



Full wwPDB NMR Structure Validation Report ⓘ

Jun 12, 2024 – 11:14 AM EDT

PDB ID : 2IUE
BMRB ID : 7313
Title : Pactolus I-domain: Functional Switching of the Rossmann Fold
Authors : Sen, M.; Legge, G.B.
Deposited on : 2006-06-02

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 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
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

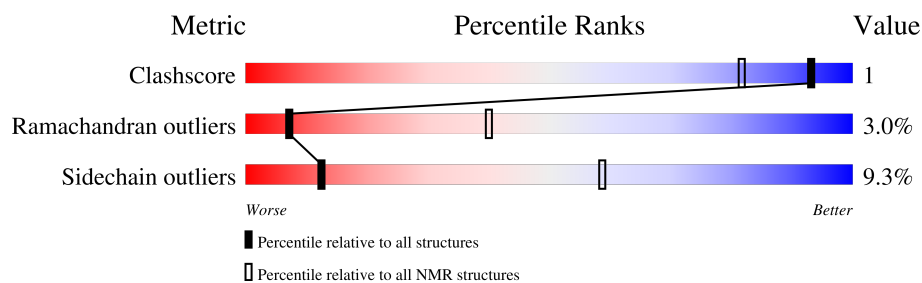
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 25%.

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	212	 67% • 28%

2 Ensemble composition and analysis

This entry contains 20 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 20 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:13, A:40-A:60, A:75-A:194 (152)	0.38	20

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2813 atoms, of which 1168 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called INTEGRIN BETA-2-LIKE PROTEIN.

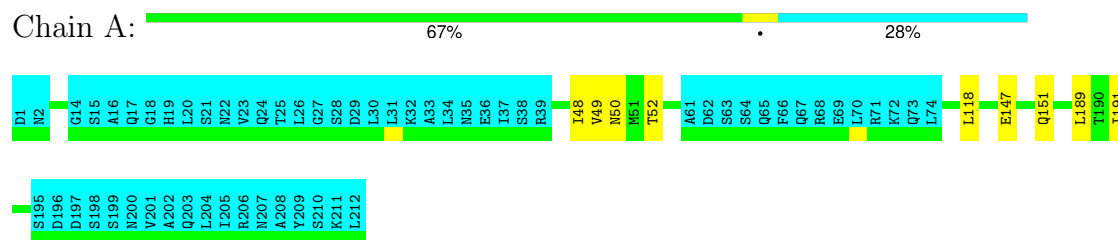
Mol	Chain	Residues	Atoms						Trace
1	A	212	Total	C	H	N	O	S	0
			2813	1029	1168	293	317	6	

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: INTEGRIN BETA-2-LIKE PROTEIN

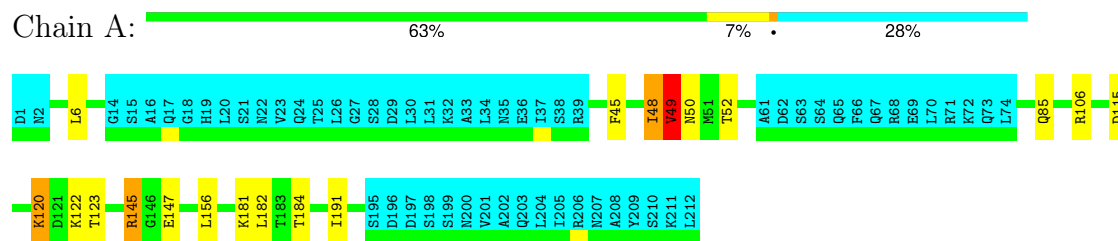


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

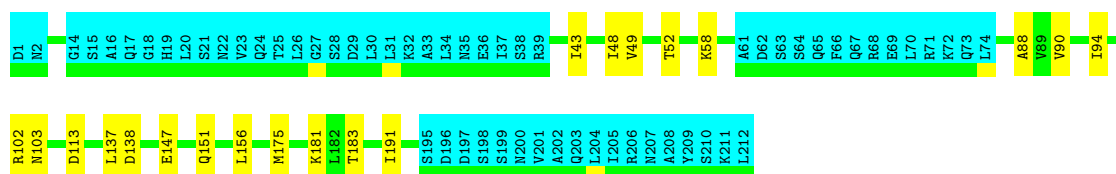
• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



4.2.2 Score per residue for model 2

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN

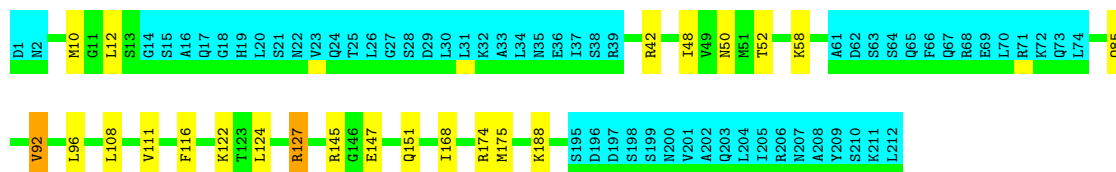




4.2.3 Score per residue for model 3

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN

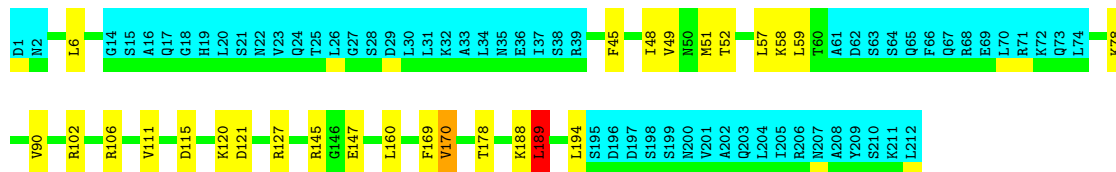
Chain A: 61% 10% 28%



4.2.4 Score per residue for model 4

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN

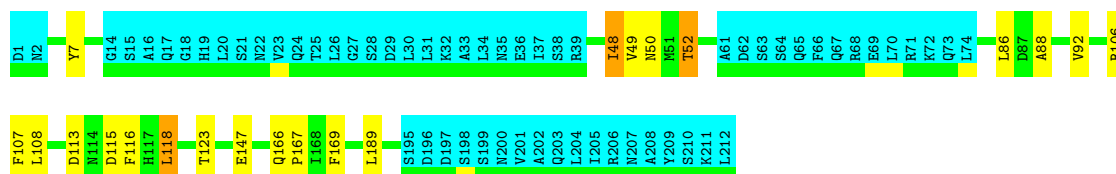
Chain A: 59% 12% 28%



4.2.5 Score per residue for model 5

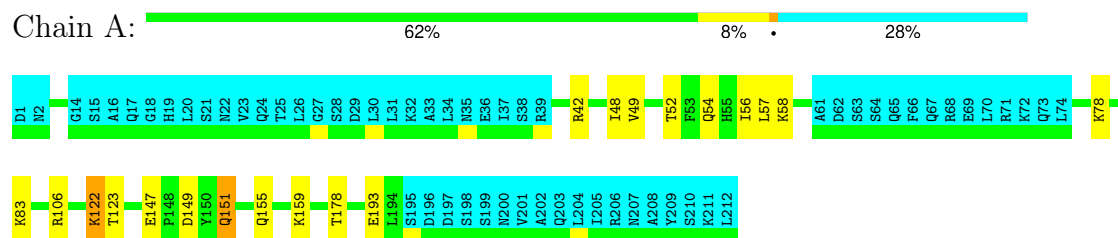
- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN

Chain A: 62% 8% 28%



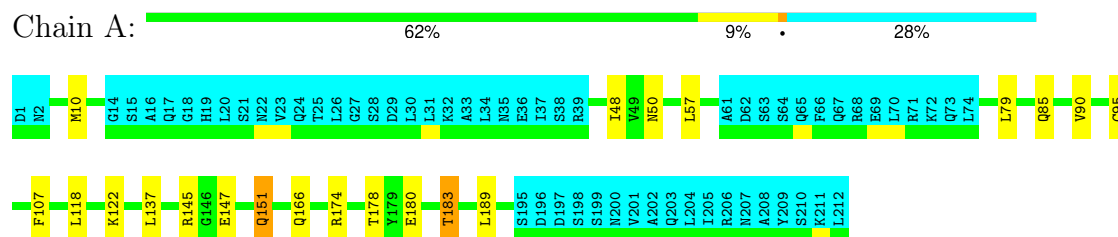
4.2.6 Score per residue for model 6

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



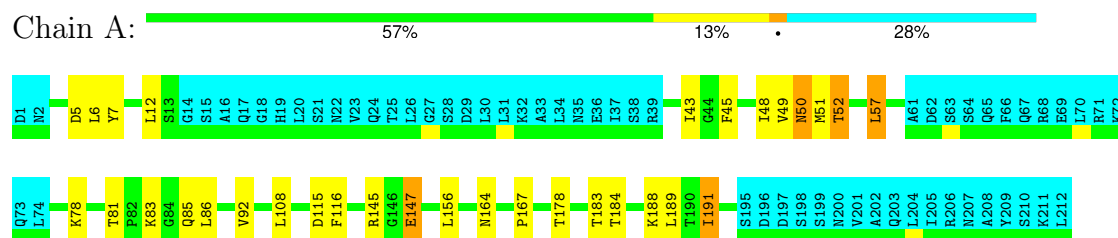
4.2.7 Score per residue for model 7

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



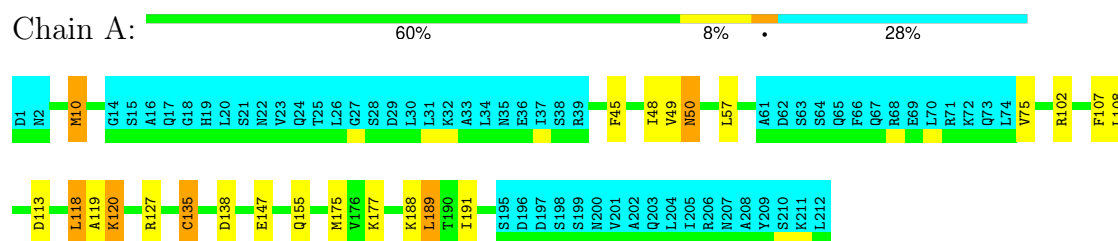
4.2.8 Score per residue for model 8

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



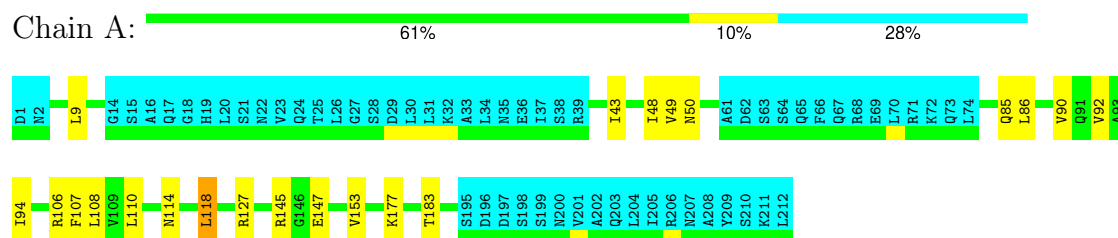
4.2.9 Score per residue for model 9

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



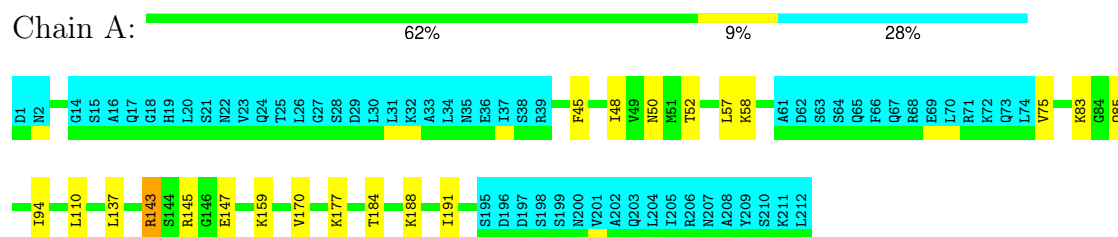
4.2.10 Score per residue for model 10

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



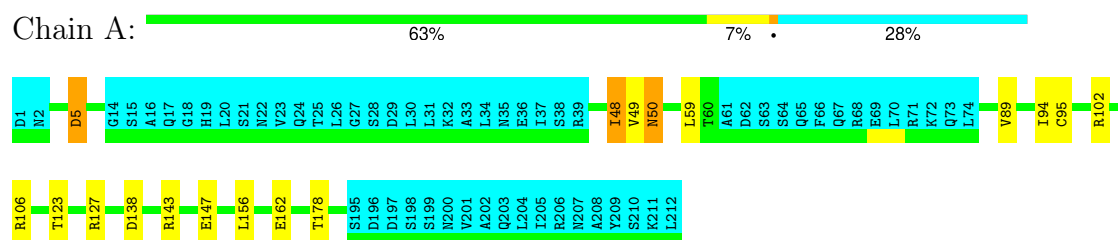
4.2.11 Score per residue for model 11

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



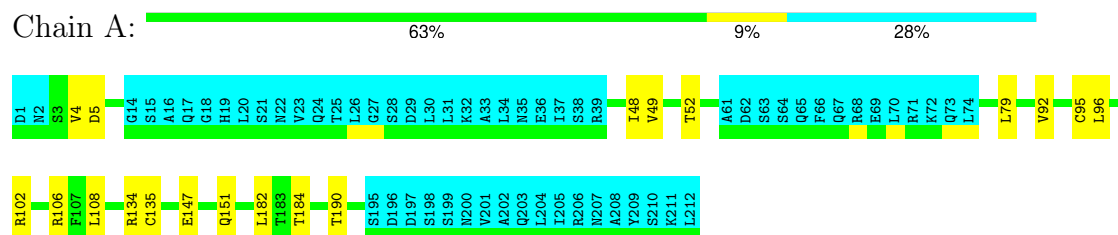
4.2.12 Score per residue for model 12

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



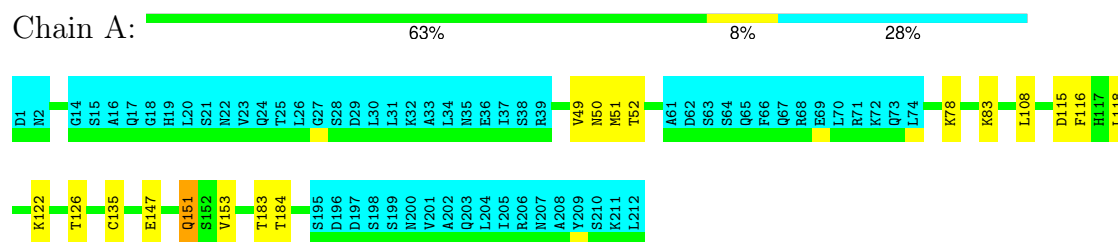
4.2.13 Score per residue for model 13

- Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



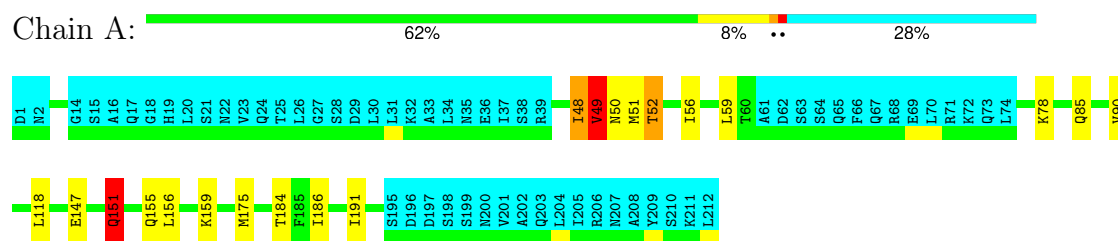
4.2.14 Score per residue for model 14

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



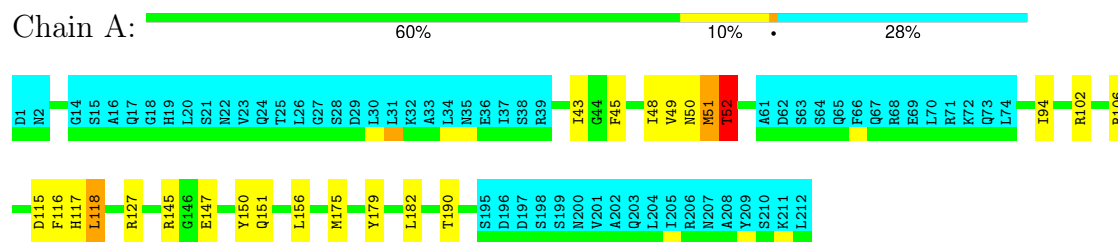
4.2.15 Score per residue for model 15

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



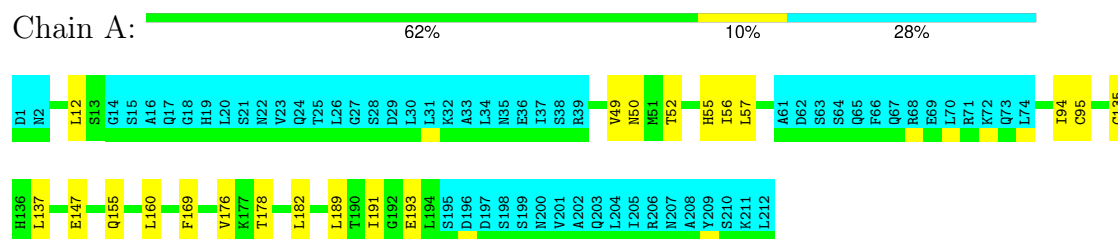
4.2.16 Score per residue for model 16

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



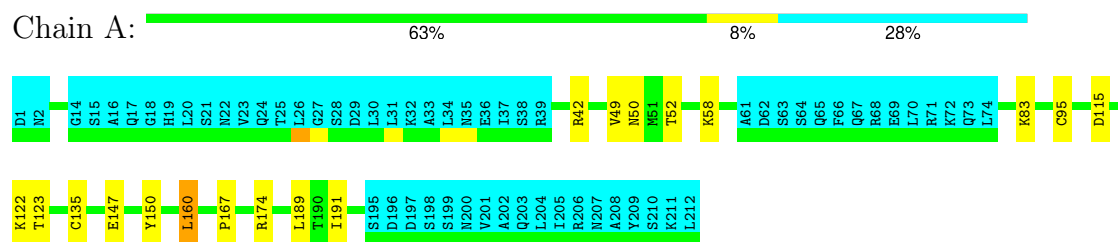
4.2.17 Score per residue for model 17

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



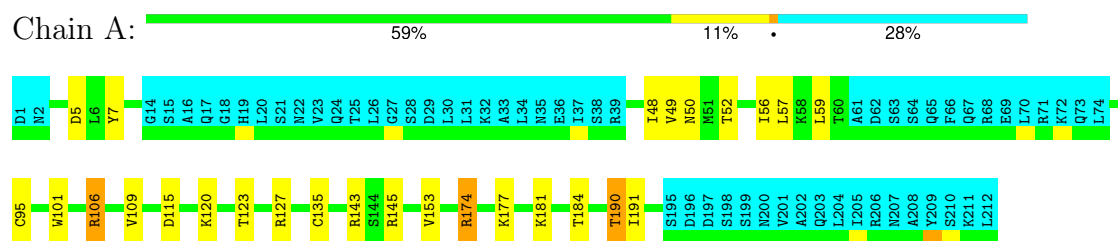
4.2.18 Score per residue for model 18

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



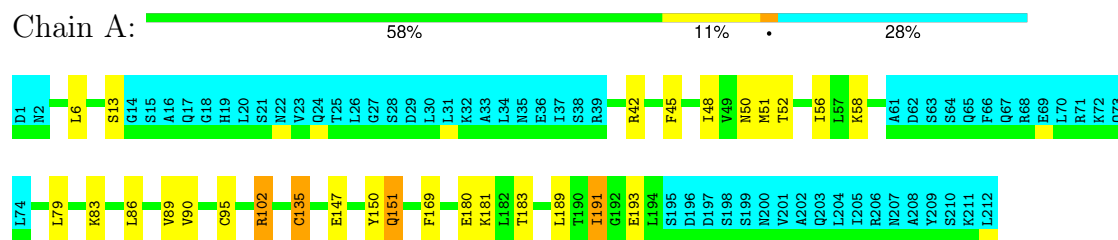
4.2.19 Score per residue for model 19

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



4.2.20 Score per residue for model 20 (medoid)

• Molecule 1: INTEGRIN BETA-2-LIKE PROTEIN



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DYANA AMBER 8.0 AND MODELLER8V2*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *LOWEST POTENTIAL ENERGY ENSEMBLES*.

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

Software name	Classification	Version
Amber	refinement	8.0
NMRPipe	structure solution	
NMRView	structure solution	
DYANA	structure solution	
Amber	structure solution	8.0
MOLMOL	structure solution	
MODELLER	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	804
Number of shifts mapped to atoms	798
Number of unparsed shifts	0
Number of shifts with mapping errors	6
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	25%

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.68±0.01	0±0/1203 (0.0± 0.0%)	1.14±0.03	2±1/1627 (0.1± 0.1%)
All	All	0.68	0/24060 (0.0%)	1.14	36/32540 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.1±1.0
All	All	0	22

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	127	ARG	NE-CZ-NH1	8.67	124.64	120.30	16	1
1	A	183	THR	CA-CB-CG2	6.25	121.15	112.40	7	1
1	A	51	MET	C-N-CA	6.25	137.32	121.70	15	4
1	A	145	ARG	NE-CZ-NH1	6.03	123.32	120.30	7	3
1	A	102	ARG	NE-CZ-NH1	6.03	123.32	120.30	16	2
1	A	5	ASP	CB-CG-OD1	5.97	123.67	118.30	12	1
1	A	189	LEU	CA-CB-CG	5.94	128.96	115.30	9	2
1	A	149	ASP	N-CA-CB	-5.75	100.26	110.60	6	1
1	A	106	ARG	NE-CZ-NH1	5.70	123.15	120.30	5	3
1	A	151	GLN	CA-CB-CG	5.54	125.60	113.40	15	1
1	A	42	ARG	NE-CZ-NH1	5.54	123.07	120.30	6	3
1	A	95	CYS	CA-CB-SG	-5.33	104.40	114.00	12	1
1	A	86	LEU	CB-CA-C	5.29	120.26	110.20	20	1
1	A	189	LEU	CB-CA-C	5.29	120.25	110.20	4	1
1	A	102	ARG	NE-CZ-NH2	-5.20	117.70	120.30	4	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	135	CYS	CA-CB-SG	-5.17	104.69	114.00	20	3
1	A	143	ARG	NE-CZ-NH1	5.16	122.88	120.30	12	2
1	A	174	ARG	NE-CZ-NH1	5.14	122.87	120.30	19	1
1	A	49	VAL	CA-CB-CG2	5.11	118.56	110.90	15	1
1	A	134	ARG	NE-CZ-NH1	5.10	122.85	120.30	13	1
1	A	190	THR	CA-CB-CG2	5.09	119.53	112.40	19	1
1	A	52	THR	CA-CB-CG2	5.00	119.41	112.40	16	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	45	PHE	Sidechain	6
1	A	145	ARG	Sidechain	4
1	A	116	PHE	Sidechain	2
1	A	7	TYR	Sidechain	2
1	A	106	ARG	Sidechain	2
1	A	174	ARG	Sidechain	1
1	A	169	PHE	Sidechain	1
1	A	127	ARG	Sidechain	1
1	A	102	ARG	Sidechain	1
1	A	42	ARG	Sidechain	1
1	A	150	TYR	Sidechain	1

6.2 Too-close contacts ⓘ

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	1182	856	1210	3±2
All	All	23640	17123	24200	60

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:VAL:HG12	1:A:170:VAL:HG22	0.70	1.63	4	1
1:A:90:VAL:HG21	1:A:156:LEU:HD22	0.65	1.69	15	1
1:A:86:LEU:HD23	1:A:156:LEU:HD21	0.62	1.72	8	1
1:A:85:GLN:CG	1:A:110:LEU:HD21	0.55	2.32	11	1
1:A:181:LYS:O	1:A:184:THR:HG22	0.54	2.02	19	1
1:A:151:GLN:H	1:A:151:GLN:CD	0.54	2.05	14	3
1:A:51:MET:O	1:A:52:THR:HG23	0.52	2.05	8	2
1:A:90:VAL:O	1:A:94:ILE:HD12	0.52	2.05	10	2
1:A:151:GLN:NE2	1:A:151:GLN:H	0.51	2.02	15	1
1:A:48:ILE:HD13	1:A:49:VAL:N	0.50	2.21	1	3
1:A:160:LEU:HD22	1:A:167:PRO:HG3	0.48	1.84	18	1
1:A:92:VAL:HG11	1:A:108:LEU:HD13	0.48	1.85	3	2
1:A:90:VAL:CG1	1:A:156:LEU:HD22	0.47	2.39	2	1
1:A:118:LEU:HD22	1:A:119:ALA:H	0.47	1.70	9	1
1:A:49:VAL:CG2	1:A:50:ASN:H	0.47	2.22	15	1
1:A:10:MET:CE	1:A:45:PHE:CZ	0.47	2.98	9	1
1:A:170:VAL:HG23	1:A:194:LEU:HB2	0.46	1.86	4	1
1:A:59:LEU:HD11	1:A:101:TRP:CE3	0.46	2.46	19	1
1:A:169:PHE:CD2	1:A:189:LEU:HD21	0.46	2.45	17	2
1:A:49:VAL:HG23	1:A:50:ASN:H	0.46	1.70	15	1
1:A:169:PHE:CD2	1:A:189:LEU:HD11	0.46	2.46	20	1
1:A:50:ASN:C	1:A:52:THR:H	0.45	2.14	15	2
1:A:167:PRO:HG2	1:A:189:LEU:HG	0.45	1.88	5	2
1:A:122:LYS:HE3	1:A:150:TYR:CZ	0.45	2.47	18	1
1:A:122:LYS:HE2	1:A:127:ARG:CG	0.45	2.42	3	1
1:A:118:LEU:HD23	1:A:118:LEU:H	0.45	1.71	16	1
1:A:90:VAL:HG21	1:A:151:GLN:CG	0.44	2.43	20	1
1:A:180:GLU:O	1:A:183:THR:HG22	0.44	2.11	7	1
1:A:107:PHE:CD2	1:A:166:GLN:HB2	0.44	2.48	7	1
1:A:9:LEU:HD12	1:A:92:VAL:HG21	0.43	1.89	10	1
1:A:48:ILE:HD13	1:A:88:ALA:HB2	0.43	1.89	5	1
1:A:5:ASP:HB2	1:A:59:LEU:HD13	0.43	1.90	19	1
1:A:122:LYS:N	1:A:122:LYS:HE2	0.43	2.29	6	1
1:A:117:HIS:HB3	1:A:150:TYR:CE2	0.43	2.49	16	1
1:A:118:LEU:HD21	1:A:153:VAL:HG23	0.43	1.90	10	1
1:A:118:LEU:H	1:A:118:LEU:CD2	0.43	2.27	16	1
1:A:7:TYR:CD1	1:A:92:VAL:HG21	0.42	2.49	5	1
1:A:86:LEU:HB2	1:A:116:PHE:CZ	0.42	2.49	8	2
1:A:120:LYS:O	1:A:123:THR:HG22	0.42	2.15	19	1
1:A:118:LEU:H	1:A:118:LEU:HD13	0.42	1.75	5	1
1:A:175:MET:CE	1:A:179:TYR:CE1	0.42	3.02	16	1
1:A:108:LEU:HD13	1:A:110:LEU:HD13	0.41	1.91	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:92:VAL:HG11	1:A:108:LEU:HD23	0.41	1.93	8	1
1:A:90:VAL:HG21	1:A:151:GLN:HG3	0.41	1.91	20	1
1:A:13:SER:OG	1:A:83:LYS:HE2	0.41	2.15	20	1
1:A:151:GLN:H	1:A:151:GLN:NE2	0.41	2.13	20	1
1:A:86:LEU:HD22	1:A:116:PHE:CE2	0.40	2.51	5	1
1:A:48:ILE:HG21	1:A:88:ALA:HB2	0.40	1.92	2	1
1:A:107:PHE:CE1	1:A:166:GLN:HG3	0.40	2.52	5	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	152/212 (72%)	133±2 (87±1%)	15±2 (10±1%)	5±2 (3±1%)	7	40
All	All	3040/4240 (72%)	2655 (87%)	294 (10%)	91 (3%)	7	40

All 15 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	147	GLU	19
1	A	49	VAL	14
1	A	52	THR	14
1	A	50	ASN	13
1	A	191	ILE	7
1	A	115	ASP	6
1	A	57	LEU	6
1	A	188	LYS	3
1	A	120	LYS	2
1	A	138	ASP	2
1	A	103	ASN	1
1	A	79	LEU	1
1	A	85	GLN	1
1	A	174	ARG	1
1	A	59	LEU	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	132/184 (72%)	120±3 (91±2%)	12±3 (9±2%)	12	59
All	All	2640/3680 (72%)	2394 (91%)	246 (9%)	12	59

All 78 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	48	ILE	16
1	A	151	GLN	9
1	A	58	LYS	7
1	A	118	LEU	7
1	A	184	THR	6
1	A	178	THR	6
1	A	95	CYS	6
1	A	135	CYS	6
1	A	85	GLN	5
1	A	123	THR	5
1	A	183	THR	5
1	A	127	ARG	5
1	A	78	LYS	5
1	A	106	ARG	5
1	A	56	ILE	5
1	A	83	LYS	5
1	A	191	ILE	5
1	A	6	LEU	4
1	A	122	LYS	4
1	A	182	LEU	4
1	A	102	ARG	4
1	A	137	LEU	4
1	A	175	MET	4
1	A	189	LEU	4
1	A	155	GLN	4
1	A	50	ASN	4
1	A	177	LYS	4
1	A	94	ILE	4
1	A	120	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	156	LEU	3
1	A	181	LYS	3
1	A	43	ILE	3
1	A	113	ASP	3
1	A	10	MET	3
1	A	12	LEU	3
1	A	160	LEU	3
1	A	108	LEU	3
1	A	159	LYS	3
1	A	193	GLU	3
1	A	5	ASP	3
1	A	57	LEU	3
1	A	145	ARG	3
1	A	190	THR	3
1	A	49	VAL	2
1	A	52	THR	2
1	A	96	LEU	2
1	A	188	LYS	2
1	A	59	LEU	2
1	A	90	VAL	2
1	A	115	ASP	2
1	A	75	VAL	2
1	A	107	PHE	2
1	A	143	ARG	2
1	A	89	VAL	2
1	A	79	LEU	2
1	A	153	VAL	2
1	A	174	ARG	2
1	A	92	VAL	1
1	A	124	LEU	1
1	A	168	ILE	1
1	A	121	ASP	1
1	A	170	VAL	1
1	A	54	GLN	1
1	A	81	THR	1
1	A	147	GLU	1
1	A	164	ASN	1
1	A	86	LEU	1
1	A	114	ASN	1
1	A	138	ASP	1
1	A	162	GLU	1
1	A	4	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	51	MET	1
1	A	126	THR	1
1	A	186	ILE	1
1	A	116	PHE	1
1	A	55	HIS	1
1	A	176	VAL	1
1	A	180	GLU	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

The completeness of assignment taking into account all chemical shift lists is 25% for the well-defined parts and 28% 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	804
Number of shifts mapped to atoms	798
Number of unparsed shifts	0
Number of shifts with mapping errors	6
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- No matching atom found in the structure. All 6 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	ASP	H	8.2	0.02	1
1	A	230	SER	H	7.6	0.02	1
1	A	230	SER	C	175.5	0.1	1
1	A	230	SER	CA	59.6	0.1	1
1	A	230	SER	CB	64.8	0.1	1
1	A	230	SER	N	121.6	0.02	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	167	0.19 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	152	0.84 ± 0.12	Should be checked

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Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}'$	163	2.97 ± 0.09	Should be applied
^{15}N	161	-0.89 ± 0.21	Should be applied

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 25%, i.e. 516 atoms were assigned a chemical shift out of a possible 2090. 0 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	420/764 (55%)	104/313 (33%)	212/304 (70%)	104/147 (71%)
Sidechain	96/1187 (8%)	0/776 (0%)	96/365 (26%)	0/46 (0%)
Aromatic	0/139 (0%)	0/69 (0%)	0/66 (0%)	0/4 (0%)
Overall	516/2090 (25%)	104/1158 (9%)	308/735 (42%)	104/197 (53%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 28%, i.e. 799 atoms were assigned a chemical shift out of a possible 2887. 0 out of 42 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	648/1067 (61%)	160/436 (37%)	328/424 (77%)	160/207 (77%)
Sidechain	151/1655 (9%)	0/1076 (0%)	151/507 (30%)	0/72 (0%)
Aromatic	0/165 (0%)	0/82 (0%)	0/78 (0%)	0/5 (0%)
Overall	799/2887 (28%)	160/1594 (10%)	479/1009 (47%)	160/284 (56%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. 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:

