



Full wwPDB NMR Structure Validation Report ⓘ

Jun 6, 2023 – 05:13 pm BST

PDB ID : 2W9V
BMRB ID : 16151
Title : Solution structure of jerdostatin from *Trimeresurus jerdonii* with end C-terminal residues N45G46 deleted
Authors : Carbajo, R.J.; Sanz, L.; Mosulen, S.; Calvete, J.J.; Pineda-Lucena, A.
Deposited on : 2009-01-29

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 : 20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

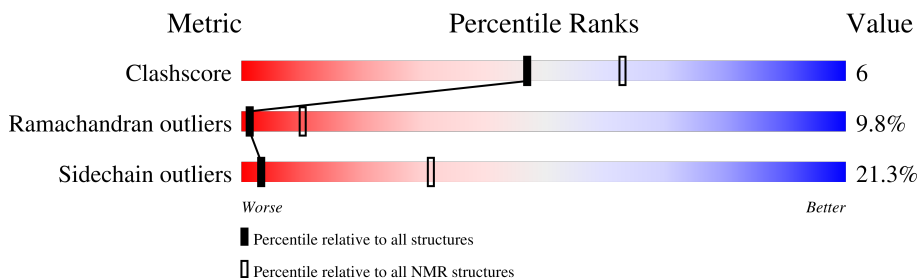
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	44	

2 Ensemble composition and analysis i

This entry contains 44 models. Model 43 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:4-A:44 (41)	1.22	43

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 7 clusters and 6 single-model clusters were found.

Cluster number	Models
1	2, 6, 7, 9, 11, 15, 20, 21, 22, 26, 27, 31, 32, 35, 38, 39, 41, 42, 43
2	3, 8, 17, 24, 33, 44
3	4, 13, 16, 18, 34
4	5, 19
5	12, 29
6	23, 30
7	25, 37
Single-model clusters	1; 10; 14; 28; 36; 40

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 622 atoms, of which 299 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SHORT DISINTEGRIN JERDOSTATIN.

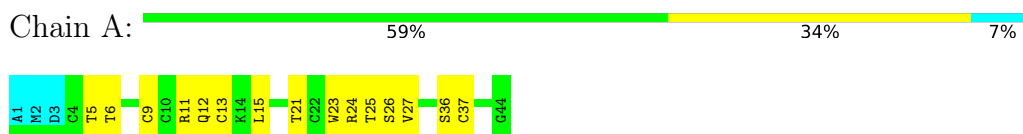
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	44	622	192	299	59	63	9	0

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

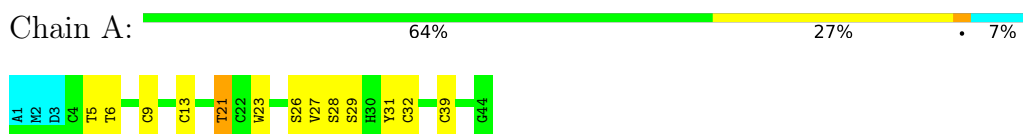


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

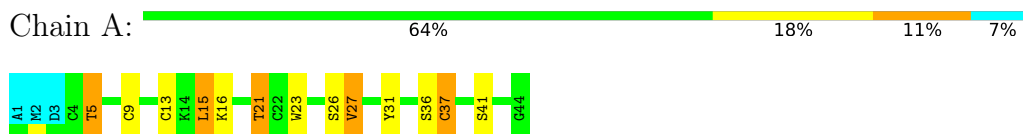
4.2.1 Score per residue for model 1

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



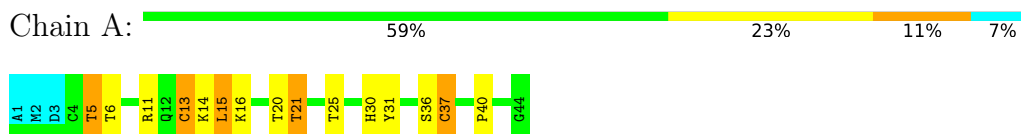
4.2.2 Score per residue for model 2

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



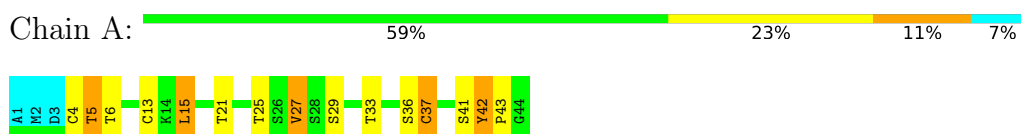
4.2.3 Score per residue for model 3

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



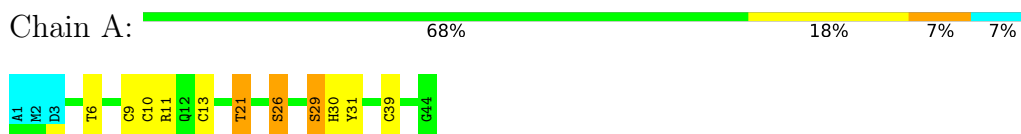
4.2.4 Score per residue for model 4

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



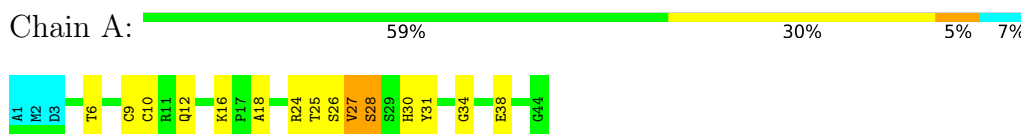
4.2.5 Score per residue for model 5

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



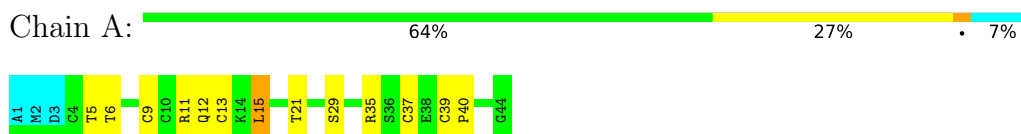
4.2.6 Score per residue for model 6

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



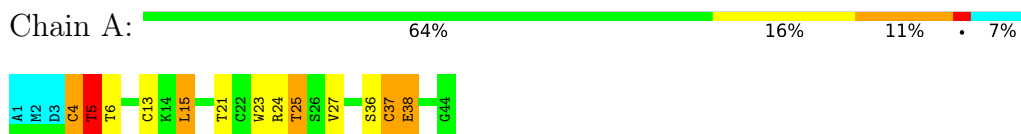
4.2.7 Score per residue for model 7

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



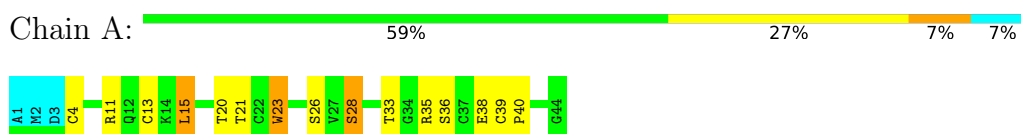
4.2.8 Score per residue for model 8

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



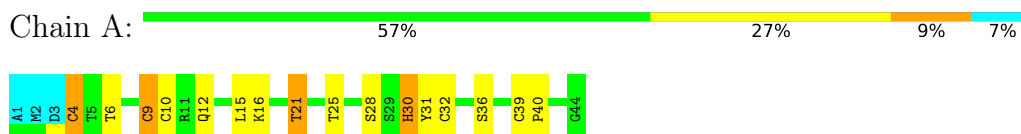
4.2.9 Score per residue for model 9

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



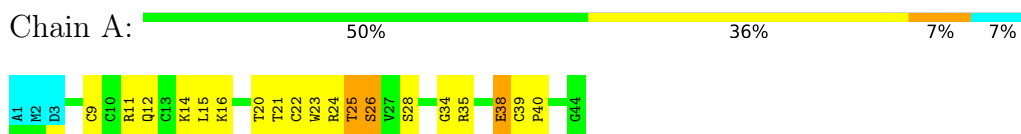
4.2.10 Score per residue for model 10

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



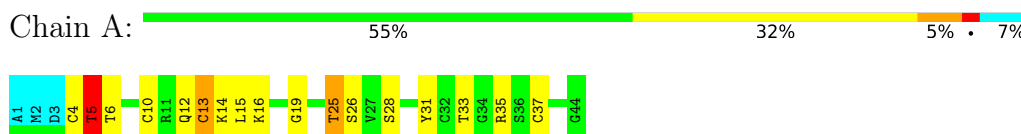
4.2.11 Score per residue for model 11

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



4.2.12 Score per residue for model 12

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



4.2.13 Score per residue for model 13

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

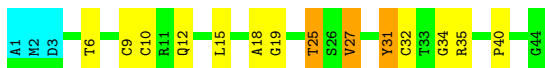
Chain A:  57% 32% 7%



4.2.14 Score per residue for model 14

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  61% 25% 7% 7%



4.2.15 Score per residue for model 15

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  61% 25% 7% 7%



4.2.16 Score per residue for model 16

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

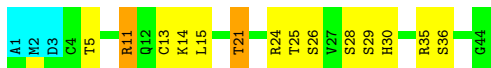
Chain A:  73% 20% 7%



4.2.17 Score per residue for model 17

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

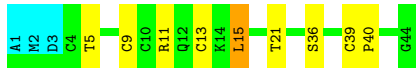
Chain A:  61% 27% 5% 7%



4.2.18 Score per residue for model 18

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

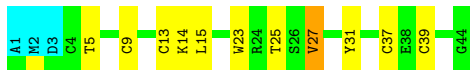
Chain A:  73% 18% 7%



4.2.19 Score per residue for model 19

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  68% 23% 7%



4.2.20 Score per residue for model 20

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  59% 25% 9% 7%



4.2.21 Score per residue for model 21

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

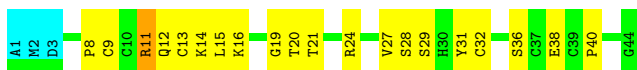
Chain A:  66% 25% 7%



4.2.22 Score per residue for model 22

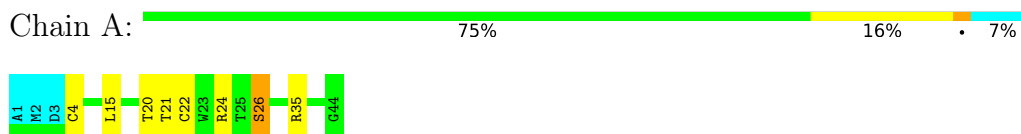
- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  48% 43% 7%



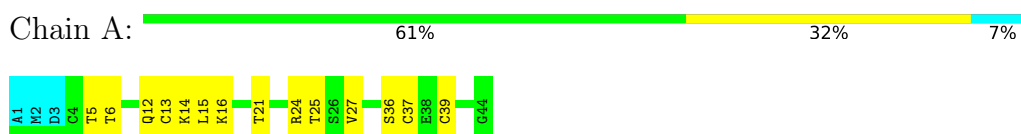
4.2.23 Score per residue for model 23

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



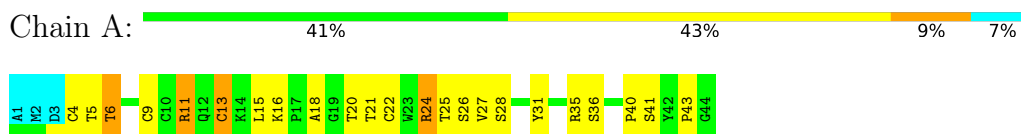
4.2.24 Score per residue for model 24

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



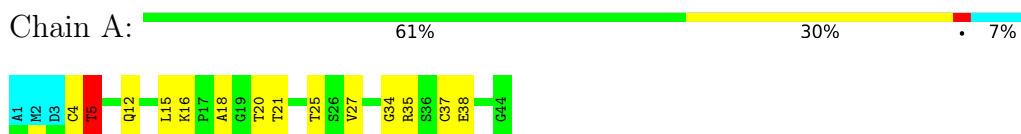
4.2.25 Score per residue for model 25

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



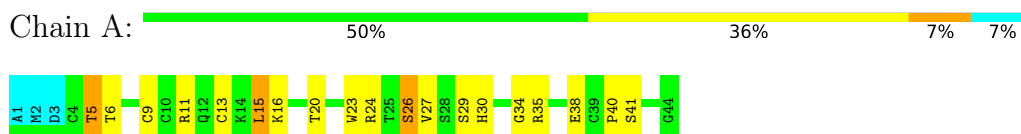
4.2.26 Score per residue for model 26

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



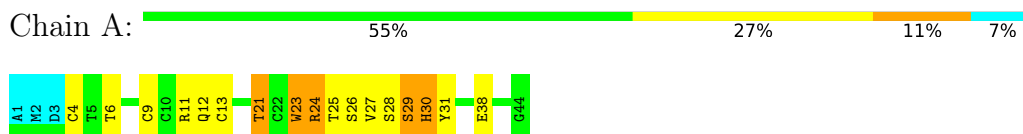
4.2.27 Score per residue for model 27

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



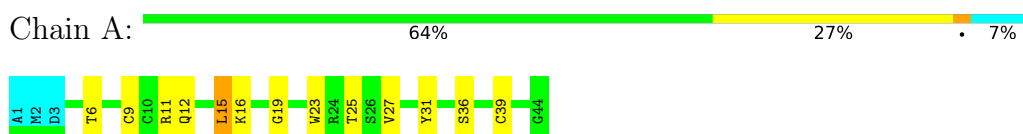
4.2.28 Score per residue for model 28

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



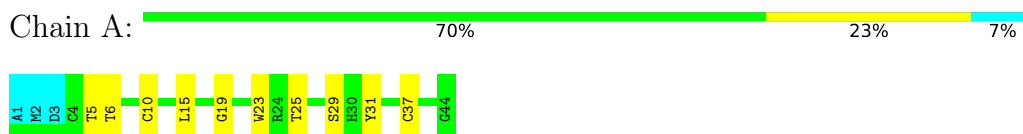
4.2.29 Score per residue for model 29

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



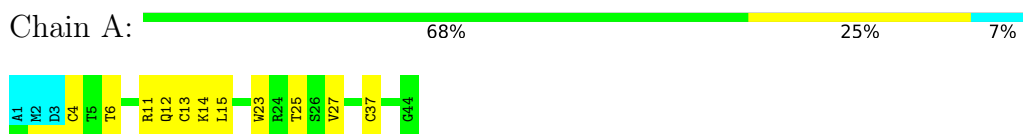
4.2.30 Score per residue for model 30

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



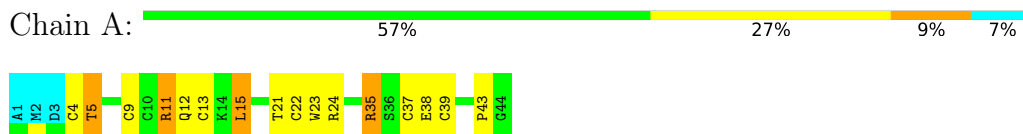
4.2.31 Score per residue for model 31

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



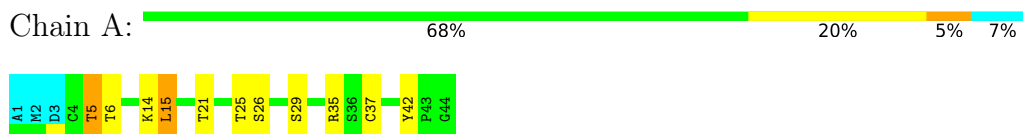
4.2.32 Score per residue for model 32

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



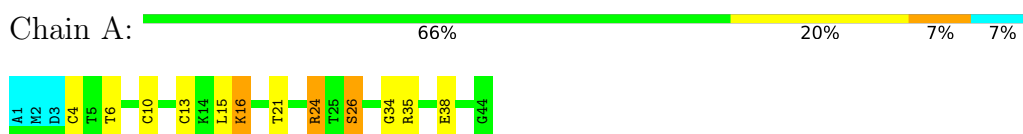
4.2.33 Score per residue for model 33

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



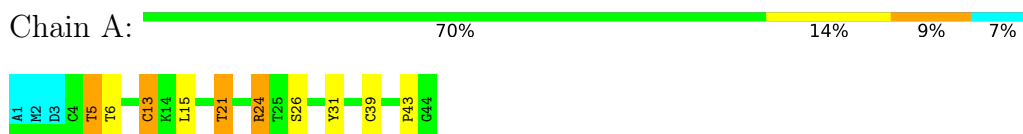
4.2.34 Score per residue for model 34

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



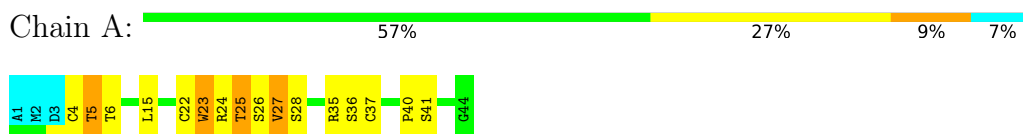
4.2.35 Score per residue for model 35

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



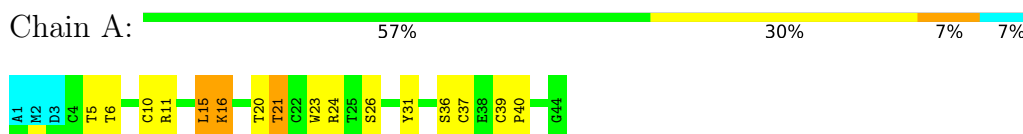
4.2.36 Score per residue for model 36

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



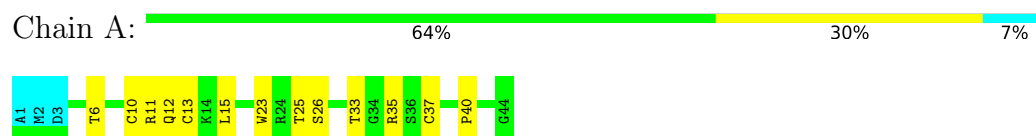
4.2.37 Score per residue for model 37

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



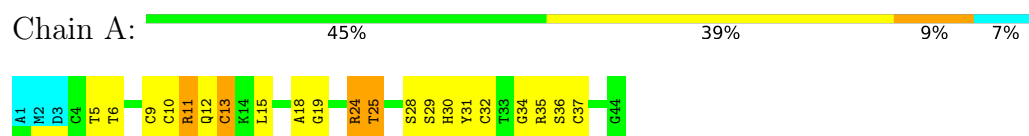
4.2.38 Score per residue for model 38

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



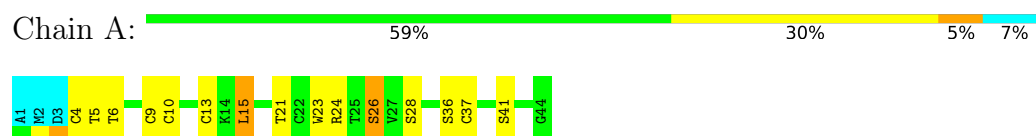
4.2.39 Score per residue for model 39

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



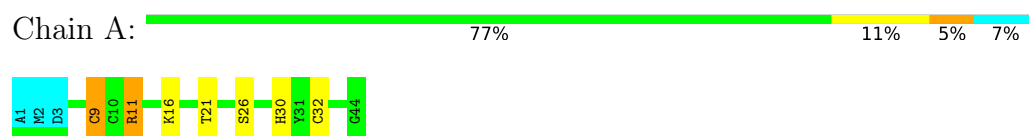
4.2.40 Score per residue for model 40

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



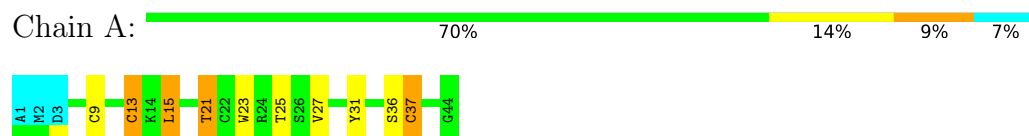
4.2.41 Score per residue for model 41

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



4.2.42 Score per residue for model 42

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN



4.2.43 Score per residue for model 43 (medoid)

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  50% 34% 7% • 7%



4.2.44 Score per residue for model 44

- Molecule 1: SHORT DISINTEGRIN JERDOSTATIN

Chain A:  57% 27% 7% • 7%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *CNS*.

Of the 50 calculated structures, 44 were deposited, based on the following criterion: *LOWEST TOTAL ENERGY*.

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

Software name	Classification	Version
CNS	refinement	
Sparky	structure solution	

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	412
Number of shifts mapped to atoms	412
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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	302	279	278	4±2
All	All	13288	12276	12232	164

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 6.

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:THR:HG23	1:A:31:TYR:CD2	0.80	2.12	42	4
1:A:23:TRP:CZ3	1:A:25:THR:HG21	0.73	2.19	31	3
1:A:6:THR:HG22	1:A:12:GLN:O	0.73	1.83	13	1
1:A:16:LYS:CE	1:A:20:THR:HG21	0.71	2.15	3	1
1:A:21:THR:HG23	1:A:30:HIS:O	0.71	1.86	10	1
1:A:15:LEU:HD13	1:A:35:ARG:C	0.71	2.06	32	2
1:A:15:LEU:HD11	1:A:36:SER:HA	0.70	1.62	15	5
1:A:15:LEU:HD11	1:A:36:SER:CA	0.70	2.16	20	4
1:A:10:CYS:SG	1:A:15:LEU:HD22	0.70	2.26	40	1
1:A:15:LEU:HD22	1:A:35:ARG:O	0.69	1.87	26	1
1:A:15:LEU:HD21	1:A:36:SER:C	0.69	2.07	42	7
1:A:16:LYS:HD2	1:A:20:THR:HG21	0.69	1.63	11	3
1:A:15:LEU:HD11	1:A:36:SER:C	0.69	2.06	43	2
1:A:21:THR:HG21	1:A:24:ARG:HD2	0.66	1.67	34	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:LEU:HD11	1:A:35:ARG:C	0.65	2.12	14	2
1:A:5:THR:HG23	1:A:37:CYS:SG	0.65	2.32	39	1
1:A:15:LEU:HD21	1:A:36:SER:N	0.65	2.06	8	2
1:A:15:LEU:HD11	1:A:36:SER:O	0.65	1.90	18	2
1:A:15:LEU:HD11	1:A:35:ARG:O	0.64	1.92	7	2
1:A:21:THR:HG23	1:A:31:TYR:CZ	0.63	2.29	3	1
1:A:21:THR:HG23	1:A:31:TYR:CE2	0.62	2.29	3	2
1:A:15:LEU:HD13	1:A:35:ARG:HA	0.62	1.71	25	1
1:A:24:ARG:O	1:A:25:THR:HG23	0.62	1.95	39	2
1:A:15:LEU:HD21	1:A:34:GLY:C	0.62	2.15	39	1
1:A:16:LYS:HD3	1:A:20:THR:HG21	0.62	1.70	37	4
1:A:15:LEU:HD22	1:A:37:CYS:SG	0.62	2.35	37	1
1:A:21:THR:HG21	1:A:29:SER:OG	0.61	1.95	44	1
1:A:15:LEU:HD22	1:A:35:ARG:C	0.60	2.16	11	5
1:A:21:THR:HG23	1:A:31:TYR:CD1	0.60	2.32	5	3
1:A:15:LEU:HD21	1:A:37:CYS:N	0.60	2.11	4	3
1:A:15:LEU:HD22	1:A:36:SER:N	0.60	2.10	25	2
1:A:15:LEU:HD12	1:A:16:LYS:O	0.60	1.95	26	3
1:A:25:THR:HG23	1:A:27:VAL:HG12	0.58	1.73	19	2
1:A:5:THR:HG22	1:A:37:CYS:SG	0.58	2.38	12	4
1:A:21:THR:HG21	1:A:24:ARG:CG	0.57	2.29	17	1
1:A:15:LEU:HD13	1:A:36:SER:C	0.56	2.21	39	1
1:A:27:VAL:O	1:A:27:VAL:HG22	0.55	2.02	36	4
1:A:21:THR:HG22	1:A:30:HIS:O	0.55	2.01	3	2
1:A:15:LEU:HD13	1:A:15:LEU:H	0.53	1.62	9	1
1:A:18:ALA:HB2	1:A:34:GLY:HA3	0.53	1.80	15	7
1:A:5:THR:HG22	1:A:37:CYS:HB3	0.52	1.80	26	1
1:A:27:VAL:O	1:A:27:VAL:HG12	0.52	2.05	1	1
1:A:15:LEU:HD12	1:A:36:SER:HA	0.51	1.82	9	1
1:A:21:THR:HG22	1:A:30:HIS:H	0.51	1.66	5	1
1:A:15:LEU:HD21	1:A:36:SER:O	0.50	2.06	2	2
1:A:15:LEU:HD23	1:A:37:CYS:SG	0.50	2.46	38	1
1:A:15:LEU:HD13	1:A:34:GLY:O	0.49	2.06	11	1
1:A:25:THR:O	1:A:27:VAL:HG23	0.49	2.06	26	2
1:A:33:THR:HG23	1:A:35:ARG:HG3	0.49	1.85	9	1
1:A:6:THR:HG23	1:A:12:GLN:HA	0.48	1.84	28	1
1:A:21:THR:HG23	1:A:31:TYR:CE1	0.48	2.43	1	2
1:A:25:THR:HG23	1:A:27:VAL:CG1	0.48	2.37	19	2
1:A:6:THR:HG22	1:A:12:GLN:C	0.47	2.29	12	1
1:A:26:SER:O	1:A:27:VAL:HG13	0.47	2.09	43	2
1:A:4:CYS:CB	1:A:13:CYS:HA	0.47	2.39	40	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:LEU:HD13	1:A:34:GLY:C	0.46	2.30	11	2
1:A:5:THR:HG22	1:A:37:CYS:CB	0.46	2.41	26	1
1:A:21:THR:HG22	1:A:29:SER:O	0.45	2.10	44	1
1:A:30:HIS:CD2	1:A:30:HIS:N	0.45	2.85	39	6
1:A:23:TRP:CE3	1:A:25:THR:CG2	0.45	3.00	13	1
1:A:15:LEU:HD12	1:A:15:LEU:C	0.45	2.32	26	2
1:A:25:THR:HG22	1:A:25:THR:O	0.45	2.12	30	1
1:A:23:TRP:CH2	1:A:25:THR:CG2	0.44	3.00	36	1
1:A:5:THR:HG23	1:A:10:CYS:SG	0.44	2.52	30	1
1:A:16:LYS:HE3	1:A:20:THR:HG21	0.44	1.88	3	1
1:A:11:ARG:O	1:A:12:GLN:CB	0.44	2.65	43	1
1:A:15:LEU:HD21	1:A:36:SER:CA	0.44	2.42	8	2
1:A:23:TRP:CH2	1:A:25:THR:HG21	0.43	2.48	36	1
1:A:5:THR:HG22	1:A:37:CYS:HB2	0.43	1.91	8	1
1:A:33:THR:HG22	1:A:42:TYR:CZ	0.43	2.49	4	1
1:A:33:THR:HG23	1:A:35:ARG:HB2	0.42	1.91	38	1
1:A:23:TRP:O	1:A:30:HIS:CD2	0.42	2.72	28	1
1:A:15:LEU:HD12	1:A:15:LEU:O	0.42	2.14	22	1
1:A:21:THR:HG22	1:A:29:SER:HA	0.42	1.90	28	1
1:A:27:VAL:HG13	1:A:28:SER:N	0.41	2.30	25	1
1:A:19:GLY:O	1:A:31:TYR:CD1	0.41	2.73	39	2
1:A:15:LEU:HD12	1:A:34:GLY:O	0.41	2.15	27	1
1:A:42:TYR:CD1	1:A:42:TYR:N	0.41	2.88	33	1
1:A:21:THR:CG2	1:A:31:TYR:CZ	0.41	3.03	3	1
1:A:30:HIS:O	1:A:31:TYR:CD1	0.41	2.74	10	1
1:A:30:HIS:O	1:A:31:TYR:CG	0.41	2.74	10	1
1:A:29:SER:O	1:A:30:HIS:CD2	0.40	2.74	5	1
1:A:19:GLY:O	1:A:31:TYR:CD2	0.40	2.74	22	4
1:A:28:SER:OG	1:A:30:HIS:CD2	0.40	2.75	17	1
1:A:5:THR:CG2	1:A:37:CYS:CB	0.40	3.00	3	2
1:A:30:HIS:CG	1:A:40:PRO:O	0.40	2.75	3	1
1:A:28:SER:O	1:A:30:HIS:CD2	0.40	2.75	6	1
1:A:11:ARG:N	1:A:14:LYS:O	0.40	2.54	22	1
1:A:23:TRP:CE2	1:A:25:THR:OG1	0.40	2.74	11	1
1:A:15:LEU:CD2	1:A:37:CYS:N	0.40	2.84	31	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	40/44 (91%)	29±2 (72±6%)	7±2 (18±5%)	4±2 (10±5%)	1	10
All	All	1760/1936 (91%)	1265 (72%)	323 (18%)	172 (10%)	1	10

All 22 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	13	CYS	21
1	A	26	SER	20
1	A	40	PRO	16
1	A	27	VAL	14
1	A	11	ARG	12
1	A	29	SER	10
1	A	5	THR	10
1	A	24	ARG	10
1	A	4	CYS	10
1	A	38	GLU	10
1	A	12	GLN	6
1	A	23	TRP	5
1	A	43	PRO	5
1	A	31	TYR	5
1	A	28	SER	5
1	A	9	CYS	3
1	A	30	HIS	2
1	A	25	THR	2
1	A	18	ALA	2
1	A	6	THR	2
1	A	8	PRO	1
1	A	15	LEU	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	36/38 (95%)	28±2 (79±6%)	8±2 (21±6%)	3	31
All	All	1584/1672 (95%)	1247 (79%)	337 (21%)	3	31

All 30 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	21	THR	29
1	A	6	THR	26
1	A	15	LEU	22
1	A	9	CYS	20
1	A	5	THR	19
1	A	25	THR	17
1	A	23	TRP	15
1	A	13	CYS	14
1	A	39	CYS	14
1	A	11	ARG	14
1	A	12	GLN	13
1	A	26	SER	12
1	A	37	CYS	12
1	A	28	SER	11
1	A	14	LYS	11
1	A	10	CYS	11
1	A	24	ARG	11
1	A	16	LYS	10
1	A	4	CYS	8
1	A	32	CYS	7
1	A	35	ARG	7
1	A	41	SER	6
1	A	29	SER	6
1	A	38	GLU	6
1	A	22	CYS	5
1	A	20	THR	4
1	A	36	SER	4
1	A	42	TYR	1
1	A	33	THR	1
1	A	30	HIS	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 monosaccharides 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 i

The completeness of assignment taking into account all chemical shift lists is 80% for the well-defined parts and 79% 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 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	412
Number of shifts mapped to atoms	412
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 i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	40	0.40 ± 0.27	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	37	-0.05 ± 0.24	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	39	0.81 ± 1.17	None needed (imprecise)

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 80%, i.e. 388 atoms were assigned a chemical shift out of a possible 486. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	156/201 (78%)	82/82 (100%)	37/82 (45%)	37/37 (100%)
Sidechain	216/247 (87%)	145/160 (91%)	67/75 (89%)	4/12 (33%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	16/38 (42%)	15/18 (83%)	0/17 (0%)	1/3 (33%)
Overall	388/486 (80%)	242/260 (93%)	104/174 (60%)	42/52 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 79%, i.e. 411 atoms were assigned a chemical shift out of a possible 519. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	166/216 (77%)	87/88 (99%)	40/88 (45%)	39/40 (98%)
Sidechain	229/265 (86%)	154/172 (90%)	71/81 (88%)	4/12 (33%)
Aromatic	16/38 (42%)	15/18 (83%)	0/17 (0%)	1/3 (33%)
Overall	411/519 (79%)	256/278 (92%)	111/186 (60%)	44/55 (80%)

7.1.4 Statistically unusual chemical shifts [i](#)

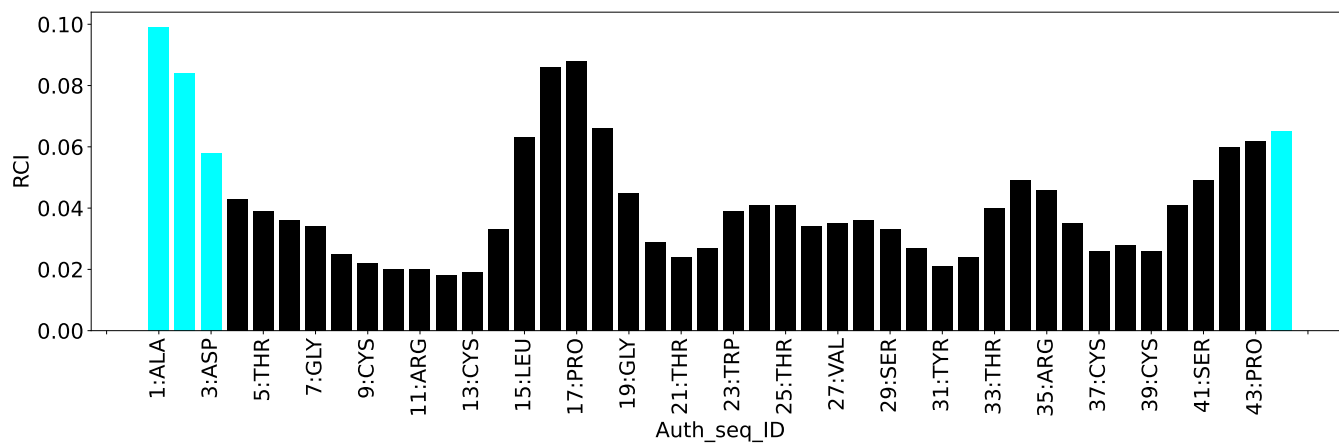
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	33	THR	HG1	5.75	0.08 – 2.19	21.9
1	A	35	ARG	NE	109.90	76.53 – 92.65	15.7
1	A	24	ARG	NE	109.60	76.53 – 92.65	15.5
1	A	11	ARG	NE	109.30	76.53 – 92.65	15.3

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	461
Intra-residue ($ i-j =0$)	93
Sequential ($ i-j =1$)	149
Medium range ($ i-j >1$ and $ i-j <5$)	67
Long range ($ i-j \geq 5$)	152
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	10.5
Number of long range restraints per residue ¹	3.5

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model

Distance violations less than 0.1 Å are not included in the calculation. There are no distance violations

8.2.2 Average number of dihedral-angle violations per model

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis [i](#)

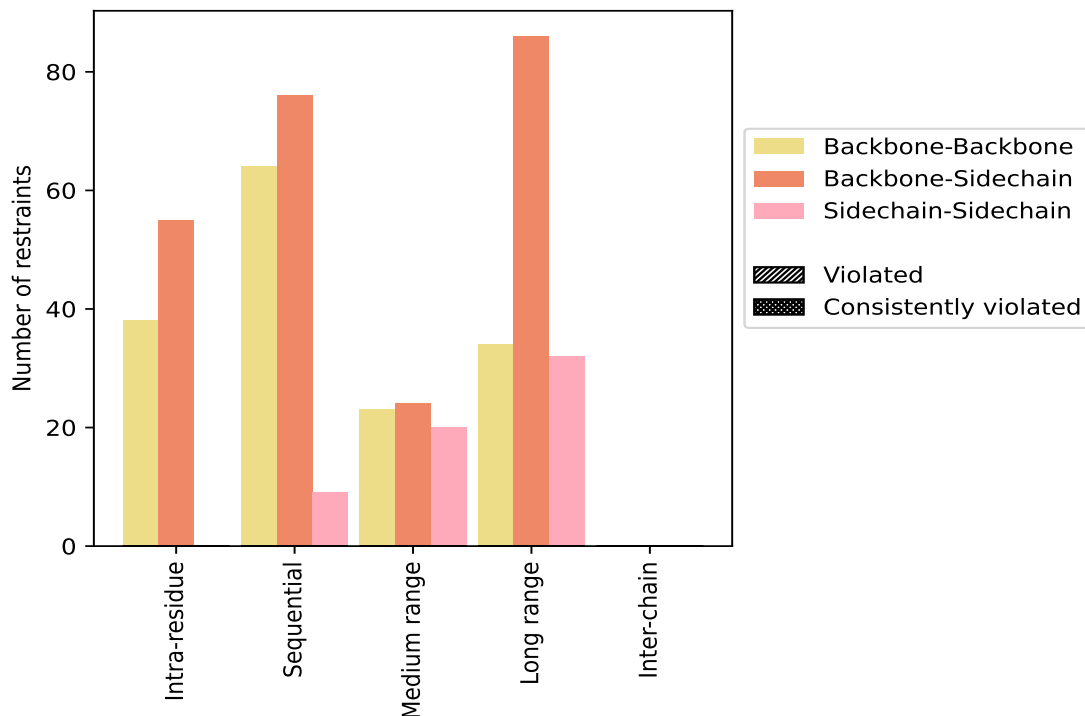
9.1 Summary of distance violations [i](#)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	93	20.2	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	38	8.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	55	11.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	149	32.3	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	64	13.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	76	16.5	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	9	2.0	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	67	14.5	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	23	5.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	24	5.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	20	4.3	0	0.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	152	33.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	34	7.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	86	18.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	32	6.9	0	0.0	0.0	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	461	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	159	34.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	241	52.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	61	13.2	0	0.0	0.0	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfid bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model [i](#)

No violations found

9.3 Distance violation statistics for the ensemble [i](#)

No violations found

9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

9.5 All violated distance restraints [i](#)

No violations found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found