
1:A:13:TYR:O	1:A:14:ARG:C	0.44	2.54	24	4
1:A:9:SER:O	1:A:10:TYR:C	0.44	2.55	9	20
1:A:16:GLN:O	1:A:17:MET:C	0.44	2.56	14	18
1:A:12:ARG:CB	1:A:12:ARG:CZ	0.44	2.96	15	1
1:A:11:SER:O	1:A:15:LYS:HD2	0.44	2.13	1	1
1:A:5:ILE:O	1:A:10:TYR:CE2	0.44	2.71	12	5
1:A:14:ARG:O	1:A:17:MET:HB3	0.43	2.13	9	1
1:A:10:TYR:CE2	1:A:14:ARG:CD	0.43	3.01	9	1
1:A:4:GLY:C	1:A:6:PHE:N	0.43	2.71	10	18
1:A:12:ARG:O	1:A:16:GLN:CD	0.43	2.57	7	3
1:A:16:GLN:HG3	1:A:17:MET:SD	0.43	2.54	7	1
1:A:17:MET:SD	1:A:17:MET:N	0.42	2.92	8	1
1:A:5:ILE:HA	1:A:10:TYR:CD2	0.42	2.49	9	1
1:A:16:GLN:OE1	1:A:17:MET:HA	0.42	2.15	14	1
1:A:10:TYR:CD2	1:A:14:ARG:CG	0.42	3.02	9	1
1:A:14:ARG:O	1:A:17:MET:CB	0.42	2.68	9	1
1:A:16:GLN:OE1	1:A:17:MET:N	0.42	2.53	14	1
1:A:16:GLN:NE2	1:A:16:GLN:HA	0.42	2.29	20	1
1:A:5:ILE:HD13	1:A:6:PHE:N	0.41	2.30	5	1
1:A:15:LYS:N	1:A:15:LYS:CD	0.41	2.80	9	1
1:A:12:ARG:O	1:A:16:GLN:OE1	0.41	2.39	1	1
1:A:11:SER:O	1:A:15:LYS:HG3	0.41	2.16	19	1
1:A:16:GLN:HA	1:A:16:GLN:NE2	0.40	2.31	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:ASP:OD1	1:A:8:ASP:C	0.40	2.59	8	1
1:A:12:ARG:O	1:A:16:GLN:HG2	0.40	2.15	13	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	18/21 (86%)	8±1 (45±6%)	7±1 (38±6%)	3±1 (17±4%)	0	3
All	All	450/525 (86%)	201 (45%)	173 (38%)	76 (17%)	0	3

All 6 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	7	THR	25
1	A	5	ILE	23
1	A	17	MET	15
1	A	3	ASP	11
1	A	4	GLY	1
1	A	20	LYS	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	16/18 (89%)	10±1 (62±6%)	6±1 (38±6%)	1	7
All	All	400/450 (89%)	249 (62%)	151 (38%)	1	7

All 11 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	13	TYR	25
1	A	10	TYR	25
1	A	9	SER	25
1	A	5	ILE	25
1	A	6	PHE	17
1	A	15	LYS	12
1	A	14	ARG	12
1	A	12	ARG	5
1	A	17	MET	3
1	A	8	ASP	1
1	A	16	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	LYN	A	21	1	9,9,9	0.54±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	LYN	A	21	1	8,10,10	1.03±0.01	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LYN	A	21	1	-	0±0,8,9,9	0±0,0,0,0

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 47% for the well-defined parts and 46% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4916

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	148
Number of shifts mapped to atoms	136
Number of unparsed shifts	0
Number of shifts with mapping errors	12
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- Residue not found in structure. All 12 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	21	LYS	H	8.359	-1.0	1
A	21	LYS	HD2	1.68	-1.0	1
A	21	LYS	HG2	1.464	-1.0	1
A	21	LYS	HE2	2.99	-1.0	1
A	21	LYS	HD3	1.68	-1.0	1
A	21	LYS	HA	4.261	-1.0	1
A	21	LYS	HB2	1.82	-1.0	1
A	22	NH2	HN2	7.124	-1.0	2
A	22	NH2	HN1	7.63	-1.0	2
A	21	LYS	HG3	1.412	-1.0	1
A	21	LYS	HE3	2.99	-1.0	1
A	21	LYS	HB3	1.76	-1.0	1

7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

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 47%, i.e. 112 atoms were assigned a chemical shift out of a possible 239. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	36/90 (40%)	36/36 (100%)	0/36 (0%)	0/18 (0%)
Sidechain	63/124 (51%)	63/74 (85%)	0/41 (0%)	0/9 (0%)
Aromatic	13/25 (52%)	13/13 (100%)	0/12 (0%)	0/0 (—%)
Overall	112/239 (47%)	112/123 (91%)	0/89 (0%)	0/27 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 46%, i.e. 120 atoms were assigned a chemical shift out of a possible 262. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	38/100 (38%)	38/40 (95%)	0/40 (0%)	0/20 (0%)
Sidechain	67/130 (52%)	67/78 (86%)	0/43 (0%)	0/9 (0%)
Aromatic	15/32 (47%)	15/17 (88%)	0/14 (0%)	0/1 (0%)
Overall	120/262 (46%)	120/135 (89%)	0/97 (0%)	0/30 (0%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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:

