



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 01:58 PM BST

PDB ID : 1C7V
Title : NMR SOLUTION STRUCTURE OF THE CALCIUM-BOUND C-TERMINAL DOMAIN (W81-S161) OF CALCIUM VECTOR PROTEIN FROM AMPHIOXUS
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Deposited on : 2000-03-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

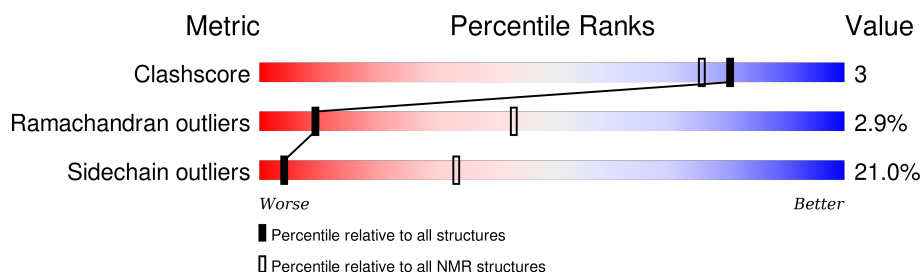
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	81	<div> <div>47%</div> <div>22%</div> <div>15%</div> <div>16%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 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:89-A:114, A:123-A:152 (56)	0.62	7

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. No single-model clusters were found.

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

3 Entry composition [i](#)

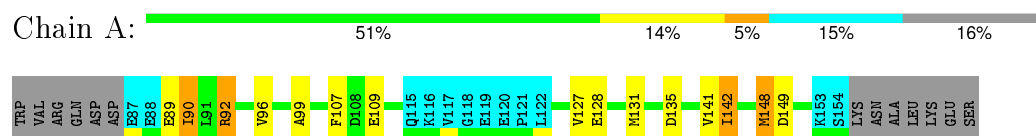
There is only 1 type of molecule in this entry. The entry contains 1049 atoms, of which 510 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CALCIUM VECTOR PROTEIN.

Mol	Chain	Residues	Atoms						Trace
1	A	68	Total	C	H	N	O	S	0
			1049	341	510	80	115	3	

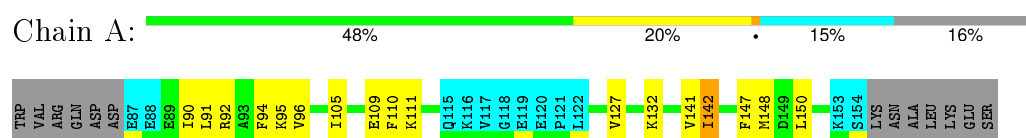
4.2.3 Score per residue for model 3

- Molecule 1: CALCIUM VECTOR PROTEIN



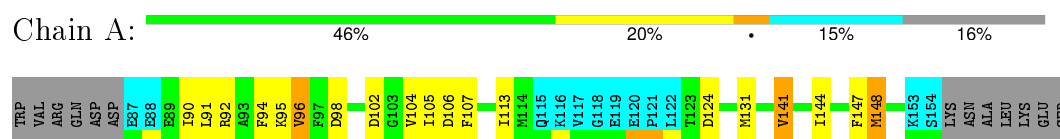
4.2.4 Score per residue for model 4

- Molecule 1: CALCIUM VECTOR PROTEIN



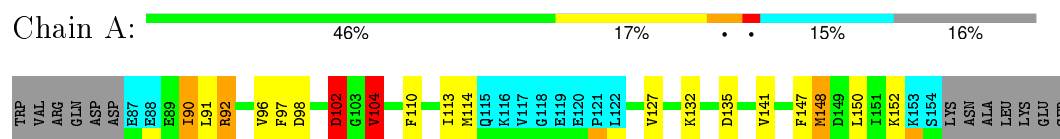
4.2.5 Score per residue for model 5

- Molecule 1: CALCIUM VECTOR PROTEIN



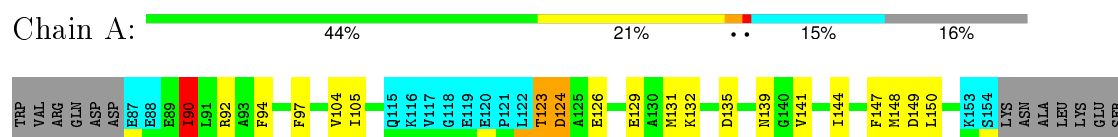
4.2.6 Score per residue for model 6

- Molecule 1: CALCIUM VECTOR PROTEIN



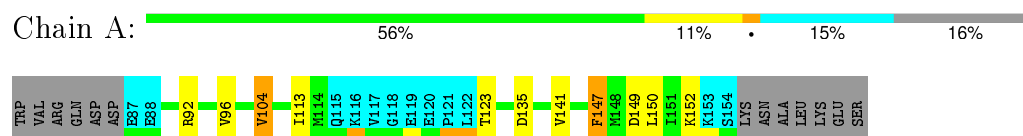
4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: CALCIUM VECTOR PROTEIN



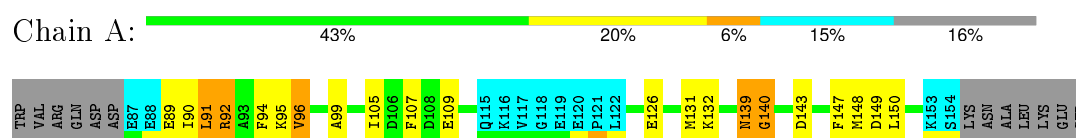
4.2.8 Score per residue for model 8

- Molecule 1: CALCIUM VECTOR PROTEIN



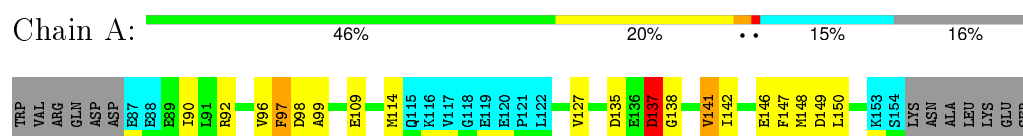
4.2.9 Score per residue for model 9

- Molecule 1: CALCIUM VECTOR PROTEIN



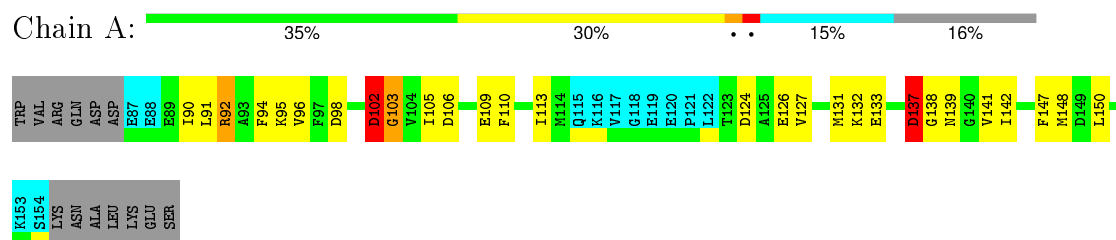
4.2.10 Score per residue for model 10

- Molecule 1: CALCIUM VECTOR PROTEIN



4.2.11 Score per residue for model 11

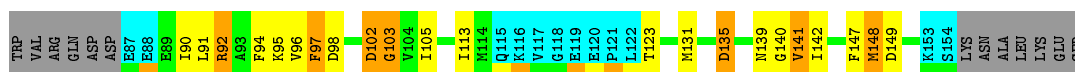
- Molecule 1: CALCIUM VECTOR PROTEIN



4.2.12 Score per residue for model 12

- Molecule 1: CALCIUM VECTOR PROTEIN

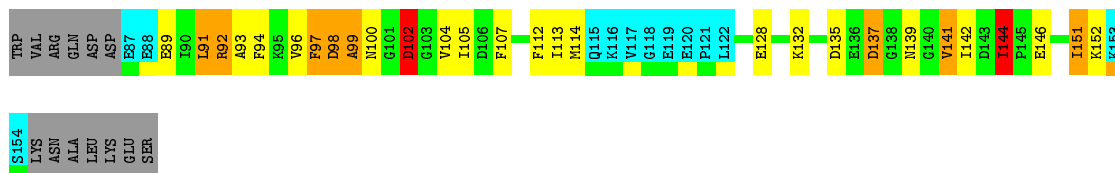




4.2.13 Score per residue for model 13

- Molecule 1: CALCIUM VECTOR PROTEIN

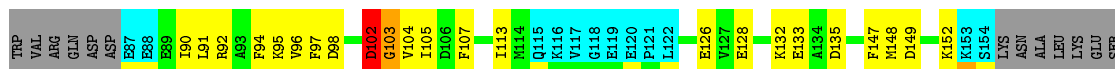
Chain A: 35% 22% 10% • 15% 16%



4.2.14 Score per residue for model 14

- Molecule 1: CALCIUM VECTOR PROTEIN

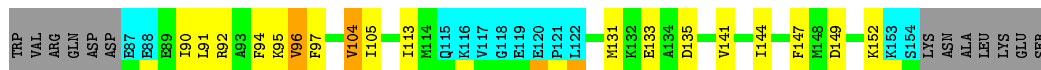
Chain A: 41% 26% •• 15% 16%



4.2.15 Score per residue for model 15

- Molecule 1: CALCIUM VECTOR PROTEIN

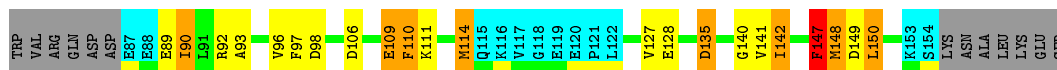
Chain A: 47% 20% • 15% 16%



4.2.16 Score per residue for model 16

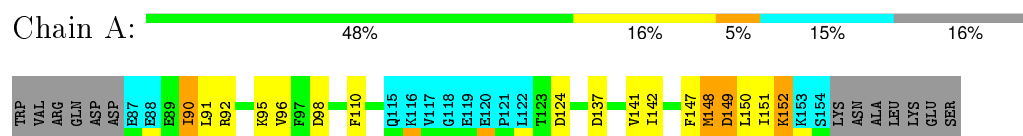
- Molecule 1: CALCIUM VECTOR PROTEIN

Chain A: 42% 16% 10% • 15% 16%



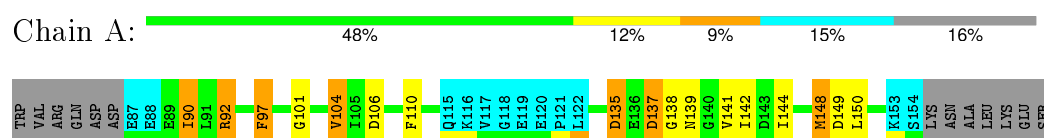
4.2.17 Score per residue for model 17

- Molecule 1: CALCIUM VECTOR PROTEIN



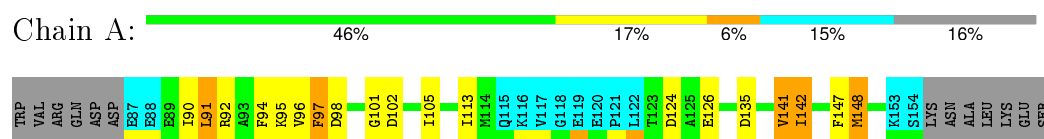
4.2.18 Score per residue for model 18

- Molecule 1: CALCIUM VECTOR PROTEIN



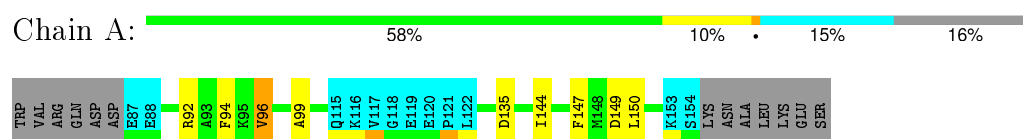
4.2.19 Score per residue for model 19

- Molecule 1: CALCIUM VECTOR PROTEIN



4.2.20 Score per residue for model 20

- Molecule 1: CALCIUM VECTOR PROTEIN



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *Distance Geometry (DGII) and Simulated Annealing (Discover)*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *agreement with NOE restraints, geometry quality*.

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

Software name	Classification	Version
Felix	structure solution	97.0
Felix	refinement	97.0

No chemical shift data was provided. 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

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	1.20±0.02	0±0/451 (0.0±0.0%)	1.73±0.20	10±4/606 (1.6±0.6%)
All	All	1.20	0/9020 (0.0%)	1.74	197/12120 (1.6%)

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	0.8±0.8
All	All	0	16

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	135	ASP	O-C-N	-37.41	62.84	122.70	18	1
1	A	135	ASP	CA-C-N	18.29	157.45	117.20	18	1
1	A	137	ASP	O-C-N	-14.43	98.67	123.20	11	2
1	A	148	MET	CA-CB-CG	12.18	134.00	113.30	1	7
1	A	135	ASP	CA-C-O	-11.33	96.31	120.10	18	1
1	A	92	ARG	NE-CZ-NH1	10.78	125.69	120.30	7	20
1	A	139	ASN	O-C-N	-10.58	105.21	123.20	9	1
1	A	135	ASP	CB-CG-OD1	10.40	127.66	118.30	12	13
1	A	141	VAL	CA-CB-CG2	10.32	126.39	110.90	5	8
1	A	127	VAL	CA-CB-CG1	9.67	125.41	110.90	2	4
1	A	90	ILE	CA-CB-CG1	8.84	127.79	111.00	16	5
1	A	102	ASP	N-CA-CB	8.67	126.21	110.60	13	2
1	A	100	ASN	N-CA-CB	8.54	125.97	110.60	13	1
1	A	141	VAL	CA-CB-CG1	8.07	123.00	110.90	19	1
1	A	137	ASP	CA-C-N	7.68	131.57	116.20	10	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	109	GLU	N-CA-CB	-7.68	96.77	110.60	16	1
1	A	91	LEU	CA-CB-CG	7.30	132.10	115.30	9	3
1	A	92	ARG	NE-CZ-NH2	-7.11	116.74	120.30	10	7
1	A	103	GLY	N-CA-C	7.08	130.80	113.10	2	4
1	A	90	ILE	N-CA-CB	6.93	126.73	110.80	16	1
1	A	141	VAL	CG1-CB-CG2	-6.88	99.90	110.90	10	4
1	A	90	ILE	CA-CB-CG2	6.66	124.22	110.90	18	1
1	A	148	MET	CG-SD-CE	6.57	110.72	100.20	16	4
1	A	95	LYS	CB-CA-C	6.47	123.33	110.40	5	9
1	A	97	PHE	CB-CG-CD2	-6.45	116.29	120.80	15	1
1	A	102	ASP	CA-C-N	-6.41	103.38	116.20	13	1
1	A	140	GLY	N-CA-C	6.40	129.10	113.10	9	1
1	A	104	VAL	CG1-CB-CG2	6.35	121.06	110.90	14	2
1	A	147	PHE	CB-CG-CD2	-6.34	116.36	120.80	16	1
1	A	97	PHE	CB-CG-CD1	-6.32	116.38	120.80	12	6
1	A	100	ASN	C-N-CA	6.31	135.55	122.30	13	1
1	A	98	ASP	CA-CB-CG	6.27	127.19	113.40	19	2
1	A	112	PHE	CB-CG-CD2	-6.18	116.48	120.80	13	1
1	A	91	LEU	CB-CG-CD1	6.17	121.48	111.00	19	2
1	A	150	LEU	CA-CB-CG	6.14	129.42	115.30	16	1
1	A	90	ILE	CG1-CB-CG2	-6.10	97.98	111.40	16	3
1	A	137	ASP	N-CA-CB	6.07	121.52	110.60	13	3
1	A	150	LEU	CB-CA-C	6.02	121.64	110.20	2	3
1	A	139	ASN	CA-C-O	-6.01	107.48	120.10	9	1
1	A	97	PHE	CA-CB-CG	5.96	128.19	113.90	15	1
1	A	98	ASP	N-CA-CB	-5.91	99.97	110.60	17	2
1	A	127	VAL	CA-CB-CG2	5.90	119.75	110.90	10	3
1	A	123	THR	N-CA-CB	5.89	121.49	110.30	8	2
1	A	104	VAL	CA-CB-CG1	5.83	119.64	110.90	6	6
1	A	142	ILE	CA-CB-CG1	5.82	122.05	111.00	1	5
1	A	96	VAL	CA-CB-CG1	5.80	119.59	110.90	5	13
1	A	102	ASP	C-N-CA	5.80	134.47	122.30	6	1
1	A	137	ASP	CB-CA-C	5.78	121.96	110.40	2	3
1	A	102	ASP	CB-CG-OD1	5.76	123.49	118.30	6	1
1	A	150	LEU	N-CA-CB	-5.76	98.87	110.40	2	1
1	A	139	ASN	CA-C-N	5.76	127.72	116.20	9	1
1	A	143	ASP	CA-CB-CG	5.74	126.03	113.40	9	1
1	A	124	ASP	N-CA-CB	-5.67	100.40	110.60	7	1
1	A	135	ASP	CB-CG-OD2	-5.65	113.22	118.30	16	4
1	A	93	ALA	N-CA-CB	5.53	117.84	110.10	16	1
1	A	147	PHE	CB-CG-CD1	5.51	124.66	120.80	16	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	135	ASP	N-CA-CB	5.44	120.40	110.60	7	1
1	A	99	ALA	C-N-CA	5.41	135.22	121.70	13	1
1	A	137	ASP	CA-C-O	-5.40	108.77	120.10	11	2
1	A	102	ASP	O-C-N	-5.38	114.06	123.20	14	1
1	A	137	ASP	N-CA-C	-5.36	96.52	111.00	2	1
1	A	124	ASP	N-CA-C	5.31	125.34	111.00	7	1
1	A	89	GLU	CA-C-N	5.29	128.83	117.20	16	1
1	A	102	ASP	CA-C-O	-5.25	109.07	120.10	11	2
1	A	144	ILE	CA-CB-CG1	5.22	120.92	111.00	2	2
1	A	149	ASP	CA-C-O	-5.14	109.30	120.10	17	1
1	A	151	ILE	CA-CB-CG1	5.14	120.77	111.00	13	1
1	A	147	PHE	CA-CB-CG	5.08	126.08	113.90	16	1
1	A	152	LYS	C-N-CA	5.06	134.35	121.70	14	1
1	A	126	GLU	CA-CB-CG	5.04	124.50	113.40	11	1
1	A	152	LYS	N-CA-CB	-5.03	101.55	110.60	13	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	102	ASP	Mainchain	4
1	A	137	ASP	Mainchain	2
1	A	92	ARG	Sidechain	2
1	A	147	PHE	Sidechain	2
1	A	135	ASP	Mainchain	1
1	A	97	PHE	Sidechain	1
1	A	123	THR	Mainchain	1
1	A	110	PHE	Sidechain	1
1	A	107	PHE	Sidechain	1
1	A	139	ASN	Mainchain	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	444	417	417	3±2
All	All	8880	8340	8339	57

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:98:ASP:OD2	1:A:102:ASP:HA	1.14	1.41	6	2
1:A:98:ASP:OD1	1:A:104:VAL:O	0.74	2.04	6	1
1:A:90:ILE:HD11	1:A:152:LYS:HE2	0.62	1.70	6	1
1:A:90:ILE:HG23	1:A:147:PHE:HE2	0.62	1.52	19	2
1:A:135:ASP:OD2	1:A:140:GLY:N	0.57	2.37	12	2
1:A:135:ASP:OD2	1:A:140:GLY:HA2	0.56	2.01	1	1
1:A:90:ILE:HG21	1:A:148:MET:HG2	0.55	1.76	10	2
1:A:90:ILE:HG23	1:A:147:PHE:CE2	0.55	2.36	11	12
1:A:99:ALA:HB2	1:A:109:GLU:HG2	0.54	1.78	10	2
1:A:90:ILE:HD12	1:A:90:ILE:H	0.54	1.60	6	1
1:A:90:ILE:HG23	1:A:148:MET:CE	0.54	2.32	18	1
1:A:90:ILE:HG23	1:A:147:PHE:CE1	0.54	2.38	6	1
1:A:135:ASP:OD2	1:A:140:GLY:CA	0.53	2.56	1	1
1:A:94:PHE:CE2	1:A:105:ILE:HD12	0.50	2.42	13	11
1:A:131:MET:SD	1:A:142:ILE:HD11	0.49	2.47	12	2
1:A:94:PHE:HB2	1:A:147:PHE:CD2	0.49	2.42	5	2
1:A:90:ILE:HG21	1:A:148:MET:HB3	0.49	1.84	6	2
1:A:90:ILE:HD11	1:A:152:LYS:CE	0.48	2.37	6	1
1:A:98:ASP:OD2	1:A:102:ASP:OD1	0.47	2.31	13	1
1:A:149:ASP:O	1:A:152:LYS:HA	0.46	2.10	17	1
1:A:89:GLU:O	1:A:93:ALA:HB3	0.44	2.11	13	1
1:A:148:MET:SD	1:A:148:MET:N	0.44	2.91	18	1
1:A:111:LYS:O	1:A:114:MET:SD	0.44	2.76	16	1
1:A:102:ASP:CG	1:A:144:ILE:HD11	0.44	2.34	13	1
1:A:90:ILE:HG23	1:A:147:PHE:HE1	0.43	1.70	6	1
1:A:94:PHE:HB2	1:A:147:PHE:CE2	0.43	2.48	5	2
1:A:99:ALA:CB	1:A:109:GLU:HG2	0.40	2.46	3	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	56/81 (69%)	51±2 (91±4%)	4±2 (6±3%)	2±1 (3±2%)	9	43
All	All	1120/1620 (69%)	1018 (91%)	70 (6%)	32 (3%)	9	43

All 14 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	137	ASP	6
1	A	138	GLY	5
1	A	103	GLY	4
1	A	101	GLY	3
1	A	99	ALA	2
1	A	98	ASP	2
1	A	114	MET	2
1	A	139	ASN	2
1	A	151	ILE	1
1	A	89	GLU	1
1	A	152	LYS	1
1	A	124	ASP	1
1	A	140	GLY	1
1	A	102	ASP	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	47/70 (67%)	37±3 (79±6%)	10±3 (21±6%)	4	33
All	All	940/1400 (67%)	743 (79%)	197 (21%)	4	33

All 37 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	148	MET	12
1	A	150	LEU	11
1	A	91	LEU	11
1	A	97	PHE	11
1	A	141	VAL	10
1	A	113	ILE	10
1	A	142	ILE	9
1	A	132	LYS	9
1	A	149	ASP	9
1	A	102	ASP	8
1	A	96	VAL	8
1	A	144	ILE	7
1	A	104	VAL	7
1	A	110	PHE	6
1	A	98	ASP	5
1	A	92	ARG	5
1	A	107	PHE	5
1	A	131	MET	5
1	A	139	ASN	4
1	A	126	GLU	4
1	A	124	ASP	4
1	A	128	GLU	4
1	A	106	ASP	4
1	A	114	MET	3
1	A	133	GLU	3
1	A	152	LYS	3
1	A	109	GLU	3
1	A	90	ILE	3
1	A	137	ASP	3
1	A	89	GLU	2
1	A	147	PHE	2
1	A	146	GLU	2
1	A	129	GLU	1
1	A	123	THR	1
1	A	151	ILE	1
1	A	127	VAL	1
1	A	111	LYS	1

6.3.3 RNA ⓘ

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

No chemical shift data were provided