



Full wwPDB NMR Structure Validation Report ⓘ

Nov 9, 2024 – 10:12 PM EST

PDB ID : 2M75
BMRB ID : 19210
Title : The C-terminal Region of Disintegrin Modulate its 3D Conformation and Co-operate with RGD Loop in Regulating Recognitions of Integrins
Authors : Chuang, W.; Chang, Y.; Shiu, J.
Deposited on : 2013-04-18

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 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 : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.39

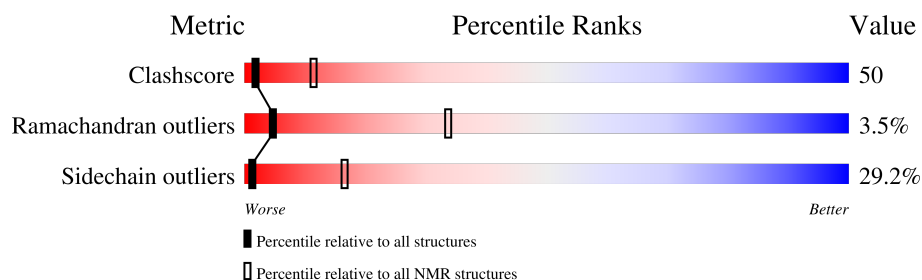
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 56%.

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	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	76	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 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:68 (66)	1.04	1

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 4 clusters and 8 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 959 atoms, of which 454 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Zinc metalloproteinase/disintegrin.

Mol	Chain	Residues	Atoms						Trace
1	A	68	Total	C	H	N	O	S	0
			959	294	454	98	101	12	

There are 11 discrepancies between the modelled and reference sequences:

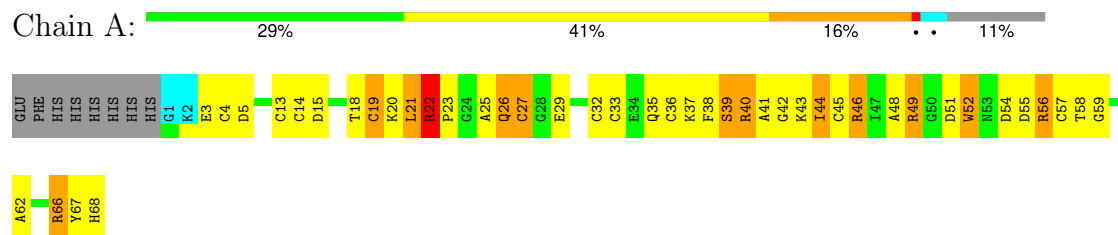
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLU	-	expression tag	UNP P30403
A	-6	PHE	-	expression tag	UNP P30403
A	-5	HIS	-	expression tag	UNP P30403
A	-4	HIS	-	expression tag	UNP P30403
A	-3	HIS	-	expression tag	UNP P30403
A	-2	HIS	-	expression tag	UNP P30403
A	-1	HIS	-	expression tag	UNP P30403
A	0	HIS	-	expression tag	UNP P30403
A	48	ALA	PRO	engineered mutation	UNP P30403
A	52	TRP	MET	engineered mutation	UNP P30403
A	53	ASN	PRO	engineered mutation	UNP P30403

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Zinc metalloproteinase/disintegrin

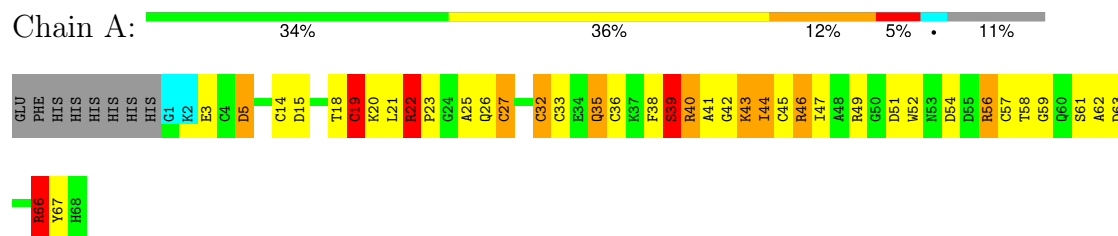


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

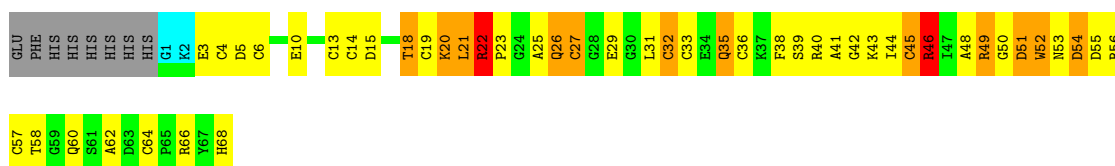
- Molecule 1: Zinc metalloproteinase/disintegrin



4.2.2 Score per residue for model 2

- Molecule 1: Zinc metalloproteinase/disintegrin

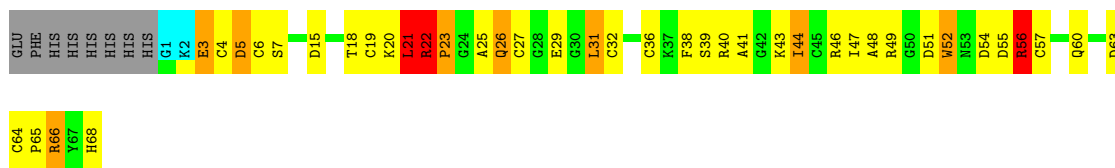




4.2.3 Score per residue for model 3

- Molecule 1: Zinc metalloproteinase/disintegrin

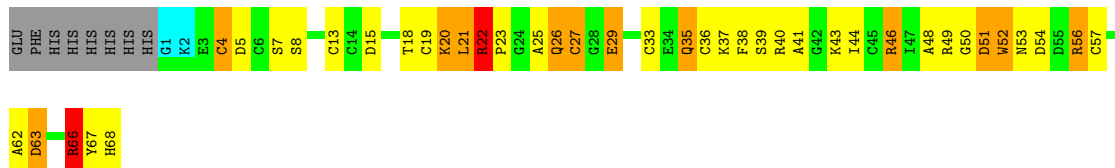
Chain A: 33% 39% 11% • • 11%



4.2.4 Score per residue for model 4

- Molecule 1: Zinc metalloproteinase/disintegrin

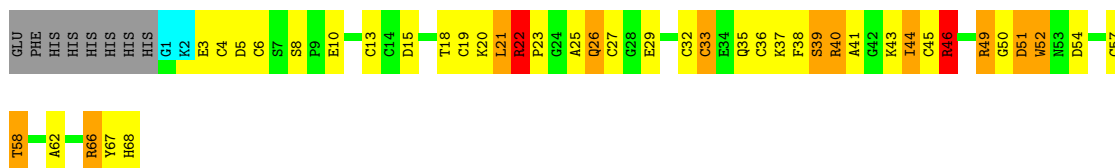
Chain A: 33% 36% 16% • • 11%



4.2.5 Score per residue for model 5

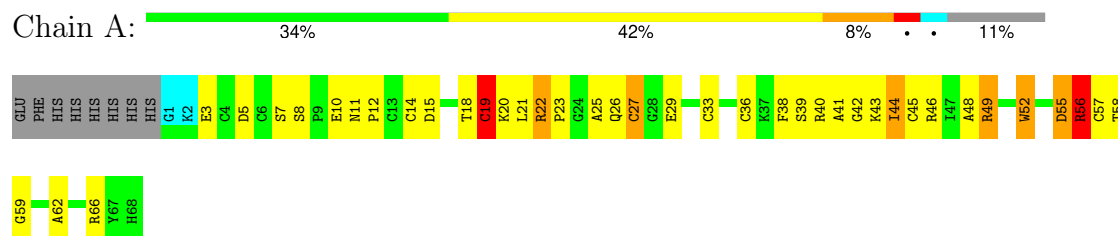
- Molecule 1: Zinc metalloproteinase/disintegrin

Chain A: 32% 38% 14% • • 11%



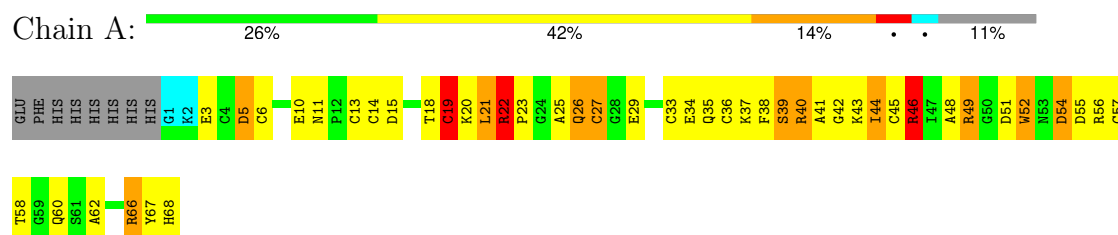
4.2.6 Score per residue for model 6

- Molecule 1: Zinc metalloproteinase/disintegrin



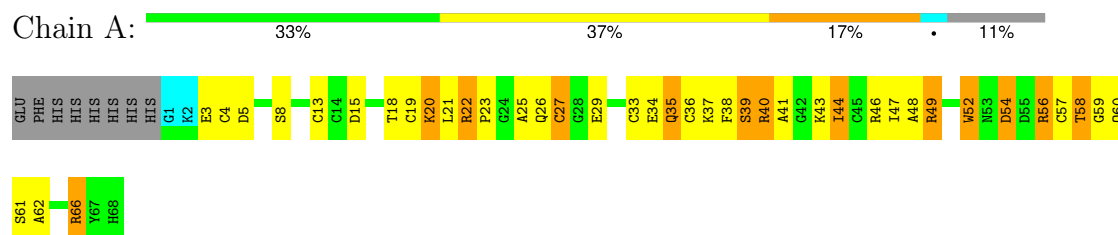
4.2.7 Score per residue for model 7

- Molecule 1: Zinc metalloproteinase/disintegrin



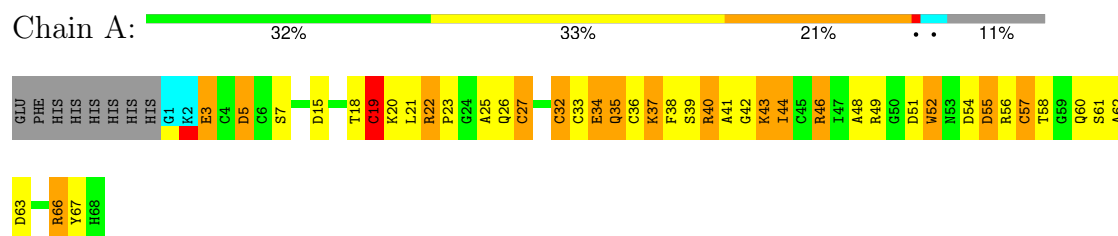
4.2.8 Score per residue for model 8

- Molecule 1: Zinc metalloproteinase/disintegrin



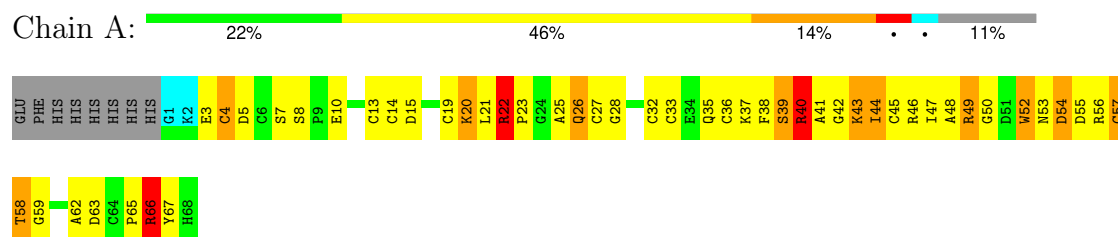
4.2.9 Score per residue for model 9

- Molecule 1: Zinc metalloproteinase/disintegrin



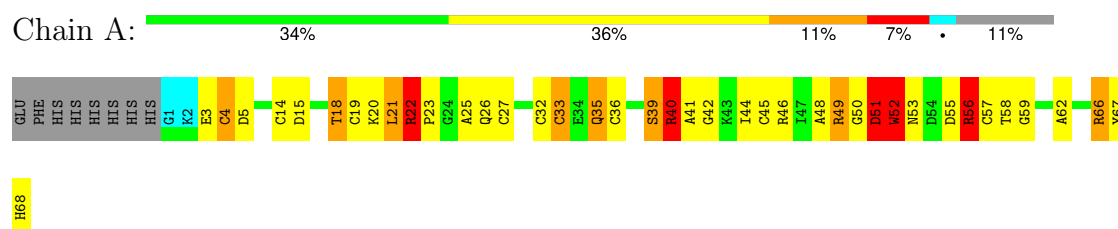
4.2.10 Score per residue for model 10

- Molecule 1: Zinc metalloproteinase/disintegrin



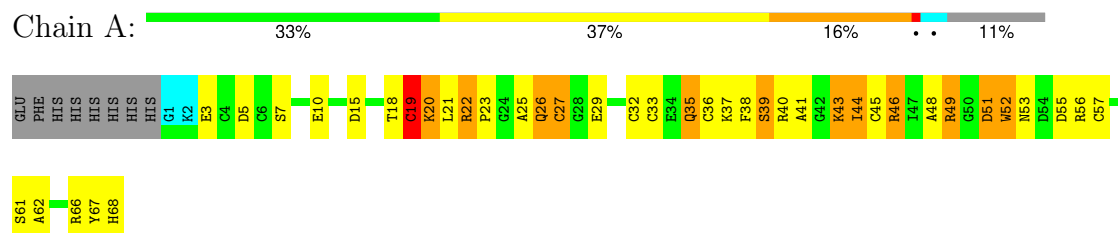
4.2.11 Score per residue for model 11

- Molecule 1: Zinc metalloproteinase/disintegrin



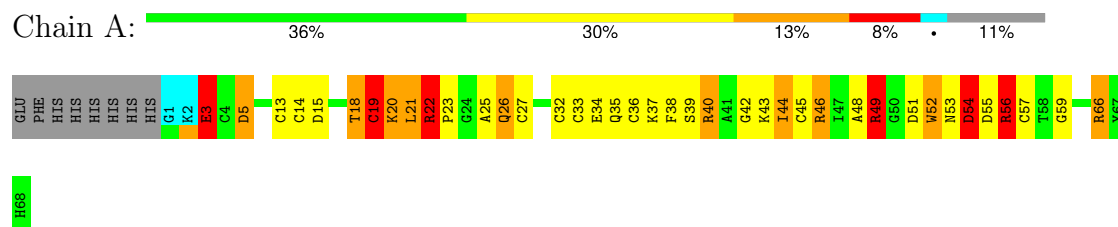
4.2.12 Score per residue for model 12

- Molecule 1: Zinc metalloproteinase/disintegrin



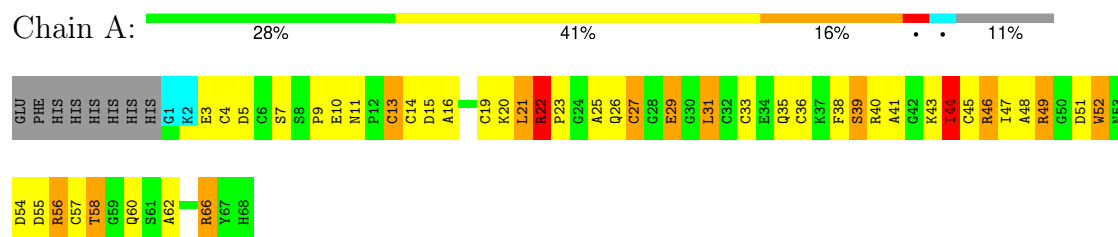
4.2.13 Score per residue for model 13

- Molecule 1: Zinc metalloproteinase/disintegrin



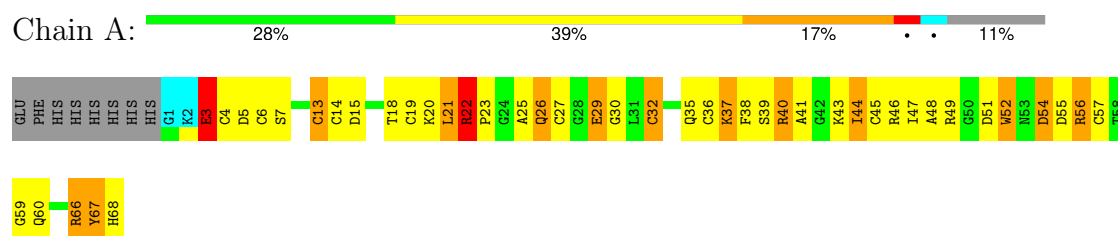
4.2.14 Score per residue for model 14

- Molecule 1: Zinc metalloproteinase/disintegrin



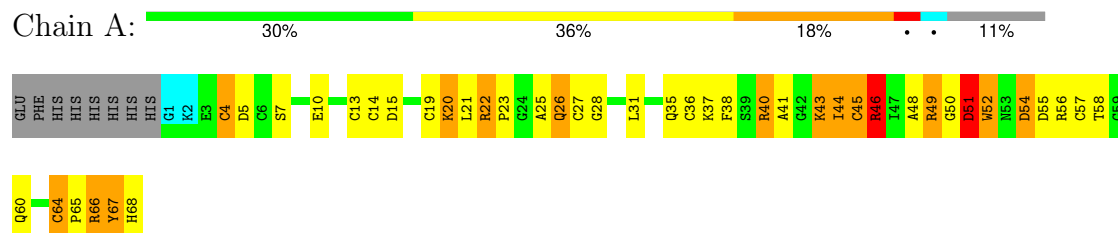
4.2.15 Score per residue for model 15

- Molecule 1: Zinc metalloproteinase/disintegrin



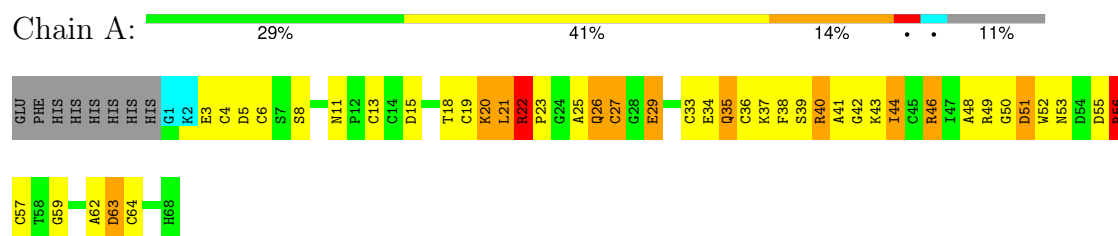
4.2.16 Score per residue for model 16

- Molecule 1: Zinc metalloproteinase/disintegrin



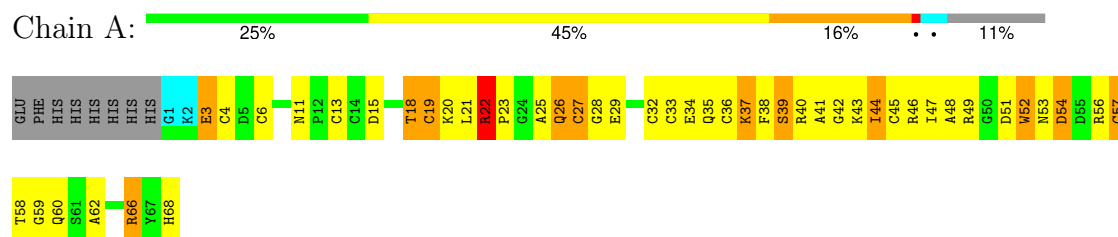
4.2.17 Score per residue for model 17

- Molecule 1: Zinc metalloproteinase/disintegrin



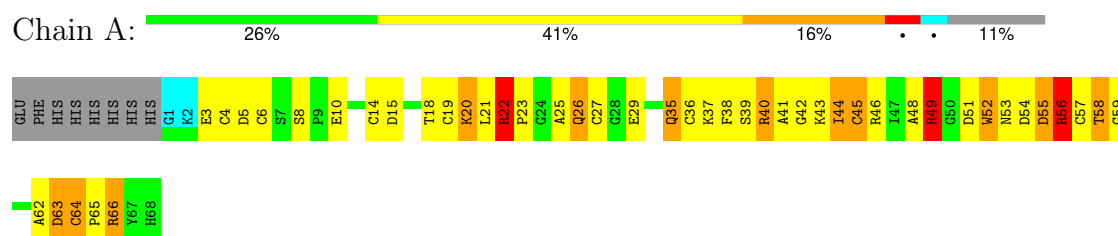
4.2.18 Score per residue for model 18

- Molecule 1: Zinc metalloproteinase/disintegrin



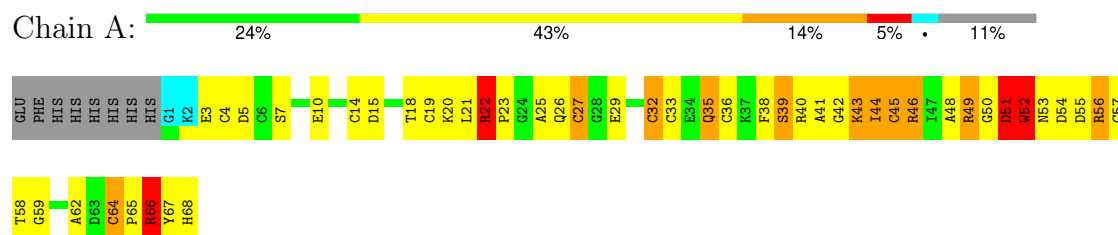
4.2.19 Score per residue for model 19

- Molecule 1: Zinc metalloproteinase/disintegrin



4.2.20 Score per residue for model 20

- Molecule 1: Zinc metalloproteinase/disintegrin



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 200 calculated structures, 20 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	refinement	3.185

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	451
Number of shifts mapped to atoms	451
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	56%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	5.8±0.4
All	All	0	115

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	40	ARG	Sidechain	20
1	A	49	ARG	Sidechain	20
1	A	22	ARG	Sidechain	19
1	A	46	ARG	Sidechain	19
1	A	66	ARG	Sidechain	19
1	A	56	ARG	Sidechain	18

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	492	438	438	47±6
All	All	9840	8760	8760	937

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 50.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:LEU:HD22	1:A:25:ALA:O	0.96	1.60	6	18
1:A:21:LEU:HD13	1:A:25:ALA:O	0.96	1.60	16	2
1:A:21:LEU:HD22	1:A:25:ALA:HB3	0.91	1.39	16	8
1:A:33:CYS:SG	1:A:62:ALA:HB1	0.91	2.06	14	12
1:A:41:ALA:HB2	1:A:58:THR:O	0.84	1.72	7	14
1:A:21:LEU:CD2	1:A:25:ALA:HB3	0.84	2.03	11	12
1:A:44:ILE:HD11	1:A:46:ARG:O	0.81	1.75	2	7
1:A:25:ALA:HB1	1:A:36:CYS:HB3	0.81	1.52	1	17
1:A:44:ILE:HD13	1:A:55:ASP:O	0.81	1.75	19	2
1:A:48:ALA:HB1	1:A:52:TRP:CD1	0.76	2.15	7	16
1:A:48:ALA:HB1	1:A:52:TRP:NE1	0.76	1.94	17	3
1:A:25:ALA:HB1	1:A:36:CYS:O	0.76	1.80	12	5
1:A:21:LEU:HD23	1:A:25:ALA:HB3	0.72	1.59	5	6
1:A:47:ILE:O	1:A:47:ILE:HG23	0.71	1.85	15	6
1:A:44:ILE:HD11	1:A:54:ASP:HB3	0.70	1.60	14	4
1:A:21:LEU:HD21	1:A:27:CYS:C	0.68	2.08	19	10
1:A:21:LEU:HD11	1:A:27:CYS:HA	0.68	1.66	15	6
1:A:48:ALA:HB1	1:A:68:HIS:CD2	0.68	2.24	4	1
1:A:44:ILE:HD13	1:A:54:ASP:HB3	0.67	1.66	2	2
1:A:21:LEU:HD22	1:A:25:ALA:C	0.66	2.10	2	7
1:A:44:ILE:HG22	1:A:44:ILE:O	0.66	1.91	3	6
1:A:41:ALA:HB2	1:A:58:THR:C	0.66	2.11	1	8
1:A:48:ALA:HB3	1:A:52:TRP:CD1	0.66	2.26	10	2
1:A:21:LEU:HD11	1:A:27:CYS:CA	0.65	2.20	16	3
1:A:42:GLY:HA2	1:A:56:ARG:CG	0.65	2.21	13	5
1:A:38:PHE:HE1	1:A:62:ALA:HB2	0.64	1.52	17	7
1:A:38:PHE:CE1	1:A:62:ALA:HB2	0.63	2.29	14	9
1:A:26:GLN:NE2	1:A:38:PHE:CD1	0.63	2.65	3	2
1:A:48:ALA:HB2	1:A:53:ASN:O	0.62	1.94	2	3
1:A:50:GLY:O	1:A:52:TRP:CE2	0.62	2.53	2	2
1:A:22:ARG:N	1:A:23:PRO:CD	0.62	2.62	9	17
1:A:21:LEU:HD21	1:A:28:GLY:N	0.61	2.11	18	1
1:A:44:ILE:HG23	1:A:44:ILE:O	0.61	1.96	7	12
1:A:26:GLN:OE1	1:A:38:PHE:CZ	0.60	2.54	8	2
1:A:50:GLY:O	1:A:52:TRP:CE3	0.59	2.56	4	2
1:A:48:ALA:HB3	1:A:52:TRP:HD1	0.59	1.56	10	2
1:A:26:GLN:OE1	1:A:38:PHE:CE2	0.58	2.56	3	2
1:A:15:ASP:HB3	1:A:18:THR:HG22	0.58	1.73	6	2
1:A:68:HIS:N	1:A:68:HIS:CD2	0.58	2.67	15	2
1:A:31:LEU:HD13	1:A:64:CYS:HB3	0.58	1.76	3	1
1:A:38:PHE:CE2	1:A:60:GLN:O	0.58	2.56	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:GLN:O	1:A:38:PHE:CZ	0.58	2.57	15	2
1:A:18:THR:O	1:A:19:CYS:CB	0.58	2.52	19	8
1:A:38:PHE:CE1	1:A:60:GLN:O	0.58	2.57	8	3
1:A:5:ASP:N	1:A:19:CYS:O	0.57	2.38	9	16
1:A:67:TYR:CD1	1:A:67:TYR:N	0.57	2.73	11	3
1:A:52:TRP:CZ3	1:A:68:HIS:CE1	0.56	2.93	3	1
1:A:22:ARG:N	1:A:23:PRO:HD2	0.56	2.15	9	16
1:A:66:ARG:O	1:A:67:TYR:CD1	0.56	2.59	1	4
1:A:43:LYS:O	1:A:45:CYS:N	0.56	2.39	6	8
1:A:55:ASP:OD1	1:A:67:TYR:CE2	0.56	2.59	12	1
1:A:13:CYS:O	1:A:21:LEU:HD23	0.56	2.01	16	1
1:A:44:ILE:O	1:A:44:ILE:CG2	0.55	2.53	14	5
1:A:14:CYS:CB	1:A:20:LYS:O	0.55	2.54	7	1
1:A:48:ALA:CB	1:A:52:TRP:O	0.55	2.55	20	2
1:A:55:ASP:OD1	1:A:67:TYR:CZ	0.55	2.59	16	2
1:A:66:ARG:O	1:A:67:TYR:CG	0.55	2.60	10	3
1:A:45:CYS:SG	1:A:57:CYS:N	0.55	2.80	19	1
1:A:21:LEU:HD11	1:A:26:GLN:O	0.55	2.02	18	2
1:A:15:ASP:O	1:A:19:CYS:N	0.54	2.40	17	18
1:A:15:ASP:N	1:A:20:LYS:O	0.54	2.41	17	18
1:A:27:CYS:SG	1:A:62:ALA:HB1	0.54	2.42	17	2
1:A:33:CYS:SG	1:A:62:ALA:CB	0.54	2.96	2	10
1:A:3:GLU:O	1:A:20:LYS:CG	0.54	2.56	19	7
1:A:26:GLN:HG2	1:A:38:PHE:N	0.54	2.18	8	2
1:A:50:GLY:O	1:A:51:ASP:CB	0.54	2.55	17	6
1:A:44:ILE:CG2	1:A:44:ILE:O	0.54	2.55	10	1
1:A:43:LYS:CG	1:A:57:CYS:SG	0.54	2.96	19	4
1:A:18:THR:HG23	1:A:20:LYS:H	0.54	1.63	5	2
1:A:47:ILE:O	1:A:47:ILE:CG2	0.53	2.56	15	2
1:A:33:CYS:SG	1:A:62:ALA:HB2	0.53	2.42	5	2
1:A:21:LEU:CD2	1:A:25:ALA:O	0.53	2.56	3	3
1:A:32:CYS:SG	1:A:43:LYS:CG	0.53	2.96	15	3
1:A:31:LEU:CB	1:A:45:CYS:SG	0.53	2.96	2	1
1:A:26:GLN:CD	1:A:38:PHE:CE2	0.53	2.82	3	1
1:A:52:TRP:CZ3	1:A:68:HIS:NE2	0.53	2.77	3	1
1:A:27:CYS:HB3	1:A:38:PHE:CE1	0.53	2.39	2	2
1:A:48:ALA:CB	1:A:52:TRP:CD1	0.53	2.91	8	3
1:A:45:CYS:SG	1:A:55:ASP:CB	0.53	2.97	14	5
1:A:22:ARG:CB	1:A:23:PRO:CD	0.53	2.87	3	8
1:A:18:THR:O	1:A:20:LYS:CG	0.53	2.56	1	5
1:A:21:LEU:CD1	1:A:26:GLN:O	0.53	2.57	18	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:ILE:CD1	1:A:46:ARG:O	0.52	2.57	5	2
1:A:26:GLN:HB3	1:A:38:PHE:CD1	0.52	2.39	1	2
1:A:26:GLN:NE2	1:A:38:PHE:CE1	0.52	2.77	3	1
1:A:22:ARG:HB3	1:A:23:PRO:HD3	0.52	1.81	3	12
1:A:11:ASN:OD1	1:A:13:CYS:N	0.52	2.42	14	2
1:A:18:THR:O	1:A:20:LYS:N	0.52	2.42	9	6
1:A:48:ALA:HB1	1:A:52:TRP:HE1	0.52	1.62	17	1
1:A:3:GLU:O	1:A:18:THR:O	0.52	2.27	13	13
1:A:22:ARG:CB	1:A:23:PRO:HD3	0.52	2.35	3	14
1:A:50:GLY:O	1:A:52:TRP:CD2	0.52	2.63	5	2
1:A:58:THR:CG2	1:A:61:SER:OG	0.52	2.57	8	1
1:A:51:ASP:HB3	1:A:52:TRP:CZ3	0.52	2.39	2	2
1:A:63:ASP:OD1	1:A:63:ASP:N	0.52	2.43	4	5
1:A:48:ALA:O	1:A:52:TRP:NE1	0.52	2.41	4	2
1:A:51:ASP:O	1:A:52:TRP:O	0.52	2.28	20	2
1:A:51:ASP:HB2	1:A:68:HIS:CE1	0.51	2.40	4	1
1:A:26:GLN:NE2	1:A:27:CYS:SG	0.51	2.83	3	1
1:A:25:ALA:CB	1:A:36:CYS:HB3	0.51	2.35	18	14
1:A:32:CYS:O	1:A:39:SER:CB	0.51	2.58	13	2
1:A:21:LEU:HD21	1:A:25:ALA:HB3	0.51	1.78	11	1
1:A:55:ASP:N	1:A:55:ASP:OD1	0.51	2.43	14	5
1:A:15:ASP:O	1:A:19:CYS:CA	0.51	2.59	14	10
1:A:41:ALA:CB	1:A:58:THR:C	0.51	2.79	1	6
1:A:23:PRO:O	1:A:25:ALA:N	0.51	2.43	19	1
1:A:38:PHE:O	1:A:39:SER:O	0.50	2.29	1	7
1:A:41:ALA:N	1:A:59:GLY:HA2	0.50	2.20	20	3
1:A:21:LEU:CD2	1:A:25:ALA:CB	0.50	2.88	2	2
1:A:31:LEU:HD13	1:A:31:LEU:O	0.50	2.06	14	1
1:A:54:ASP:N	1:A:54:ASP:OD1	0.50	2.45	8	4
1:A:48:ALA:HB1	1:A:52:TRP:HD1	0.50	1.65	18	5
1:A:42:GLY:N	1:A:57:CYS:O	0.50	2.43	1	6
1:A:14:CYS:CA	1:A:20:LYS:O	0.50	2.60	15	1
1:A:27:CYS:O	1:A:36:CYS:CA	0.50	2.60	5	3
1:A:26:GLN:NE2	1:A:38:PHE:CE2	0.50	2.80	18	1
1:A:50:GLY:O	1:A:51:ASP:HB2	0.50	2.07	2	4
1:A:44:ILE:HD11	1:A:54:ASP:CB	0.50	2.37	19	3
1:A:21:LEU:HD11	1:A:27:CYS:N	0.50	2.21	16	1
1:A:26:GLN:HG2	1:A:38:PHE:CD2	0.49	2.41	2	7
1:A:26:GLN:HB3	1:A:38:PHE:CD2	0.49	2.41	4	6
1:A:43:LYS:O	1:A:56:ARG:HA	0.49	2.07	1	10
1:A:54:ASP:OD1	1:A:54:ASP:N	0.49	2.44	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:41:ALA:N	1:A:59:GLY:CA	0.49	2.75	8	5
1:A:66:ARG:C	1:A:67:TYR:CD1	0.49	2.86	4	2
1:A:52:TRP:CD1	1:A:68:HIS:NE2	0.49	2.81	11	1
1:A:21:LEU:HD22	1:A:25:ALA:CB	0.49	2.37	19	1
1:A:41:ALA:HA	1:A:59:GLY:N	0.49	2.23	15	5
1:A:42:GLY:C	1:A:56:ARG:HG3	0.49	2.28	13	1
1:A:44:ILE:HD12	1:A:55:ASP:O	0.49	2.07	20	2
1:A:53:ASN:OD1	1:A:53:ASN:N	0.49	2.45	18	1
1:A:18:THR:O	1:A:19:CYS:C	0.49	2.51	9	6
1:A:34:GLU:O	1:A:35:GLN:CB	0.49	2.59	17	3
1:A:29:GLU:OE1	1:A:30:GLY:N	0.48	2.46	15	1
1:A:26:GLN:HB3	1:A:38:PHE:CE2	0.48	2.42	2	1
1:A:43:LYS:HB3	1:A:57:CYS:CB	0.48	2.39	1	1
1:A:42:GLY:CA	1:A:56:ARG:CG	0.48	2.89	13	3
1:A:38:PHE:CG	1:A:60:GLN:O	0.48	2.66	15	1
1:A:41:ALA:N	1:A:59:GLY:HA3	0.48	2.24	8	3
1:A:15:ASP:O	1:A:19:CYS:HA	0.48	2.09	6	6
1:A:42:GLY:HA2	1:A:56:ARG:HG2	0.48	1.84	13	2
1:A:43:LYS:O	1:A:57:CYS:N	0.47	2.39	9	4
1:A:32:CYS:HB3	1:A:39:SER:OG	0.47	2.09	11	1
1:A:52:TRP:CD2	1:A:52:TRP:N	0.47	2.83	5	1
1:A:14:CYS:SG	1:A:20:LYS:N	0.47	2.88	16	1
1:A:19:CYS:SG	1:A:19:CYS:O	0.47	2.72	11	3
1:A:26:GLN:OE1	1:A:26:GLN:O	0.47	2.33	3	1
1:A:5:ASP:OD2	1:A:21:LEU:CD1	0.47	2.63	5	1
1:A:47:ILE:HG13	1:A:48:ALA:N	0.47	2.25	10	1
1:A:3:GLU:O	1:A:19:CYS:SG	0.47	2.73	9	5
1:A:64:CYS:SG	1:A:65:PRO:HD2	0.47	2.50	20	3
1:A:45:CYS:SG	1:A:57:CYS:SG	0.47	3.13	2	3
1:A:15:ASP:CB	1:A:22:ARG:HG3	0.47	2.39	13	1
1:A:14:CYS:O	1:A:14:CYS:SG	0.47	2.73	11	5
1:A:5:ASP:CG	1:A:21:LEU:CD1	0.47	2.84	5	1
1:A:49:ARG:O	1:A:52:TRP:CZ2	0.47	2.68	19	2
1:A:44:ILE:CD1	1:A:54:ASP:HB2	0.47	2.40	4	2
1:A:5:ASP:CG	1:A:21:LEU:HD12	0.46	2.31	5	1
1:A:18:THR:O	1:A:20:LYS:HG3	0.46	2.10	13	3
1:A:66:ARG:C	1:A:67:TYR:CG	0.46	2.88	4	2
1:A:45:CYS:SG	1:A:55:ASP:O	0.46	2.73	10	1
1:A:32:CYS:SG	1:A:43:LYS:HG2	0.46	2.50	2	3
1:A:21:LEU:HD21	1:A:27:CYS:CA	0.46	2.41	5	1
1:A:42:GLY:HA2	1:A:56:ARG:HB3	0.46	1.86	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:ARG:O	1:A:67:TYR:CD2	0.46	2.68	7	1
1:A:4:CYS:SG	1:A:19:CYS:O	0.46	2.74	15	1
1:A:27:CYS:SG	1:A:37:LYS:N	0.46	2.89	15	3
1:A:43:LYS:O	1:A:43:LYS:HD2	0.46	2.10	1	1
1:A:4:CYS:HA	1:A:19:CYS:O	0.46	2.11	17	14
1:A:31:LEU:HB3	1:A:45:CYS:SG	0.46	2.51	2	1
1:A:68:HIS:O	1:A:68:HIS:ND1	0.46	2.49	5	1
1:A:7:SER:OG	1:A:29:GLU:OE2	0.46	2.34	15	1
1:A:44:ILE:HD13	1:A:54:ASP:HB2	0.46	1.88	4	1
1:A:40:ARG:C	1:A:59:GLY:CA	0.46	2.84	8	3
1:A:13:CYS:HB3	1:A:28:GLY:HA2	0.46	1.88	16	2
1:A:42:GLY:HA2	1:A:56:ARG:CD	0.46	2.40	20	3
1:A:32:CYS:HB3	1:A:61:SER:O	0.45	2.12	1	1
1:A:4:CYS:SG	1:A:6:CYS:O	0.45	2.74	19	5
1:A:27:CYS:SG	1:A:37:LYS:O	0.45	2.74	13	2
1:A:55:ASP:OD1	1:A:67:TYR:CE1	0.45	2.69	16	1
1:A:43:LYS:N	1:A:56:ARG:HG3	0.45	2.26	17	2
1:A:27:CYS:O	1:A:36:CYS:HA	0.45	2.11	20	6
1:A:22:ARG:CD	1:A:22:ARG:C	0.45	2.83	19	1
1:A:41:ALA:HB2	1:A:59:GLY:N	0.45	2.27	1	1
1:A:26:GLN:CD	1:A:38:PHE:CD2	0.45	2.89	3	1
1:A:27:CYS:SG	1:A:29:GLU:O	0.45	2.74	4	6
1:A:19:CYS:O	1:A:19:CYS:SG	0.45	2.73	16	2
1:A:42:GLY:HA2	1:A:56:ARG:CB	0.45	2.40	13	1
1:A:40:ARG:C	1:A:59:GLY:HA2	0.45	2.32	11	4
1:A:27:CYS:O	1:A:33:CYS:SG	0.45	2.74	10	2
1:A:43:LYS:CG	1:A:57:CYS:HB2	0.45	2.41	9	1
1:A:54:ASP:O	1:A:67:TYR:CE2	0.45	2.69	20	1
1:A:18:THR:C	1:A:19:CYS:SG	0.45	2.94	12	6
1:A:53:ASN:O	1:A:54:ASP:C	0.45	2.55	10	3
1:A:3:GLU:O	1:A:20:LYS:HG3	0.45	2.11	8	3
1:A:26:GLN:CD	1:A:27:CYS:HB3	0.45	2.32	8	1
1:A:32:CYS:HB2	1:A:61:SER:O	0.45	2.12	9	1
1:A:35:GLN:O	1:A:36:CYS:CB	0.45	2.64	12	1
1:A:6:CYS:SG	1:A:11:ASN:ND2	0.45	2.90	17	1
1:A:21:LEU:HD21	1:A:27:CYS:N	0.44	2.27	5	2
1:A:41:ALA:HA	1:A:57:CYS:O	0.44	2.12	10	18
1:A:45:CYS:SG	1:A:55:ASP:HB2	0.44	2.52	11	5
1:A:43:LYS:CB	1:A:57:CYS:HB2	0.44	2.43	9	1
1:A:45:CYS:SG	1:A:55:ASP:HB3	0.44	2.52	11	3
1:A:46:ARG:NH2	1:A:65:PRO:O	0.44	2.49	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:CYS:N	1:A:55:ASP:O	0.44	2.44	2	1
1:A:15:ASP:HB3	1:A:18:THR:CG2	0.44	2.40	6	2
1:A:26:GLN:O	1:A:38:PHE:CE2	0.44	2.71	16	1
1:A:34:GLU:O	1:A:35:GLN:HB3	0.44	2.12	7	1
1:A:66:ARG:C	1:A:67:TYR:CD2	0.44	2.91	7	1
1:A:3:GLU:O	1:A:20:LYS:HG2	0.44	2.12	19	1
1:A:39:SER:O	1:A:59:GLY:O	0.44	2.35	6	1
1:A:6:CYS:O	1:A:6:CYS:SG	0.43	2.76	2	1
1:A:51:ASP:HB3	1:A:52:TRP:CE3	0.43	2.48	2	1
1:A:22:ARG:HB3	1:A:23:PRO:CD	0.43	2.43	3	1
1:A:11:ASN:OD1	1:A:11:ASN:C	0.43	2.57	18	1
1:A:35:GLN:O	1:A:36:CYS:HB2	0.43	2.12	18	16
1:A:33:CYS:HA	1:A:37:LYS:O	0.43	2.13	5	4
1:A:48:ALA:CB	1:A:68:HIS:CD2	0.43	3.00	4	1
1:A:15:ASP:HB2	1:A:22:ARG:CG	0.43	2.43	13	1
1:A:52:TRP:CD1	1:A:52:TRP:N	0.43	2.87	6	1
1:A:55:ASP:CG	1:A:64:CYS:SG	0.43	2.97	17	1
1:A:46:ARG:CB	1:A:55:ASP:HB2	0.43	2.44	9	1
1:A:32:CYS:C	1:A:39:SER:OG	0.43	2.57	18	2
1:A:13:CYS:HB3	1:A:28:GLY:CA	0.43	2.43	18	2
1:A:42:GLY:HA2	1:A:56:ARG:NE	0.43	2.29	11	1
1:A:44:ILE:CD1	1:A:54:ASP:HB3	0.43	2.43	5	2
1:A:9:PRO:O	1:A:16:ALA:HB2	0.43	2.14	14	1
1:A:26:GLN:N	1:A:36:CYS:O	0.43	2.51	1	1
1:A:55:ASP:OD2	1:A:65:PRO:O	0.43	2.36	3	1
1:A:14:CYS:SG	1:A:19:CYS:C	0.42	2.98	10	2
1:A:22:ARG:HG2	1:A:23:PRO:N	0.42	2.29	18	1
1:A:14:CYS:HA	1:A:20:LYS:O	0.42	2.14	19	1
1:A:20:LYS:O	1:A:21:LEU:C	0.42	2.56	8	3
1:A:32:CYS:O	1:A:39:SER:OG	0.42	2.33	10	1
1:A:41:ALA:CA	1:A:59:GLY:N	0.42	2.81	1	2
1:A:33:CYS:SG	1:A:37:LYS:O	0.42	2.77	5	1
1:A:11:ASN:CG	1:A:14:CYS:SG	0.42	2.98	7	2
1:A:51:ASP:O	1:A:52:TRP:C	0.42	2.57	11	1
1:A:6:CYS:SG	1:A:6:CYS:O	0.42	2.77	3	1
1:A:43:LYS:NZ	1:A:44:ILE:O	0.42	2.50	19	1
1:A:27:CYS:SG	1:A:37:LYS:C	0.42	2.98	13	2
1:A:42:GLY:CA	1:A:56:ARG:HB3	0.42	2.44	6	2
1:A:44:ILE:O	1:A:44:ILE:HG13	0.42	2.15	20	1
1:A:55:ASP:OD2	1:A:64:CYS:HB3	0.42	2.14	2	1
1:A:26:GLN:OE1	1:A:26:GLN:C	0.42	2.58	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:CYS:SG	1:A:55:ASP:CG	0.42	2.98	13	1
1:A:46:ARG:HB3	1:A:55:ASP:CB	0.42	2.44	17	1
1:A:18:THR:O	1:A:19:CYS:HB3	0.41	2.14	4	2
1:A:5:ASP:O	1:A:5:ASP:OD1	0.41	2.38	6	1
1:A:44:ILE:O	1:A:44:ILE:HG22	0.41	2.15	10	1
1:A:15:ASP:CA	1:A:22:ARG:HB2	0.41	2.45	15	1
1:A:27:CYS:SG	1:A:36:CYS:C	0.41	2.99	15	2
1:A:15:ASP:CB	1:A:22:ARG:HG2	0.41	2.46	17	1
1:A:13:CYS:O	1:A:23:PRO:HD2	0.41	2.14	15	2
1:A:21:LEU:HD13	1:A:26:GLN:O	0.41	2.15	1	1
1:A:44:ILE:HA	1:A:55:ASP:O	0.41	2.15	17	4
1:A:5:ASP:CB	1:A:20:LYS:HA	0.41	2.44	11	1
1:A:43:LYS:HB3	1:A:57:CYS:SG	0.41	2.56	19	1
1:A:26:GLN:NE2	1:A:27:CYS:HB3	0.41	2.30	3	1
1:A:50:GLY:O	1:A:52:TRP:CZ2	0.41	2.73	2	1
1:A:5:ASP:HB2	1:A:20:LYS:CD	0.41	2.45	8	1
1:A:15:ASP:CG	1:A:22:ARG:CG	0.41	2.89	14	1
1:A:27:CYS:HB2	1:A:38:PHE:CE1	0.41	2.51	7	1
1:A:67:TYR:O	1:A:68:HIS:CB	0.41	2.69	16	1
1:A:26:GLN:NE2	1:A:38:PHE:CG	0.41	2.89	8	1
1:A:32:CYS:O	1:A:39:SER:N	0.41	2.48	12	1
1:A:14:CYS:HB2	1:A:20:LYS:O	0.41	2.16	15	1
1:A:54:ASP:O	1:A:67:TYR:CD2	0.41	2.74	20	1
1:A:43:LYS:CE	1:A:57:CYS:HB2	0.41	2.46	1	1
1:A:26:GLN:HG2	1:A:38:PHE:CE2	0.41	2.51	10	1
1:A:14:CYS:SG	1:A:20:LYS:C	0.40	3.00	16	1
1:A:48:ALA:HB2	1:A:53:ASN:C	0.40	2.37	20	1
1:A:53:ASN:OD1	1:A:53:ASN:O	0.40	2.38	12	1
1:A:38:PHE:CD2	1:A:60:GLN:O	0.40	2.74	15	1
1:A:34:GLU:O	1:A:37:LYS:HG2	0.40	2.17	18	1
1:A:39:SER:O	1:A:59:GLY:HA2	0.40	2.16	13	2
1:A:41:ALA:CB	1:A:58:THR:O	0.40	2.58	7	1
1:A:55:ASP:OD2	1:A:65:PRO:HG2	0.40	2.16	10	1
1:A:49:ARG:NH1	1:A:49:ARG:HG2	0.40	2.31	13	1
1:A:4:CYS:N	1:A:20:LYS:HD3	0.40	2.31	20	1
1:A:51:ASP:CG	1:A:51:ASP:O	0.40	2.59	1	1
1:A:11:ASN:OD1	1:A:12:PRO:HD2	0.40	2.17	6	1
1:A:26:GLN:HB2	1:A:38:PHE:CE2	0.40	2.52	8	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	65/76 (86%)	54±2 (83±3%)	9±2 (13±2%)	2±1 (4±2%)	5	34
All	All	1300/1520 (86%)	1083 (83%)	171 (13%)	46 (4%)	5	34

All 12 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	39	SER	14
1	A	44	ILE	11
1	A	19	CYS	6
1	A	51	ASP	5
1	A	52	TRP	2
1	A	3	GLU	2
1	A	21	LEU	1
1	A	22	ARG	1
1	A	23	PRO	1
1	A	60	GLN	1
1	A	54	ASP	1
1	A	67	TYR	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	54/63 (86%)	38±3 (71±5%)	16±3 (29±5%)	1	16
All	All	1080/1260 (86%)	765 (71%)	315 (29%)	1	16

All 45 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	52	TRP	19
1	A	22	ARG	16
1	A	26	GLN	15
1	A	51	ASP	15
1	A	66	ARG	14
1	A	27	CYS	12
1	A	35	GLN	12
1	A	49	ARG	12
1	A	29	GLU	11
1	A	40	ARG	10
1	A	10	GLU	10
1	A	21	LEU	10
1	A	20	LYS	9
1	A	7	SER	9
1	A	5	ASP	8
1	A	13	CYS	8
1	A	54	ASP	8
1	A	3	GLU	8
1	A	19	CYS	7
1	A	43	LYS	7
1	A	46	ARG	7
1	A	44	ILE	7
1	A	8	SER	7
1	A	37	LYS	7
1	A	56	ARG	6
1	A	32	CYS	5
1	A	63	ASP	5
1	A	58	THR	5
1	A	18	THR	4
1	A	45	CYS	4
1	A	68	HIS	4
1	A	4	CYS	4
1	A	39	SER	3
1	A	31	LEU	3
1	A	55	ASP	3
1	A	34	GLU	3
1	A	57	CYS	3
1	A	64	CYS	3
1	A	60	GLN	2
1	A	33	CYS	2
1	A	14	CYS	2
1	A	67	TYR	2
1	A	53	ASN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	6	CYS	1
1	A	61	SER	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 56% for the well-defined parts and 55% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	451
Number of shifts mapped to atoms	451
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

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	64	1.05 ± 0.96	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 56%, i.e. 441 atoms were assigned a chemical shift out of a possible 793. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	196/328 (60%)	134/134 (100%)	0/132 (0%)	62/62 (100%)
Sidechain	231/427 (54%)	225/270 (83%)	0/131 (0%)	6/26 (23%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	14/38 (37%)	14/19 (74%)	0/17 (0%)	0/2 (0%)
Overall	441/793 (56%)	373/423 (88%)	0/280 (0%)	68/90 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 55%, i.e. 451 atoms were assigned a chemical shift out of a possible 817. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	202/339 (60%)	138/139 (99%)	0/136 (0%)	64/64 (100%)
Sidechain	235/440 (53%)	229/278 (82%)	0/135 (0%)	6/27 (22%)
Aromatic	14/38 (37%)	14/19 (74%)	0/17 (0%)	0/2 (0%)
Overall	451/817 (55%)	381/436 (87%)	0/288 (0%)	70/93 (75%)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	56	ARG	NE	126.44	76.53 – 92.65	26.0
1	A	22	ARG	NE	125.13	76.53 – 92.65	25.1
1	A	26	GLN	HB2	0.57	0.80 – 3.29	-5.9
1	A	17	ALA	N	104.93	106.13 – 140.55	-5.3

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. 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:

