



Full wwPDB NMR Structure Validation Report ⓘ

Feb 16, 2018 – 06:26 am GMT

PDB ID : 1Z0Q
Title : Aqueous Solution Structure of the Alzheimer's Disease Abeta Peptide (1-42)
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Deposited on : 2005-03-02

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

<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	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk30686
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30686

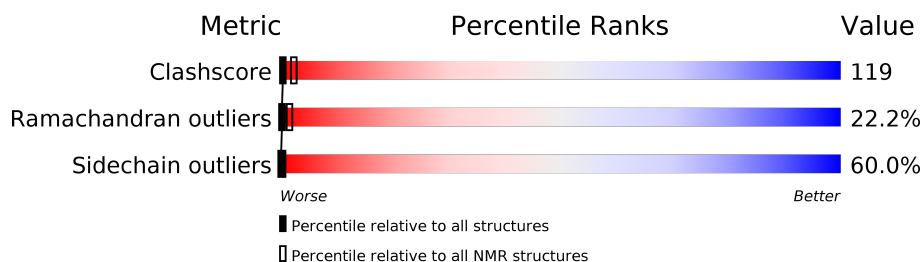
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 43%.

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	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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	42	

2 Ensemble composition and analysis

This entry contains 30 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 25 as representative, based on the following criterion: *closest to the average*.

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:7-A:26 (20)	0.77	3

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 5 clusters and 2 single-model clusters were found.

Cluster number	Models
1	2, 3, 6, 14, 18, 23, 24
2	5, 9, 10, 13, 15, 17, 19
3	1, 7, 8, 11, 16, 27, 28
4	4, 12, 25, 26
5	20, 29, 30
Single-model clusters	21; 22

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 588 atoms, of which 270 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Alzheimer's disease amyloid.

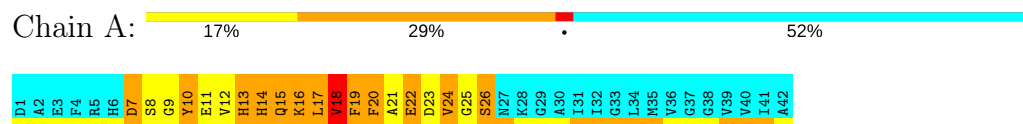
Mol	Chain	Residues	Atoms						Trace
1	A	42	Total	C	H	N	O	S	0
			588	203	270	55	59	1	

4 Residue-property plots [i](#)

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: Alzheimer's disease amyloid

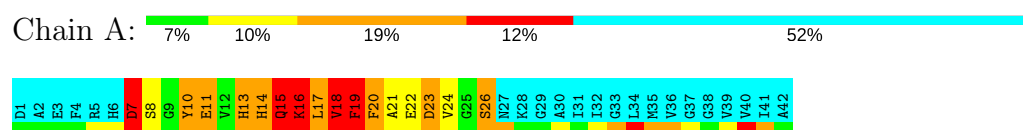


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

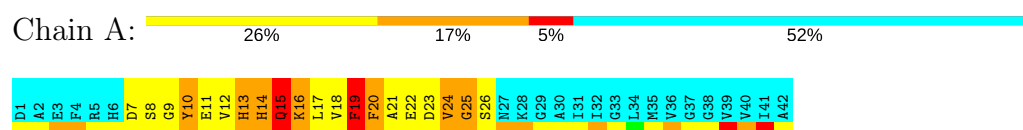
4.2.1 Score per residue for model 1

- Molecule 1: Alzheimer's disease amyloid



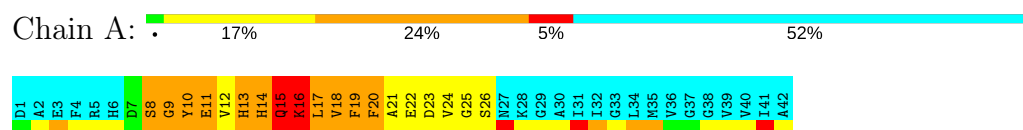
4.2.2 Score per residue for model 2

- Molecule 1: Alzheimer's disease amyloid



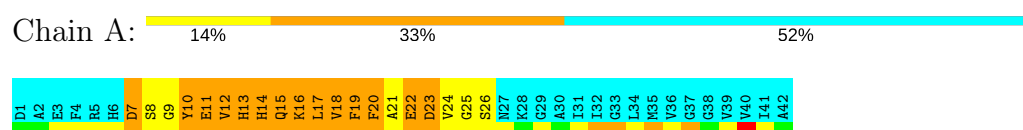
4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Alzheimer's disease amyloid



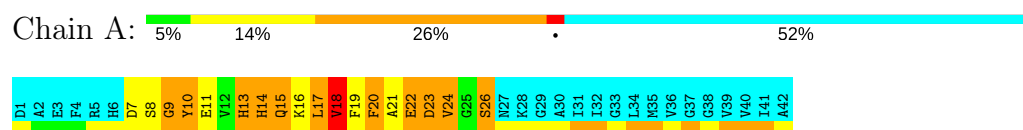
4.2.4 Score per residue for model 4

- Molecule 1: Alzheimer's disease amyloid



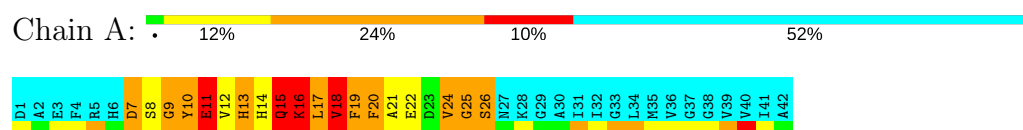
4.2.5 Score per residue for model 5

- Molecule 1: Alzheimer's disease amyloid



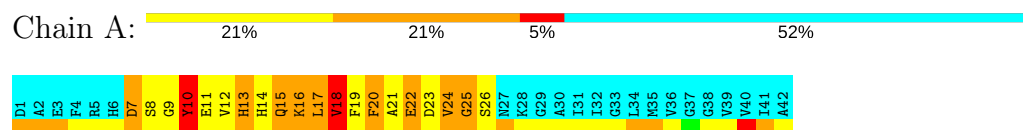
4.2.6 Score per residue for model 6

- Molecule 1: Alzheimer's disease amyloid



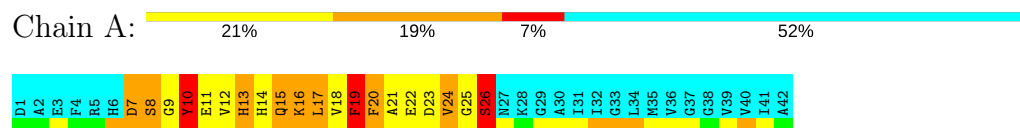
4.2.7 Score per residue for model 7

- Molecule 1: Alzheimer's disease amyloid



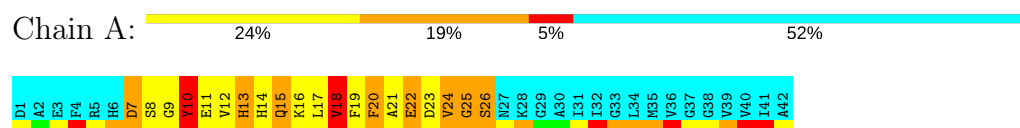
4.2.8 Score per residue for model 8

- Molecule 1: Alzheimer's disease amyloid



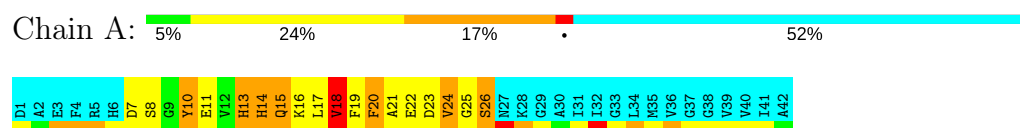
4.2.9 Score per residue for model 9

- Molecule 1: Alzheimer's disease amyloid



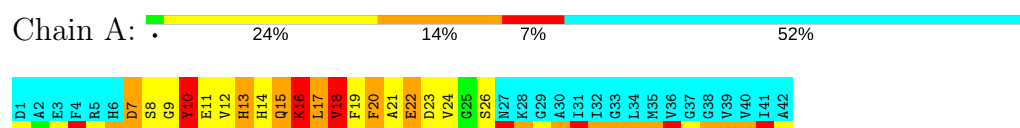
4.2.10 Score per residue for model 10

- Molecule 1: Alzheimer's disease amyloid



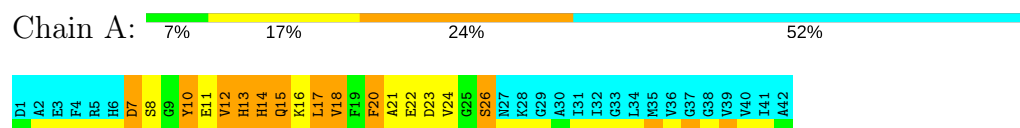
4.2.11 Score per residue for model 11

- Molecule 1: Alzheimer's disease amyloid



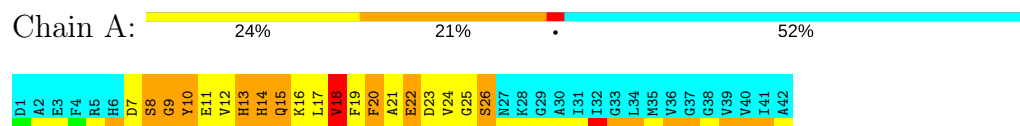
4.2.12 Score per residue for model 12

- Molecule 1: Alzheimer's disease amyloid



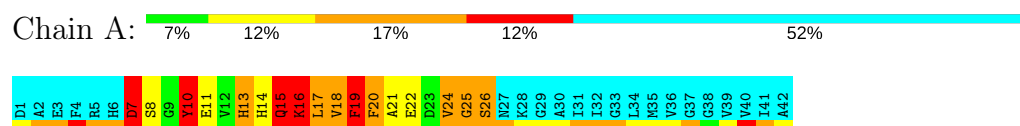
4.2.13 Score per residue for model 13

- Molecule 1: Alzheimer's disease amyloid



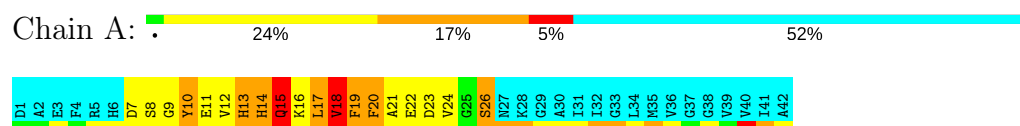
4.2.14 Score per residue for model 14

- Molecule 1: Alzheimer's disease amyloid



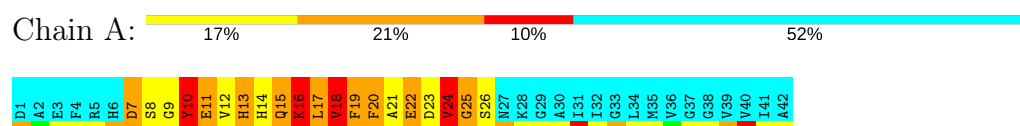
4.2.15 Score per residue for model 15

- Molecule 1: Alzheimer's disease amyloid



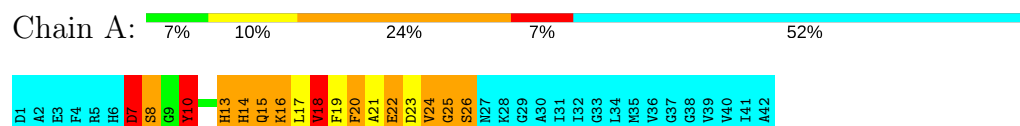
4.2.16 Score per residue for model 16

- Molecule 1: Alzheimer's disease amyloid



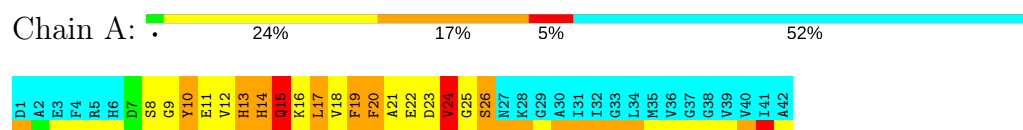
4.2.17 Score per residue for model 17

- Molecule 1: Alzheimer's disease amyloid



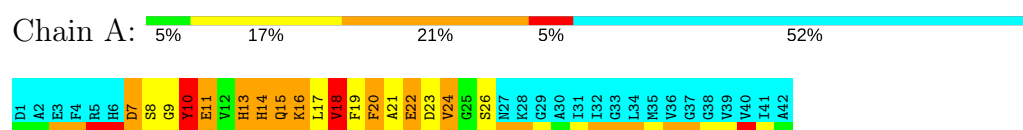
4.2.18 Score per residue for model 18

- Molecule 1: Alzheimer's disease amyloid



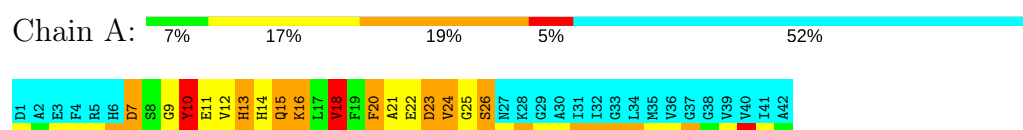
4.2.19 Score per residue for model 19

- Molecule 1: Alzheimer's disease amyloid



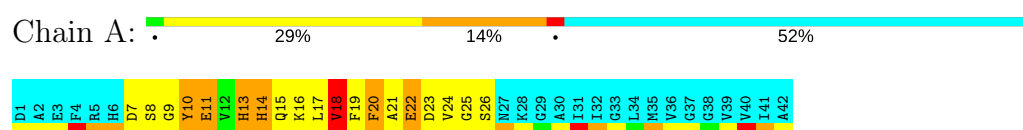
4.2.20 Score per residue for model 20

- Molecule 1: Alzheimer's disease amyloid



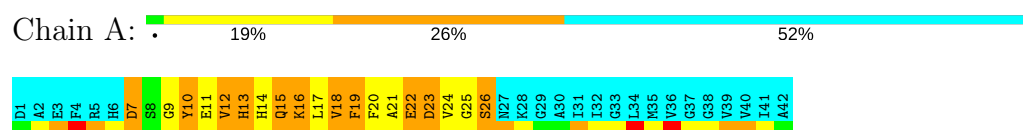
4.2.21 Score per residue for model 21

- Molecule 1: Alzheimer's disease amyloid



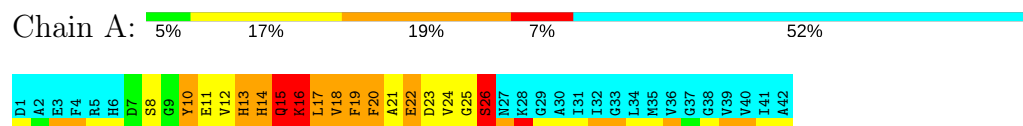
4.2.22 Score per residue for model 22

- Molecule 1: Alzheimer's disease amyloid



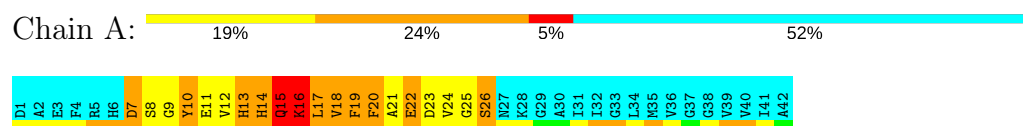
4.2.23 Score per residue for model 23

- Molecule 1: Alzheimer's disease amyloid



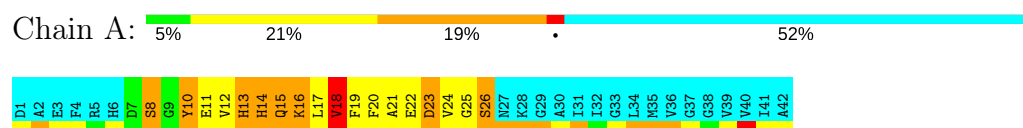
4.2.24 Score per residue for model 24

- Molecule 1: Alzheimer's disease amyloid



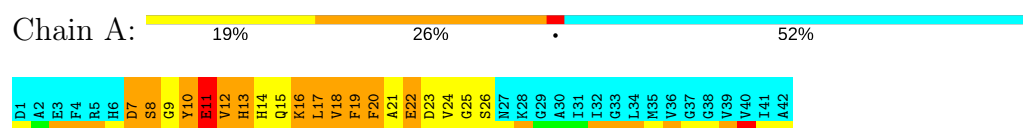
4.2.25 Score per residue for model 25

- Molecule 1: Alzheimer's disease amyloid



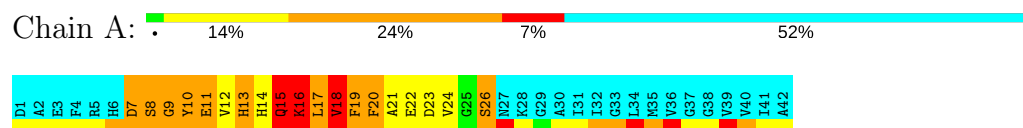
4.2.26 Score per residue for model 26

- Molecule 1: Alzheimer's disease amyloid



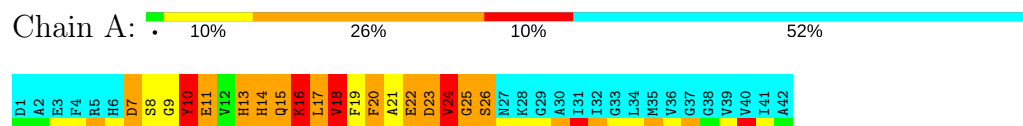
4.2.27 Score per residue for model 27

- Molecule 1: Alzheimer's disease amyloid



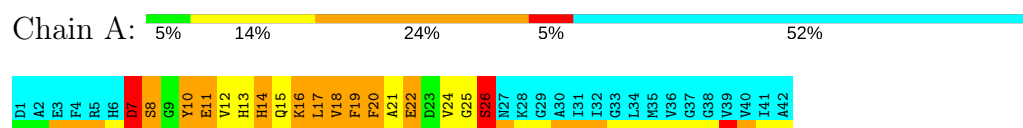
4.2.28 Score per residue for model 28

- Molecule 1: Alzheimer's disease amyloid



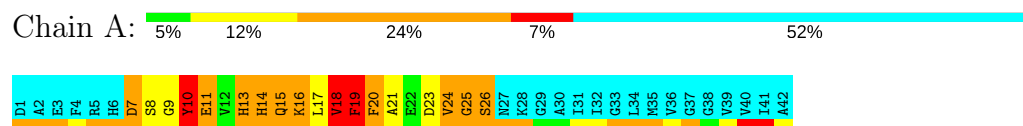
4.2.29 Score per residue for model 29

- Molecule 1: Alzheimer's disease amyloid



4.2.30 Score per residue for model 30

- Molecule 1: Alzheimer's disease amyloid



5 Refinement protocol and experimental data overview

Of the 100 calculated structures, 30 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DYANA	refinement	1.5
DYANA	structure solution	1.5

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 6554
Number of chemical shift lists	1
Total number of shifts	255
Number of shifts mapped to atoms	255
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

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	160	123	141	36±7
All	All	4800	3690	4230	1075

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 119.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:HIS:O	1:A:16:LYS:N	0.98	1.96	28	30
1:A:14:HIS:O	1:A:18:VAL:HG23	0.95	1.62	18	22
1:A:15:GLN:HA	1:A:18:VAL:HG21	0.93	1.40	21	7
1:A:15:GLN:HA	1:A:18:VAL:CG2	0.93	1.94	21	23
1:A:8:SER:O	1:A:12:VAL:HG12	0.92	1.63	18	8
1:A:14:HIS:O	1:A:18:VAL:CG2	0.87	2.23	6	22
1:A:14:HIS:CD2	1:A:18:VAL:HG21	0.86	2.04	18	9
1:A:20:PHE:O	1:A:24:VAL:HG13	0.84	1.71	5	1
1:A:15:GLN:HA	1:A:18:VAL:HG23	0.83	1.50	11	15
1:A:15:GLN:C	1:A:18:VAL:CG2	0.82	2.48	25	8
1:A:17:LEU:HD23	1:A:20:PHE:HB3	0.82	1.50	26	3
1:A:14:HIS:O	1:A:18:VAL:HG13	0.81	1.76	4	2
1:A:10:TYR:N	1:A:10:TYR:CD1	0.80	2.47	30	6
1:A:10:TYR:CD1	1:A:10:TYR:N	0.79	2.51	8	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:LEU:O	1:A:20:PHE:N	0.79	2.15	6	22
1:A:15:GLN:O	1:A:18:VAL:HG23	0.79	1.78	21	6
1:A:17:LEU:CD1	1:A:21:ALA:HB2	0.78	2.08	18	1
1:A:7:ASP:O	1:A:10:TYR:CD1	0.77	2.38	26	6
1:A:15:GLN:CA	1:A:18:VAL:CG2	0.76	2.63	21	12
1:A:14:HIS:CD2	1:A:18:VAL:CG2	0.76	2.69	18	8
1:A:17:LEU:HD22	1:A:17:LEU:H	0.75	1.41	15	1
1:A:10:TYR:CD2	1:A:11:GLU:N	0.75	2.55	13	15
1:A:15:GLN:O	1:A:18:VAL:CG2	0.74	2.35	30	8
1:A:15:GLN:C	1:A:18:VAL:HG22	0.72	2.05	4	7
1:A:17:LEU:HD12	1:A:21:ALA:HB2	0.72	1.61	18	1
1:A:14:HIS:CG	1:A:18:VAL:HG21	0.72	2.19	18	2
1:A:18:VAL:O	1:A:22:GLU:N	0.71	2.23	15	26
1:A:15:GLN:CA	1:A:18:VAL:HG23	0.71	2.16	19	17
1:A:16:LYS:NZ	1:A:17:LEU:HD12	0.71	2.00	26	1
1:A:10:TYR:CG	1:A:11:GLU:N	0.70	2.59	10	16
1:A:10:TYR:O	1:A:14:HIS:N	0.70	2.24	19	29
1:A:16:LYS:O	1:A:19:PHE:CE2	0.70	2.44	4	3
1:A:9:GLY:C	1:A:10:TYR:CG	0.69	2.66	8	9
1:A:10:TYR:C	1:A:10:TYR:CD1	0.69	2.65	26	1
1:A:15:GLN:O	1:A:17:LEU:N	0.68	2.27	6	12
1:A:17:LEU:O	1:A:19:PHE:N	0.68	2.26	15	12
1:A:16:LYS:O	1:A:19:PHE:CZ	0.68	2.46	30	1
1:A:15:GLN:O	1:A:19:PHE:CZ	0.67	2.48	26	4
1:A:8:SER:O	1:A:9:GLY:C	0.67	2.33	27	2
1:A:21:ALA:HA	1:A:24:VAL:HG12	0.67	1.65	11	15
1:A:10:TYR:CD1	1:A:11:GLU:N	0.66	2.64	26	1
1:A:15:GLN:C	1:A:18:VAL:HG23	0.66	2.11	21	1
1:A:16:LYS:HZ1	1:A:17:LEU:HD12	0.66	1.49	26	1
1:A:18:VAL:HG12	1:A:22:GLU:CG	0.66	2.20	15	1
1:A:7:ASP:O	1:A:9:GLY:N	0.64	2.30	13	3
1:A:15:GLN:O	1:A:19:PHE:CD1	0.64	2.50	8	8
1:A:10:TYR:O	1:A:12:VAL:N	0.64	2.31	26	1
1:A:7:ASP:O	1:A:11:GLU:HB3	0.64	1.92	27	3
1:A:13:HIS:O	1:A:14:HIS:C	0.63	2.36	1	25
1:A:9:GLY:C	1:A:10:TYR:CD1	0.63	2.72	30	4
1:A:15:GLN:O	1:A:19:PHE:CE1	0.63	2.52	26	8
1:A:18:VAL:HG12	1:A:22:GLU:CB	0.63	2.22	15	1
1:A:13:HIS:O	1:A:16:LYS:HE2	0.63	1.94	29	2
1:A:14:HIS:C	1:A:18:VAL:CG2	0.62	2.67	19	13
1:A:7:ASP:O	1:A:11:GLU:CB	0.62	2.47	27	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:LEU:HD13	1:A:17:LEU:N	0.62	2.09	15	1
1:A:20:PHE:O	1:A:24:VAL:HG22	0.62	1.95	28	7
1:A:18:VAL:HG12	1:A:22:GLU:HB2	0.62	1.69	15	2
1:A:15:GLN:O	1:A:16:LYS:C	0.61	2.38	27	20
1:A:24:VAL:O	1:A:24:VAL:HG13	0.61	1.93	30	2
1:A:19:PHE:CD1	1:A:20:PHE:N	0.61	2.67	27	9
1:A:17:LEU:O	1:A:18:VAL:C	0.61	2.39	15	18
1:A:18:VAL:O	1:A:22:GLU:CB	0.61	2.49	1	12
1:A:7:ASP:O	1:A:10:TYR:N	0.60	2.22	26	1
1:A:15:GLN:O	1:A:19:PHE:N	0.60	2.34	22	1
1:A:7:ASP:O	1:A:11:GLU:N	0.59	2.34	28	5
1:A:16:LYS:HG2	1:A:17:LEU:N	0.59	2.11	11	4
1:A:7:ASP:O	1:A:8:SER:C	0.59	2.41	26	1
1:A:15:GLN:O	1:A:15:GLN:NE2	0.59	2.36	20	2
1:A:24:VAL:HG13	1:A:25:GLY:H	0.58	1.58	26	7
1:A:12:VAL:HG22	1:A:16:LYS:CE	0.58	2.28	20	1
1:A:24:VAL:HG13	1:A:24:VAL:O	0.58	1.99	7	1
1:A:19:PHE:C	1:A:19:PHE:CD1	0.58	2.76	18	1
1:A:19:PHE:CD1	1:A:19:PHE:N	0.58	2.70	29	3
1:A:14:HIS:O	1:A:18:VAL:HG22	0.58	1.98	21	7
1:A:14:HIS:O	1:A:16:LYS:N	0.58	2.36	1	17
1:A:20:PHE:O	1:A:24:VAL:CG2	0.58	2.52	9	9
1:A:8:SER:O	1:A:10:TYR:N	0.57	2.37	13	8
1:A:21:ALA:HA	1:A:24:VAL:CG2	0.57	2.29	27	5
1:A:15:GLN:CA	1:A:18:VAL:HG22	0.57	2.28	30	7
1:A:18:VAL:HG23	1:A:19:PHE:CE1	0.57	2.34	4	2
1:A:21:ALA:HA	1:A:24:VAL:HG23	0.57	1.76	10	5
1:A:15:GLN:OE1	1:A:19:PHE:CD2	0.57	2.58	2	1
1:A:15:GLN:OE1	1:A:19:PHE:CB	0.57	2.52	2	2
1:A:10:TYR:O	1:A:13:HIS:N	0.56	2.37	9	18
1:A:7:ASP:HA	1:A:10:TYR:CE1	0.56	2.35	27	2
1:A:14:HIS:C	1:A:16:LYS:N	0.56	2.59	24	19
1:A:14:HIS:C	1:A:18:VAL:HG23	0.56	2.20	1	4
1:A:16:LYS:O	1:A:19:PHE:CD2	0.56	2.59	29	2
1:A:11:GLU:CG	1:A:12:VAL:N	0.55	2.69	13	7
1:A:11:GLU:HG3	1:A:12:VAL:N	0.55	2.17	11	4
1:A:13:HIS:O	1:A:15:GLN:N	0.54	2.41	30	13
1:A:21:ALA:O	1:A:24:VAL:O	0.54	2.25	27	5
1:A:14:HIS:C	1:A:16:LYS:H	0.54	2.06	24	11
1:A:10:TYR:O	1:A:11:GLU:C	0.54	2.46	27	8
1:A:24:VAL:O	1:A:26:SER:N	0.54	2.41	7	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:ALA:O	1:A:25:GLY:N	0.53	2.42	6	8
1:A:12:VAL:O	1:A:15:GLN:CG	0.53	2.56	7	4
1:A:16:LYS:HA	1:A:19:PHE:CZ	0.52	2.39	26	3
1:A:7:ASP:O	1:A:11:GLU:HB2	0.52	2.04	19	5
1:A:17:LEU:O	1:A:21:ALA:N	0.52	2.40	14	8
1:A:19:PHE:CE1	1:A:20:PHE:HB2	0.52	2.39	1	2
1:A:15:GLN:HG3	1:A:15:GLN:O	0.52	2.03	26	6
1:A:15:GLN:HG2	1:A:19:PHE:CD2	0.52	2.39	11	2
1:A:16:LYS:HA	1:A:19:PHE:CE2	0.52	2.39	29	1
1:A:15:GLN:CA	1:A:18:VAL:HG21	0.52	2.24	21	1
1:A:24:VAL:HG13	1:A:25:GLY:N	0.52	2.19	3	7
1:A:18:VAL:O	1:A:22:GLU:HB2	0.51	2.05	11	23
1:A:12:VAL:HG22	1:A:16:LYS:NZ	0.51	2.21	20	1
1:A:21:ALA:C	1:A:24:VAL:HG22	0.51	2.25	18	1
1:A:15:GLN:C	1:A:17:LEU:N	0.51	2.62	6	8
1:A:16:LYS:CE	1:A:17:LEU:N	0.51	2.73	29	1
1:A:15:GLN:HA	1:A:18:VAL:HG22	0.51	1.81	26	3
1:A:17:LEU:O	1:A:20:PHE:CB	0.51	2.59	27	6
1:A:15:GLN:CG	1:A:15:GLN:O	0.51	2.59	26	3
1:A:22:GLU:O	1:A:26:SER:CB	0.51	2.59	22	11
1:A:10:TYR:CE1	1:A:11:GLU:HB3	0.51	2.41	26	1
1:A:13:HIS:O	1:A:16:LYS:CB	0.50	2.59	21	2
1:A:18:VAL:C	1:A:20:PHE:N	0.50	2.65	8	9
1:A:7:ASP:C	1:A:10:TYR:CE1	0.50	2.85	27	1
1:A:22:GLU:OE2	1:A:26:SER:CB	0.49	2.60	10	1
1:A:21:ALA:O	1:A:24:VAL:CG2	0.49	2.60	18	1
1:A:10:TYR:CE2	1:A:11:GLU:HB2	0.49	2.42	10	1
1:A:8:SER:N	1:A:11:GLU:OE2	0.49	2.45	11	1
1:A:19:PHE:O	1:A:23:ASP:N	0.49	2.45	25	4
1:A:21:ALA:HA	1:A:24:VAL:HG22	0.49	1.84	5	1
1:A:8:SER:O	1:A:9:GLY:O	0.49	2.29	27	1
1:A:21:ALA:C	1:A:24:VAL:CG2	0.49	2.80	18	1
1:A:26:SER:O	1:A:26:SER:OG	0.49	2.31	30	2
1:A:15:GLN:NE2	1:A:19:PHE:CD2	0.49	2.79	7	2
1:A:18:VAL:O	1:A:20:PHE:N	0.49	2.46	1	6
1:A:13:HIS:CD2	1:A:16:LYS:HE2	0.48	2.43	30	1
1:A:13:HIS:CD2	1:A:16:LYS:HD3	0.48	2.43	26	2
1:A:9:GLY:O	1:A:10:TYR:C	0.48	2.51	27	1
1:A:15:GLN:NE2	1:A:19:PHE:CB	0.48	2.76	27	1
1:A:13:HIS:O	1:A:16:LYS:HB3	0.48	2.08	11	2
1:A:23:ASP:O	1:A:25:GLY:N	0.48	2.46	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:VAL:O	1:A:16:LYS:CE	0.48	2.61	20	2
1:A:9:GLY:O	1:A:13:HIS:HB2	0.48	2.08	13	1
1:A:7:ASP:O	1:A:8:SER:O	0.48	2.32	27	1
1:A:24:VAL:O	1:A:24:VAL:CG1	0.48	2.61	30	1
1:A:17:LEU:C	1:A:19:PHE:N	0.48	2.67	19	10
1:A:15:GLN:HG3	1:A:19:PHE:CE1	0.48	2.43	21	1
1:A:24:VAL:CG1	1:A:24:VAL:O	0.48	2.61	21	3
1:A:21:ALA:O	1:A:24:VAL:N	0.48	2.47	23	3
1:A:8:SER:N	1:A:11:GLU:OE1	0.48	2.46	9	2
1:A:7:ASP:CG	1:A:7:ASP:O	0.48	2.52	20	1
1:A:14:HIS:O	1:A:16:LYS:HE2	0.48	2.08	6	3
1:A:22:GLU:O	1:A:22:GLU:CD	0.47	2.52	14	3
1:A:9:GLY:O	1:A:13:HIS:ND1	0.47	2.47	6	10
1:A:7:ASP:CA	1:A:10:TYR:CE1	0.47	2.97	27	1
1:A:11:GLU:CD	1:A:12:VAL:N	0.47	2.68	12	1
1:A:17:LEU:HD23	1:A:20:PHE:CB	0.47	2.31	26	2
1:A:15:GLN:OE1	1:A:19:PHE:HB3	0.47	2.10	18	1
1:A:19:PHE:N	1:A:19:PHE:CD1	0.47	2.80	21	2
1:A:7:ASP:O	1:A:10:TYR:CE1	0.47	2.67	14	1
1:A:15:GLN:O	1:A:15:GLN:HG3	0.47	2.10	19	2
1:A:18:VAL:O	1:A:22:GLU:HB3	0.47	2.10	18	1
1:A:8:SER:C	1:A:10:TYR:N	0.46	2.66	13	9
1:A:13:HIS:C	1:A:15:GLN:N	0.46	2.68	29	3
1:A:25:GLY:O	1:A:26:SER:C	0.46	2.53	17	3
1:A:7:ASP:N	1:A:7:ASP:OD1	0.46	2.47	7	2
1:A:15:GLN:NE2	1:A:15:GLN:O	0.46	2.48	8	1
1:A:22:GLU:CD	1:A:22:GLU:O	0.46	2.53	23	2
1:A:24:VAL:O	1:A:25:GLY:C	0.46	2.54	7	7
1:A:21:ALA:HA	1:A:24:VAL:CG1	0.46	2.41	24	7
1:A:14:HIS:O	1:A:18:VAL:CG1	0.46	2.59	4	2
1:A:7:ASP:OD1	1:A:8:SER:N	0.45	2.50	14	1
1:A:9:GLY:O	1:A:12:VAL:CG1	0.45	2.64	27	1
1:A:19:PHE:O	1:A:22:GLU:N	0.45	2.50	25	1
1:A:20:PHE:O	1:A:24:VAL:HG23	0.45	2.12	8	5
1:A:24:VAL:C	1:A:26:SER:N	0.45	2.70	18	10
1:A:7:ASP:CG	1:A:8:SER:N	0.45	2.71	14	1
1:A:15:GLN:CG	1:A:19:PHE:HB3	0.45	2.42	24	5
1:A:7:ASP:O	1:A:11:GLU:CG	0.45	2.66	11	2
1:A:20:PHE:O	1:A:24:VAL:HG12	0.44	2.12	26	1
1:A:7:ASP:C	1:A:11:GLU:OE1	0.44	2.56	9	1
1:A:15:GLN:NE2	1:A:19:PHE:HB3	0.44	2.28	27	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:ALA:O	1:A:22:GLU:C	0.44	2.55	15	3
1:A:9:GLY:O	1:A:13:HIS:CG	0.44	2.71	26	3
1:A:16:LYS:HA	1:A:16:LYS:CE	0.44	2.43	1	2
1:A:17:LEU:HD22	1:A:17:LEU:N	0.44	2.19	15	1
1:A:21:ALA:O	1:A:25:GLY:CA	0.44	2.66	8	1
1:A:22:GLU:CD	1:A:26:SER:CB	0.43	2.87	10	1
1:A:23:ASP:O	1:A:26:SER:CB	0.43	2.66	24	1
1:A:7:ASP:CB	1:A:11:GLU:HB3	0.43	2.42	8	1
1:A:12:VAL:O	1:A:15:GLN:HG2	0.43	2.13	16	1
1:A:14:HIS:O	1:A:17:LEU:HD22	0.43	2.13	15	1
1:A:23:ASP:O	1:A:26:SER:C	0.43	2.57	13	3
1:A:12:VAL:O	1:A:16:LYS:HD3	0.43	2.13	25	1
1:A:24:VAL:O	1:A:24:VAL:CG2	0.43	2.66	5	1
1:A:15:GLN:OE1	1:A:19:PHE:CG	0.43	2.71	2	1
1:A:18:VAL:HG12	1:A:22:GLU:HG2	0.43	1.88	15	1
1:A:18:VAL:CG1	1:A:22:GLU:HB2	0.43	2.42	15	1
1:A:7:ASP:O	1:A:11:GLU:HG2	0.43	2.13	11	2
1:A:13:HIS:CD2	1:A:16:LYS:CE	0.42	3.02	30	1
1:A:16:LYS:HE2	1:A:17:LEU:N	0.42	2.29	26	2
1:A:17:LEU:N	1:A:17:LEU:CD1	0.42	2.77	15	1
1:A:22:GLU:O	1:A:26:SER:C	0.42	2.57	8	2
1:A:13:HIS:CA	1:A:16:LYS:HE2	0.42	2.45	30	1
1:A:10:TYR:CD1	1:A:11:GLU:HB3	0.42	2.49	26	1
1:A:17:LEU:HD22	1:A:17:LEU:HA	0.42	1.73	18	1
1:A:21:ALA:HA	1:A:24:VAL:HG21	0.42	1.90	18	1
1:A:17:LEU:O	1:A:20:PHE:CA	0.42	2.67	6	1
1:A:12:VAL:O	1:A:15:GLN:HG3	0.42	2.15	7	1
1:A:8:SER:HA	1:A:11:GLU:CG	0.42	2.44	12	1
1:A:9:GLY:O	1:A:10:TYR:CG	0.42	2.73	30	1
1:A:17:LEU:CD1	1:A:21:ALA:CB	0.42	2.92	18	1
1:A:8:SER:HA	1:A:11:GLU:HG2	0.42	1.90	8	1
1:A:22:GLU:O	1:A:22:GLU:OE1	0.41	2.38	9	2
1:A:12:VAL:O	1:A:16:LYS:HB2	0.41	2.15	20	1
1:A:11:GLU:C	1:A:13:HIS:N	0.41	2.73	21	2
1:A:19:PHE:O	1:A:23:ASP:OD2	0.41	2.38	24	2
1:A:22:GLU:O	1:A:26:SER:OG	0.41	2.37	14	2
1:A:18:VAL:C	1:A:20:PHE:H	0.41	2.17	4	3
1:A:16:LYS:C	1:A:17:LEU:HD13	0.41	2.35	15	1
1:A:13:HIS:O	1:A:16:LYS:HB2	0.41	2.15	7	1
1:A:21:ALA:CA	1:A:24:VAL:CG2	0.41	2.98	18	1
1:A:15:GLN:CD	1:A:15:GLN:O	0.41	2.59	30	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:ASP:HB3	1:A:10:TYR:CZ	0.41	2.50	26	1
1:A:8:SER:O	1:A:11:GLU:HG2	0.41	2.16	13	1
1:A:11:GLU:O	1:A:12:VAL:C	0.41	2.58	27	1
1:A:11:GLU:C	1:A:11:GLU:CD	0.41	2.78	27	1
1:A:26:SER:OG	1:A:26:SER:O	0.41	2.36	7	1
1:A:22:GLU:HA	1:A:26:SER:CB	0.41	2.46	12	1
1:A:8:SER:CA	1:A:11:GLU:HG2	0.40	2.46	8	1
1:A:15:GLN:OE1	1:A:19:PHE:CA	0.40	2.70	19	1
1:A:7:ASP:CB	1:A:11:GLU:HB2	0.40	2.46	30	1
1:A:16:LYS:HE3	1:A:17:LEU:CB	0.40	2.47	29	1
1:A:21:ALA:CA	1:A:24:VAL:HG22	0.40	2.46	18	1
1:A:22:GLU:OE1	1:A:22:GLU:C	0.40	2.60	1	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	20/42 (48%)	9±3 (47±14%)	6±2 (31±11%)	4±2 (22±10%)	0	2
All	All	600/1260 (48%)	282 (47%)	185 (31%)	133 (22%)	0	2

All 13 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	18	VAL	22
1	A	15	GLN	16
1	A	14	HIS	15
1	A	11	GLU	13
1	A	16	LYS	12
1	A	7	ASP	12
1	A	25	GLY	11
1	A	10	TYR	11
1	A	19	PHE	5
1	A	9	GLY	5

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Mol	Chain	Res	Type	Models (Total)
1	A	24	VAL	5
1	A	8	SER	3
1	A	26	SER	3

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	17/32 (53%)	7±2 (40±11%)	10±2 (60±11%)	0	0
All	All	510/960 (53%)	204 (40%)	306 (60%)	0	0

All 17 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	20	PHE	30
1	A	10	TYR	30
1	A	13	HIS	29
1	A	26	SER	25
1	A	18	VAL	23
1	A	17	LEU	22
1	A	15	GLN	21
1	A	16	LYS	20
1	A	23	ASP	19
1	A	7	ASP	18
1	A	19	PHE	17
1	A	22	GLU	16
1	A	24	VAL	13
1	A	8	SER	10
1	A	12	VAL	5
1	A	14	HIS	4
1	A	11	GLU	4

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 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 43% for the well-defined parts and 44% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6554

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	255
Number of shifts mapped to atoms	255
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

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

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 43%, i.e. 102 atoms were assigned a chemical shift out of a possible 237. 0 out of 4 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	52/95 (55%)	52/55 (95%)	0/38 (0%)	0/2 (0%)
Aromatic	12/42 (29%)	12/22 (55%)	0/16 (0%)	0/4 (0%)
Overall	102/237 (43%)	102/117 (87%)	0/94 (0%)	0/26 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 44%, i.e. 215 atoms were assigned a chemical shift out of a possible 487. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	82/210 (39%)	81/84 (96%)	1/84 (1%)	0/42 (0%)
Sidechain	116/218 (53%)	116/125 (93%)	0/86 (0%)	0/7 (0%)
Aromatic	17/59 (29%)	17/31 (55%)	0/22 (0%)	0/6 (0%)
Overall	215/487 (44%)	214/240 (89%)	1/192 (1%)	0/55 (0%)

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.

Mol	Chain	Res	Type	Atom	Shift, <i>ppm</i>	Expected range, <i>ppm</i>	Z-score
1	A	5	ARG	HD2	0.00	4.27 – 1.97	-13.6
1	A	13	HIS	HB2	0.00	4.91 – 1.31	-8.6
1	A	11	GLU	HG2	3.43	3.33 – 1.23	5.5

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_1). RCI is only applicable to proteins.