



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 02:27 PM UTC

PDB ID : 1RY4 / pdb_00001ry4
Title : NMR Structure of the CRIB-PDZ module of Par-6
Authors : Peterson, F.C.; Penkert, R.R.; Volkman, B.F.; Prehoda, K.E.
Deposited on : 2003-12-19

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 : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.49

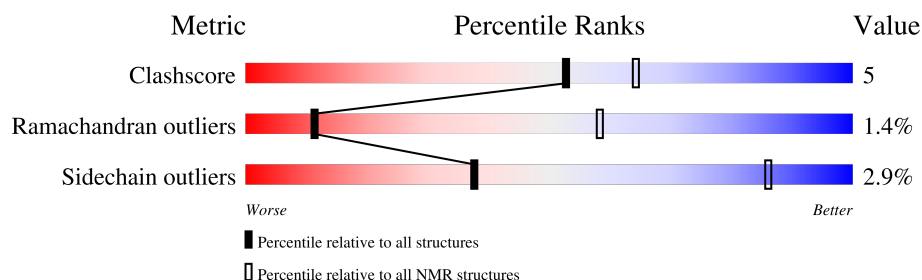
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	128	

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 3 as representative, based on the following criterion: *closest to the average*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:133-A:143 (11)	1.65	14
2	A:154-A:253 (100)	1.68	9

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 3 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1972 atoms, of which 1006 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CG5884-PA.

Mol	Chain	Residues	Atoms						Trace
1	A	128	Total	C	H	N	O	S	0
			1972	604	1006	174	186	2	

There are 2 discrepancies between the modelled and reference sequences:

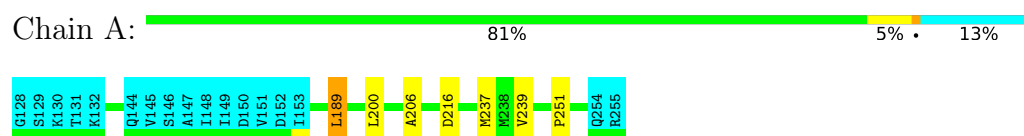
Chain	Residue	Modelled	Actual	Comment	Reference
A	128	GLY	-	cloning artifact	GB 18860099
A	129	SER	-	cloning artifact	GB 18860099

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: CG5884-PA

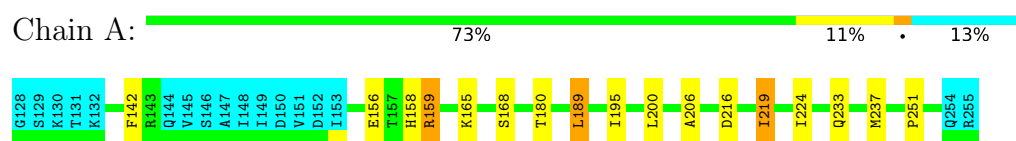


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

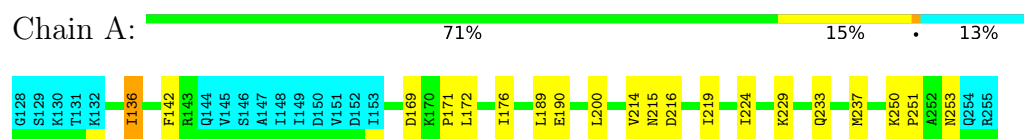
4.2.1 Score per residue for model 1

- Molecule 1: CG5884-PA



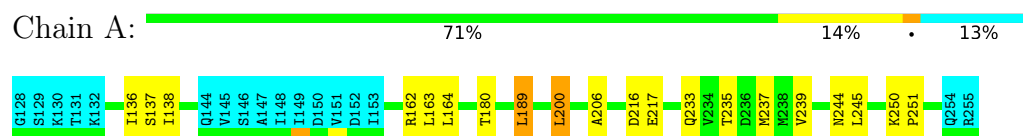
4.2.2 Score per residue for model 2

- Molecule 1: CG5884-PA



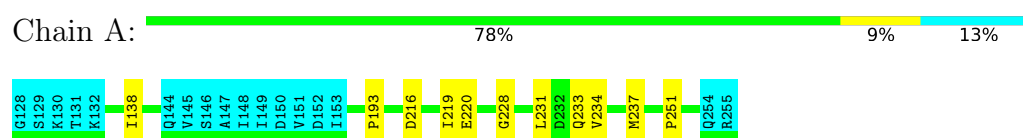
4.2.3 Score per residue for model 3

- Molecule 1: CG5884-PA



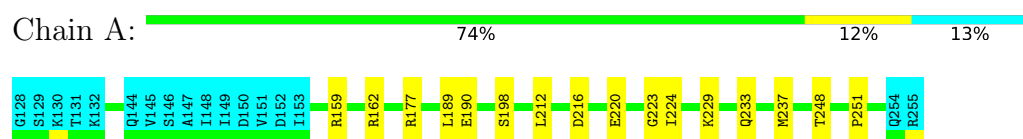
4.2.4 Score per residue for model 4

- Molecule 1: CG5884-PA



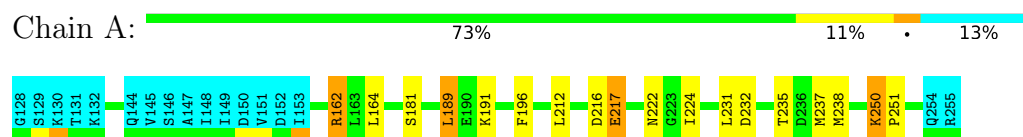
4.2.5 Score per residue for model 5

- Molecule 1: CG5884-PA



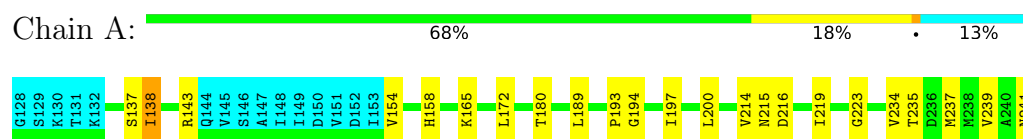
4.2.6 Score per residue for model 6

- Molecule 1: CG5884-PA



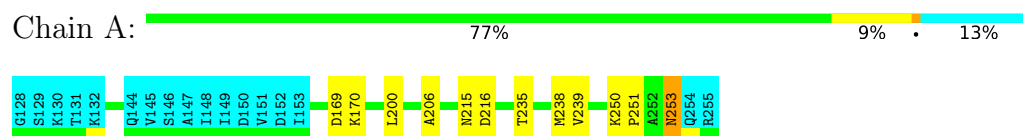
4.2.7 Score per residue for model 7

- Molecule 1: CG5884-PA



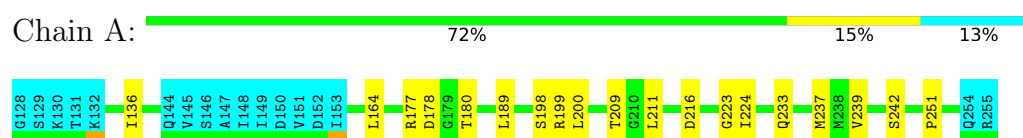
4.2.8 Score per residue for model 8

- Molecule 1: CG5884-PA



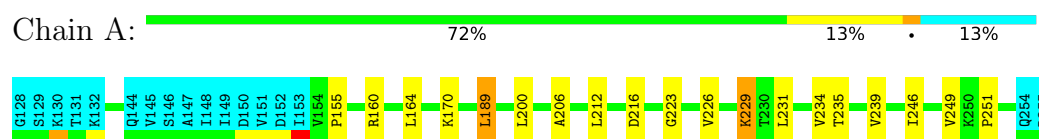
4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: CG5884-PA



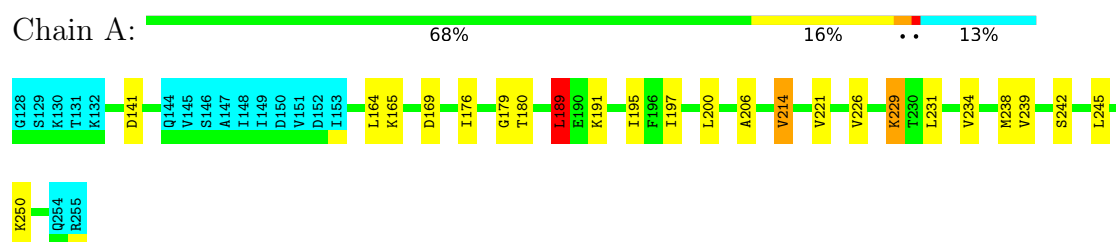
4.2.10 Score per residue for model 10

- Molecule 1: CG5884-PA



4.2.11 Score per residue for model 11

- Molecule 1: CG5884-PA



4.2.12 Score per residue for model 12

- Molecule 1: CG5884-PA





4.2.13 Score per residue for model 13

- Molecule 1: CG5884-PA

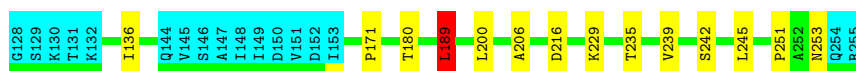
Chain A: 73% 12% .. 13%



4.2.14 Score per residue for model 14

- Molecule 1: CG5884-PA

Chain A: 76% 10% . 13%



4.2.15 Score per residue for model 15

- Molecule 1: CG5884-PA

Chain A: 72% 14% . 13%



4.2.16 Score per residue for model 16

- Molecule 1: CG5884-PA

Chain A: 70% 15% .. 13%



4.2.17 Score per residue for model 17

- Molecule 1: CG5884-PA

Chain A: 71% 15% . 13%



4.2.18 Score per residue for model 18

- Molecule 1: CG5884-PA



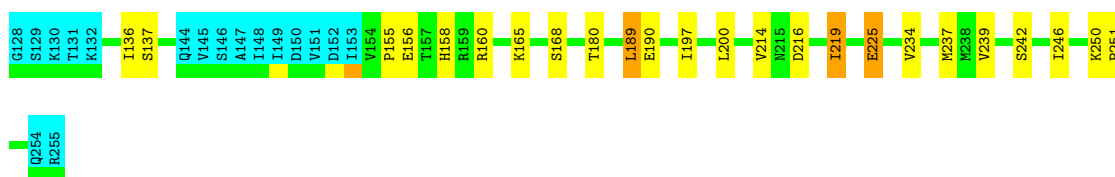
4.2.19 Score per residue for model 19

- Molecule 1: CG5884-PA



4.2.20 Score per residue for model 20

- Molecule 1: CG5884-PA



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	1.0.6
XPLOR-NIH	refinement	2.0.6

No chemical shift data was provided.

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	1.30±0.05	2±2/850 (0.3± 0.3%)	0.98±0.03	0±1/1155 (0.0± 0.1%)
All	All	1.30	48/17000 (0.3%)	0.98	7/23100 (0.0%)

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	241	ASN	N-CA	-7.46	1.39	1.46	7	1
1	A	137	SER	C-N	-7.38	1.26	1.33	7	4
1	A	137	SER	N-CA	-6.55	1.38	1.46	7	1
1	A	136	ILE	C-N	-6.54	1.24	1.33	2	1
1	A	138	ILE	N-CA	-6.50	1.41	1.46	7	4
1	A	193	PRO	C-N	-6.48	1.27	1.33	7	1
1	A	154	VAL	CA-CB	6.14	1.58	1.54	7	1
1	A	189	LEU	N-CA	-6.13	1.38	1.46	14	10
1	A	200	LEU	N-CA	-6.07	1.39	1.46	16	2
1	A	180	THR	N-CA	-5.91	1.39	1.46	19	6
1	A	158	HIS	C-N	-5.61	1.25	1.33	20	3
1	A	141	ASP	C-N	-5.50	1.26	1.33	11	1
1	A	191	LYS	C-N	-5.46	1.26	1.33	11	1
1	A	194	GLY	CA-C	-5.43	1.48	1.52	7	1
1	A	180	THR	C-N	-5.37	1.25	1.33	3	2
1	A	159	ARG	N-CA	-5.36	1.39	1.46	13	2
1	A	245	LEU	C-N	-5.28	1.26	1.33	14	1
1	A	200	LEU	C-N	-5.26	1.27	1.32	3	1
1	A	179	GLY	CA-C	-5.25	1.47	1.52	11	1
1	A	168	SER	N-CA	-5.21	1.39	1.46	15	1
1	A	250	LYS	CA-C	-5.13	1.48	1.52	3	1
1	A	154	VAL	N-CA	-5.13	1.42	1.46	17	1
1	A	136	ILE	N-CA	-5.05	1.40	1.46	14	1

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	211	LEU	N-CA-C	-7.83	103.87	113.50	18	1
1	A	216	ASP	N-CA-C	6.61	119.25	110.53	13	1
1	A	216	ASP	N-CA-CB	5.74	118.57	110.36	13	1
1	A	216	ASP	CA-CB-CG	5.69	118.29	112.60	13	1
1	A	154	VAL	N-CA-C	5.41	112.91	107.55	16	1
1	A	138	ILE	N-CA-C	5.32	113.13	107.76	12	1
1	A	219	ILE	CB-CA-C	-5.05	107.42	111.71	7	1

There are no chirality outliers.

There are no planarity outliers.

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	836	865	862	9±2
All	All	16720	17300	17240	179

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:239:VAL:HA	1:A:242:SER:OG	0.64	1.92	17	8
1:A:216:ASP:CG	1:A:251:PRO:HA	0.62	2.19	10	15
1:A:200:LEU:HD21	1:A:206:ALA:HB3	0.61	1.72	15	10
1:A:216:ASP:HB3	1:A:250:LYS:O	0.58	1.98	8	1
1:A:233:GLN:O	1:A:237:MET:HG3	0.57	2.00	2	8
1:A:229:LYS:HD2	1:A:229:LYS:C	0.56	2.25	11	2
1:A:177:ARG:HB2	1:A:198:SER:HB3	0.56	1.78	16	2
1:A:212:LEU:HA	1:A:216:ASP:OD2	0.55	2.02	6	2
1:A:216:ASP:OD1	1:A:251:PRO:HA	0.54	2.02	4	8
1:A:231:LEU:O	1:A:234:VAL:HG12	0.54	2.03	10	2
1:A:196:PHE:CE2	1:A:217:GLU:HG2	0.53	2.38	17	1
1:A:231:LEU:HD12	1:A:232:ASP:N	0.53	2.18	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:165:LYS:O	1:A:165:LYS:HD2	0.53	2.03	18	2
1:A:226:VAL:O	1:A:229:LYS:HG3	0.53	2.04	11	2
1:A:235:THR:O	1:A:239:VAL:HG23	0.51	2.04	3	8
1:A:165:LYS:HE2	1:A:168:SER:O	0.50	2.07	20	1
1:A:209:THR:OG1	1:A:211:LEU:HG	0.50	2.07	9	1
1:A:238:MET:SD	1:A:245:LEU:HD21	0.50	2.47	11	1
1:A:189:LEU:H	1:A:189:LEU:HD23	0.50	1.67	6	11
1:A:197:ILE:HB	1:A:214:VAL:HA	0.50	1.83	11	1
1:A:224:ILE:HG21	1:A:237:MET:SD	0.50	2.46	2	4
1:A:242:SER:HA	1:A:245:LEU:HB2	0.49	1.85	13	2
1:A:160:ARG:HA	1:A:247:ILE:O	0.49	2.08	13	1
1:A:162:ARG:HD3	1:A:162:ARG:H	0.49	1.68	5	2
1:A:176:ILE:HB	1:A:195:ILE:CG2	0.49	2.38	11	1
1:A:158:HIS:CE1	1:A:250:LYS:HE3	0.48	2.42	17	1
1:A:177:ARG:HG2	1:A:178:ASP:N	0.48	2.23	9	1
1:A:225:GLU:H	1:A:225:GLU:CD	0.48	2.16	20	1
1:A:160:ARG:HB2	1:A:246:ILE:CG2	0.48	2.39	15	2
1:A:212:LEU:HD21	1:A:249:VAL:CG2	0.48	2.39	10	1
1:A:197:ILE:HB	1:A:214:VAL:O	0.47	2.08	7	3
1:A:163:LEU:O	1:A:244:ASN:HA	0.47	2.10	3	1
1:A:156:GLU:HA	1:A:251:PRO:CG	0.47	2.39	20	2
1:A:181:SER:O	1:A:191:LYS:HA	0.47	2.10	6	1
1:A:177:ARG:CB	1:A:198:SER:HB3	0.47	2.39	16	1
1:A:226:VAL:HG12	1:A:237:MET:SD	0.47	2.49	18	1
1:A:163:LEU:O	1:A:245:LEU:HD23	0.47	2.09	19	1
1:A:178:ASP:HA	1:A:195:ILE:HG22	0.46	1.87	16	1
1:A:219:ILE:HD12	1:A:219:ILE:N	0.46	2.26	12	5
1:A:195:ILE:HD11	1:A:229:LYS:CE	0.46	2.40	11	1
1:A:198:SER:C	1:A:199:ARG:HD2	0.46	2.35	9	1
1:A:216:ASP:HB3	1:A:252:ALA:N	0.46	2.25	13	1
1:A:160:ARG:HB3	1:A:246:ILE:CG2	0.45	2.42	10	1
1:A:193:PRO:HD2	1:A:228:GLY:HA2	0.45	1.89	16	1
1:A:191:LYS:N	1:A:191:LYS:HD2	0.44	2.27	16	1
1:A:234:VAL:HA	1:A:237:MET:SD	0.44	2.52	20	1
1:A:176:ILE:O	1:A:176:ILE:HD12	0.44	2.13	15	1
1:A:142:PHE:C	1:A:143:ARG:HD2	0.44	2.37	13	1
1:A:159:ARG:NE	1:A:159:ARG:HA	0.44	2.28	5	2
1:A:229:LYS:HA	1:A:229:LYS:HE2	0.43	1.89	14	4
1:A:174:PHE:HE1	1:A:238:MET:SD	0.43	2.36	15	1
1:A:221:VAL:HG13	1:A:238:MET:SD	0.43	2.52	11	1
1:A:164:LEU:HB2	1:A:166:HIS:CE1	0.43	2.49	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:219:ILE:HD11	1:A:250:LYS:CB	0.43	2.43	18	2
1:A:231:LEU:HA	1:A:234:VAL:HG12	0.43	1.91	4	1
1:A:220:GLU:H	1:A:248:THR:HB	0.43	1.72	19	2
1:A:239:VAL:HA	1:A:242:SER:HG	0.43	1.74	16	1
1:A:189:LEU:HD12	1:A:189:LEU:O	0.42	2.13	20	2
1:A:230:THR:O	1:A:234:VAL:HG23	0.42	2.14	19	1
1:A:189:LEU:H	1:A:189:LEU:HD13	0.42	1.74	16	2
1:A:217:GLU:OE2	1:A:250:LYS:HB3	0.42	2.15	6	1
1:A:170:LYS:HD3	1:A:170:LYS:H	0.42	1.75	8	1
1:A:219:ILE:HD11	1:A:250:LYS:HB2	0.42	1.90	12	1
1:A:189:LEU:O	1:A:189:LEU:HD22	0.42	2.14	16	1
1:A:235:THR:HA	1:A:238:MET:SD	0.42	2.54	8	1
1:A:196:PHE:CD2	1:A:217:GLU:HB3	0.42	2.50	6	1
1:A:234:VAL:HA	1:A:237:MET:HG2	0.42	1.92	18	1
1:A:164:LEU:O	1:A:164:LEU:HD12	0.42	2.15	10	1
1:A:251:PRO:HB2	1:A:253:ASN:ND2	0.42	2.30	2	1
1:A:200:LEU:CD1	1:A:206:ALA:HB3	0.41	2.45	16	2
1:A:160:ARG:H	1:A:160:ARG:HD3	0.41	1.75	15	1
1:A:231:LEU:HD22	1:A:232:ASP:N	0.41	2.29	15	1
1:A:183:ARG:O	1:A:189:LEU:HA	0.41	2.15	18	1
1:A:234:VAL:O	1:A:237:MET:HB3	0.41	2.16	7	1
1:A:189:LEU:HD22	1:A:189:LEU:O	0.41	2.16	12	1
1:A:219:ILE:HG22	1:A:220:GLU:HG3	0.41	1.91	4	1
1:A:224:ILE:CG2	1:A:237:MET:HE3	0.41	2.46	17	1
1:A:193:PRO:O	1:A:228:GLY:HA2	0.41	2.16	4	1
1:A:177:ARG:HB3	1:A:198:SER:HB3	0.41	1.92	5	1
1:A:218:VAL:HA	1:A:248:THR:O	0.41	2.16	19	1
1:A:162:ARG:HA	1:A:245:LEU:O	0.40	2.15	3	1
1:A:233:GLN:O	1:A:237:MET:HB2	0.40	2.16	4	1
1:A:163:LEU:HD23	1:A:164:LEU:N	0.40	2.32	19	1
1:A:235:THR:HA	1:A:238:MET:HG2	0.40	1.94	6	1
1:A:165:LYS:HG2	1:A:168:SER:O	0.40	2.15	1	1
1:A:165:LYS:HG3	1:A:168:SER:O	0.40	2.17	13	1
1:A:172:LEU:H	1:A:172:LEU:HD13	0.40	1.76	19	1
1:A:143:ARG:HE	1:A:143:ARG:HA	0.40	1.76	17	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	111/128 (87%)	101±3 (91±3%)	8±3 (8±3%)	2±1 (1±1%)	11	58
All	All	2220/2560 (87%)	2020 (91%)	169 (8%)	31 (1%)	11	58

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	169	ASP	4
1	A	223	GLY	4
1	A	222	ASN	3
1	A	156	GLU	3
1	A	142	PHE	2
1	A	171	PRO	2
1	A	214	VAL	2
1	A	172	LEU	2
1	A	253	ASN	2
1	A	136	ILE	2
1	A	170	LYS	2
1	A	143	ARG	1
1	A	210	GLY	1
1	A	137	SER	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	94/109 (86%)	91±2 (97±2%)	3±2 (3±2%)	38	86
All	All	1880/2180 (86%)	1826 (97%)	54 (3%)	38	86

All 27 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	164	LEU	5
1	A	189	LEU	5
1	A	215	ASN	4
1	A	136	ILE	3
1	A	190	GLU	3
1	A	200	LEU	3
1	A	250	LYS	3
1	A	156	GLU	2
1	A	159	ARG	2
1	A	219	ILE	2
1	A	172	LEU	2
1	A	176	ILE	2
1	A	217	GLU	2
1	A	253	ASN	2
1	A	229	LYS	2
1	A	195	ILE	1
1	A	162	ARG	1
1	A	138	ILE	1
1	A	165	LYS	1
1	A	224	ILE	1
1	A	180	THR	1
1	A	170	LYS	1
1	A	207	GLU	1
1	A	216	ASP	1
1	A	231	LEU	1
1	A	249	VAL	1
1	A	225	GLU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided