



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 05:40 AM BST

PDB ID : 2RQ0
Title : Solution Structure of Mouse Lipocalin-type Prostaglandin D Synthase Possessing the Intrinsic Disulfide Bond
Authors : Miyamoto, Y.; Nishimura, S.; Inui, T.
Deposited on : 2008-12-24

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

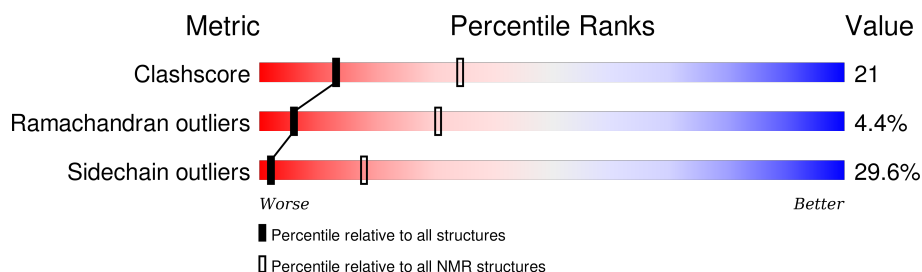
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 70%.

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	167	

2 Ensemble composition and analysis ⓘ

This entry contains 10 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:30-A:182 (153)	0.74	10

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 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 6, 8, 10
2	3, 4
Single-model clusters	7; 9

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2591 atoms, of which 1280 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Prostaglandin-H2 D-isomerase.

Mol	Chain	Residues	Atoms						Trace
1	A	167	Total	C	H	N	O	S	0
			2591	828	1280	223	255	5	

There are 3 discrepancies between the modelled and reference sequences:

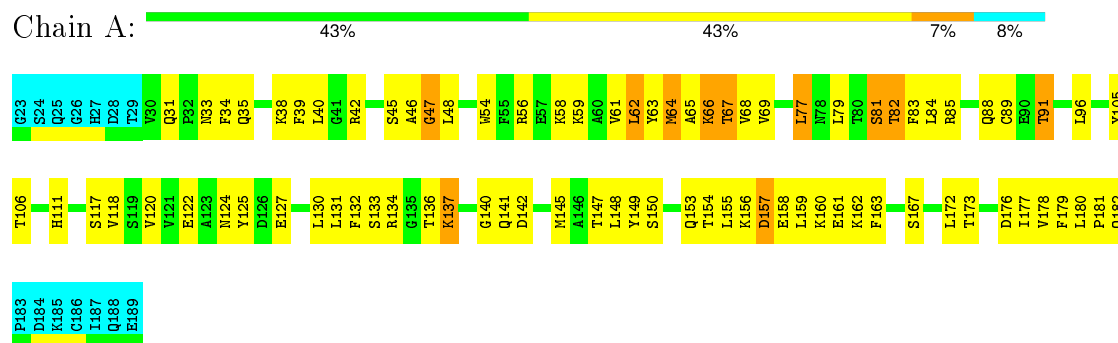
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	GLY	-	EXPRESSION TAG	UNP O09114
A	24	SER	-	EXPRESSION TAG	UNP O09114
A	65	ALA	CYS	ENGINEERED	UNP O09114

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Prostaglandin-H2 D-isomerase

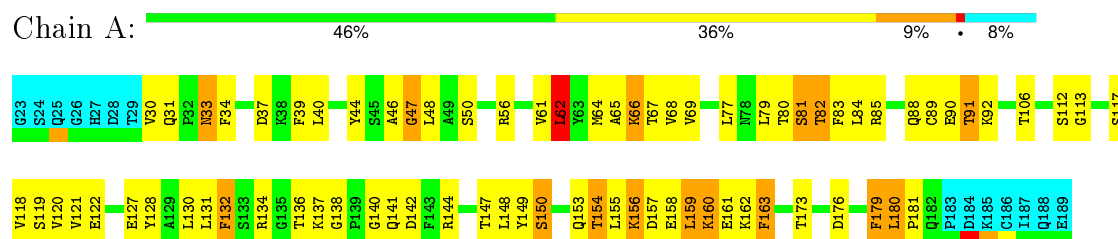


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

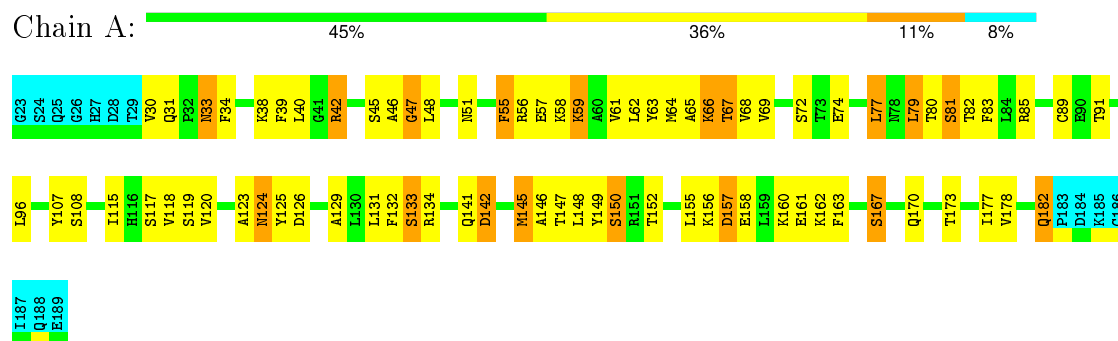
4.2.1 Score per residue for model 1

- Molecule 1: Prostaglandin-H2 D-isomerase



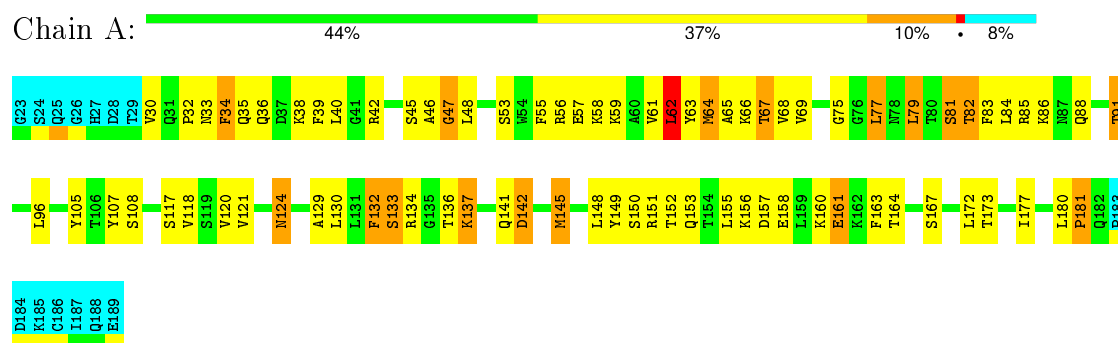
4.2.2 Score per residue for model 2

- Molecule 1: Prostaglandin-H2 D-isomerase



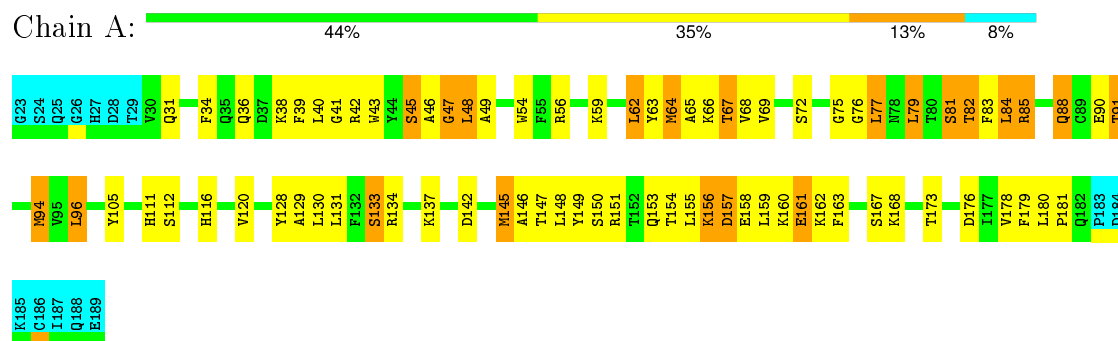
4.2.3 Score per residue for model 3

- Molecule 1: Prostaglandin-H2 D-isomerase



4.2.4 Score per residue for model 4

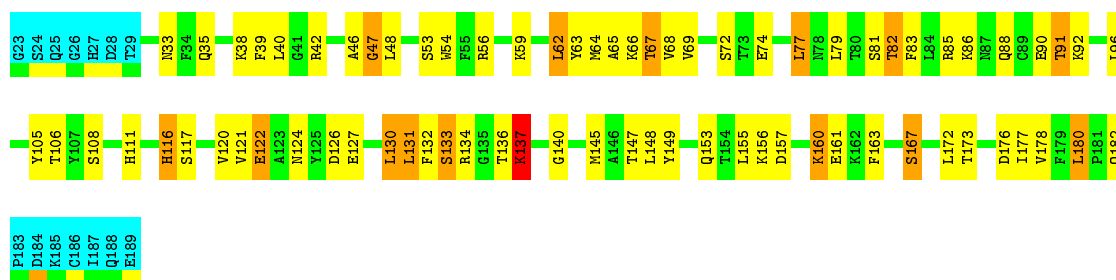
- Molecule 1: Prostaglandin-H2 D-isomerase



4.2.5 Score per residue for model 5

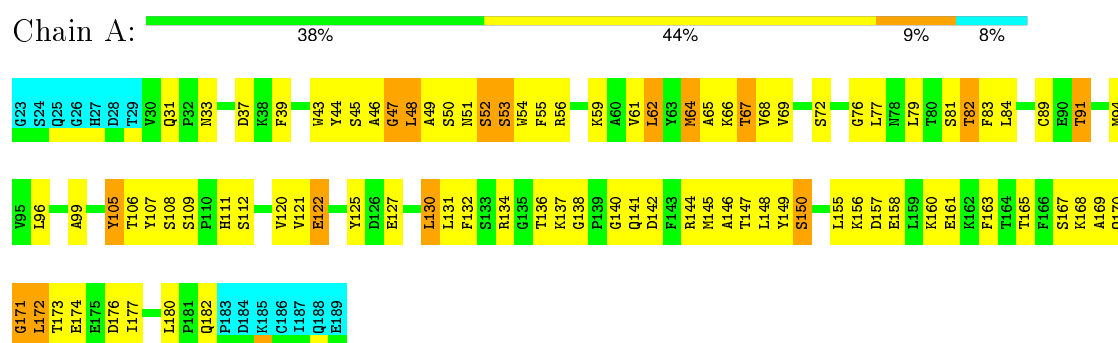
- Molecule 1: Prostaglandin-H2 D-isomerase





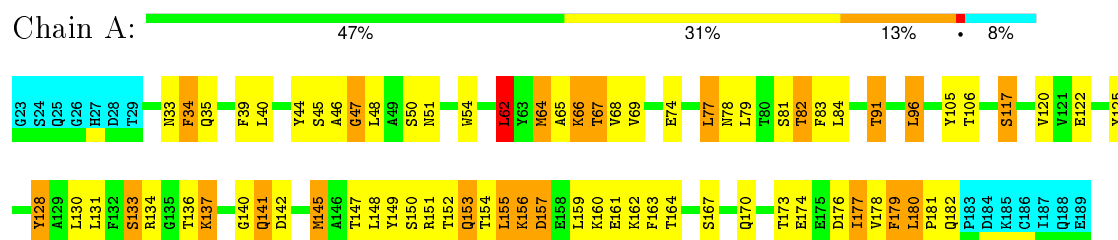
4.2.6 Score per residue for model 6

- Molecule 1: Prostaglandin-H2 D-isomerase



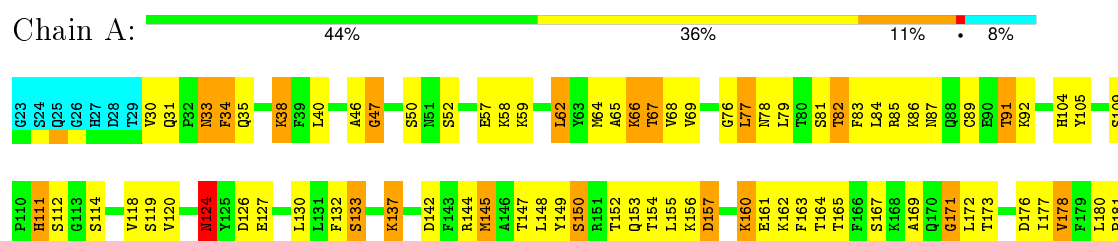
4.2.7 Score per residue for model 7

- Molecule 1: Prostaglandin-H2 D-isomerase



4.2.8 Score per residue for model 8

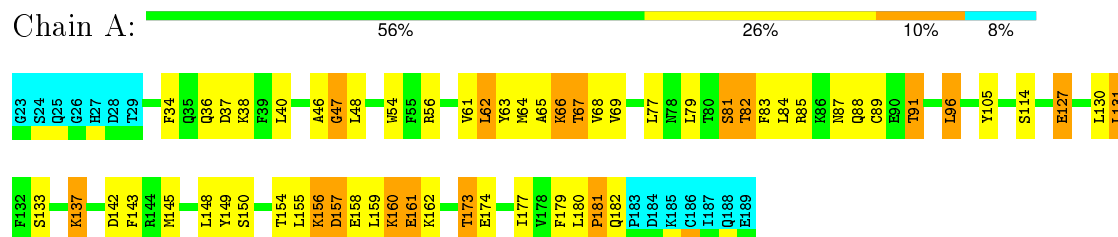
- Molecule 1: Prostaglandin-H2 D-isomerase



Q182
P183
D184
K185
G186
I187
Q188
E189

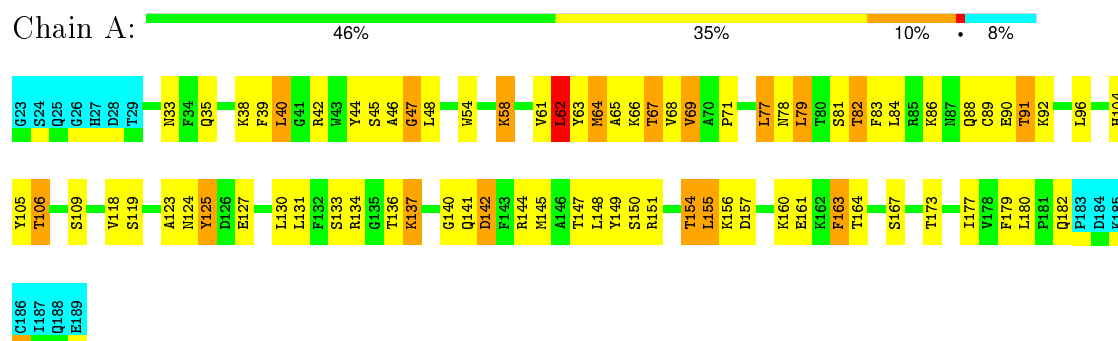
4.2.9 Score per residue for model 9

- Molecule 1: Prostaglandin-H2 D-isomerase



4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Prostaglandin-H2 D-isomerase



5 Refinement protocol and experimental data overview

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

Of the 3000 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.2
CNS	structure solution	1.2

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)	BMRB entry 11062
Number of chemical shift lists	1
Total number of shifts	1471
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	70%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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 ⓘ

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	1206	1187	1184	51±4
All	All	12060	11870	11840	512

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 21.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:LEU:HD21	1:A:96:LEU:HD13	0.88	1.45	6	2
1:A:155:LEU:HD13	1:A:179:PHE:CD1	0.82	2.10	10	1
1:A:64:MET:O	1:A:83:PHE:HA	0.81	1.75	4	10
1:A:58:LYS:O	1:A:61:VAL:HG12	0.80	1.77	2	2
1:A:69:VAL:HG22	1:A:79:LEU:HB3	0.79	1.55	4	8
1:A:96:LEU:HD21	1:A:105:TYR:CD1	0.78	2.13	5	1
1:A:131:LEU:HD13	1:A:132:PHE:N	0.78	1.93	1	1
1:A:120:VAL:HG22	1:A:131:LEU:HD13	0.76	1.56	6	1
1:A:69:VAL:HG12	1:A:77:LEU:HB3	0.74	1.57	6	9
1:A:68:VAL:O	1:A:79:LEU:HA	0.73	1.83	9	10
1:A:148:LEU:HD22	1:A:163:PHE:CD1	0.73	2.18	1	3
1:A:48:LEU:HD22	1:A:180:LEU:HD11	0.73	1.58	9	1
1:A:48:LEU:HD13	1:A:180:LEU:HD11	0.72	1.60	3	2
1:A:39:PHE:O	1:A:77:LEU:HD13	0.72	1.85	2	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:VAL:HG22	1:A:79:LEU:HB2	0.71	1.62	7	2
1:A:79:LEU:CD2	1:A:96:LEU:HD13	0.70	2.17	6	2
1:A:69:VAL:HG12	1:A:77:LEU:CB	0.70	2.16	6	9
1:A:153:GLN:O	1:A:155:LEU:HD23	0.69	1.86	7	3
1:A:62:LEU:HD23	1:A:181:PRO:CB	0.69	2.17	3	1
1:A:172:LEU:HD11	1:A:176:ASP:HB2	0.69	1.64	6	1
1:A:46:ALA:HB3	1:A:149:TYR:HA	0.69	1.63	5	10
1:A:67:THR:HG23	1:A:81:SER:CB	0.68	2.17	2	3
1:A:67:THR:CG2	1:A:79:LEU:HD13	0.67	2.19	9	2
1:A:79:LEU:HD23	1:A:96:LEU:CD1	0.67	2.20	9	1
1:A:62:LEU:HD12	1:A:62:LEU:O	0.67	1.90	10	1
1:A:82:THR:CG2	1:A:91:THR:HG23	0.67	2.19	5	5
1:A:69:VAL:HG12	1:A:77:LEU:HB2	0.67	1.66	10	3
1:A:76:GLY:C	1:A:77:LEU:HD12	0.66	2.10	6	1
1:A:48:LEU:HD13	1:A:180:LEU:CD1	0.66	2.20	3	1
1:A:156:LYS:O	1:A:160:LYS:N	0.66	2.28	5	10
1:A:130:LEU:C	1:A:131:LEU:HD22	0.65	2.12	7	1
1:A:61:VAL:O	1:A:62:LEU:HD12	0.64	1.91	3	1
1:A:99:ALA:HB2	1:A:106:THR:HG23	0.64	1.67	6	1
1:A:79:LEU:HD23	1:A:96:LEU:HD12	0.64	1.68	9	1
1:A:128:TYR:CD1	1:A:159:LEU:HD21	0.64	2.28	1	1
1:A:69:VAL:HG22	1:A:79:LEU:HD12	0.64	1.68	7	2
1:A:64:MET:O	1:A:83:PHE:CA	0.64	2.46	4	10
1:A:67:THR:CG2	1:A:79:LEU:HD21	0.64	2.22	8	2
1:A:67:THR:HG22	1:A:79:LEU:HD21	0.63	1.70	7	2
1:A:131:LEU:HD21	1:A:149:TYR:CD1	0.63	2.29	5	1
1:A:62:LEU:HD13	1:A:181:PRO:HG3	0.63	1.69	8	1
1:A:155:LEU:HD13	1:A:179:PHE:CG	0.63	2.28	10	1
1:A:120:VAL:HG23	1:A:130:LEU:O	0.63	1.93	5	1
1:A:69:VAL:HG22	1:A:79:LEU:CB	0.62	2.23	6	9
1:A:106:THR:HG22	1:A:117:SER:HA	0.62	1.69	5	2
1:A:63:TYR:O	1:A:180:LEU:HD13	0.62	1.95	10	1
1:A:67:THR:HG23	1:A:81:SER:HB3	0.61	1.71	2	1
1:A:39:PHE:O	1:A:77:LEU:HD22	0.61	1.96	7	1
1:A:30:VAL:HG13	1:A:120:VAL:O	0.61	1.95	3	2
1:A:40:LEU:HG	1:A:77:LEU:HD23	0.61	1.73	3	1
1:A:40:LEU:HD12	1:A:40:LEU:O	0.60	1.96	9	2
1:A:77:LEU:HD22	1:A:77:LEU:N	0.60	2.09	8	1
1:A:40:LEU:CD2	1:A:77:LEU:HD23	0.60	2.25	3	1
1:A:48:LEU:HD22	1:A:55:PHE:CE2	0.60	2.32	2	1
1:A:77:LEU:N	1:A:77:LEU:HD22	0.60	2.11	4	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:LEU:HD12	1:A:160:LYS:CD	0.60	2.27	9	1
1:A:107:TYR:O	1:A:115:ILE:HG23	0.60	1.96	2	1
1:A:130:LEU:HD23	1:A:148:LEU:CD1	0.59	2.27	1	1
1:A:155:LEU:HD12	1:A:179:PHE:CE2	0.59	2.32	7	1
1:A:118:VAL:CG1	1:A:131:LEU:HD11	0.59	2.27	1	1
1:A:128:TYR:CD1	1:A:159:LEU:HD11	0.58	2.34	7	1
1:A:79:LEU:O	1:A:79:LEU:HD12	0.58	1.99	9	1
1:A:130:LEU:HD12	1:A:148:LEU:HD13	0.58	1.76	9	1
1:A:47:GLY:O	1:A:147:THR:HG23	0.58	1.98	4	2
1:A:154:THR:HG23	1:A:182:GLN:OE1	0.57	1.99	10	1
1:A:77:LEU:HD23	1:A:77:LEU:N	0.57	2.13	10	1
1:A:120:VAL:HG22	1:A:131:LEU:CD2	0.57	2.30	1	1
1:A:120:VAL:HG22	1:A:131:LEU:HD12	0.57	1.76	4	1
1:A:148:LEU:HD22	1:A:163:PHE:HB2	0.57	1.75	8	2
1:A:48:LEU:HD22	1:A:180:LEU:HD12	0.57	1.75	1	1
1:A:62:LEU:HD23	1:A:180:LEU:HD23	0.57	1.76	6	1
1:A:65:ALA:HB2	1:A:83:PHE:HB3	0.57	1.77	3	10
1:A:38:LYS:CD	1:A:123:ALA:HB2	0.56	2.29	2	1
1:A:155:LEU:HD12	1:A:179:PHE:CE1	0.56	2.35	4	1
1:A:48:LEU:HD22	1:A:180:LEU:HD21	0.56	1.77	3	1
1:A:48:LEU:CD1	1:A:180:LEU:HD11	0.56	2.29	3	1
1:A:77:LEU:HD12	1:A:77:LEU:N	0.56	2.15	3	1
1:A:136:THR:HG22	1:A:140:GLY:HA2	0.56	1.76	1	5
1:A:62:LEU:HD23	1:A:180:LEU:CD2	0.56	2.30	6	1
1:A:67:THR:HG22	1:A:79:LEU:HB2	0.56	1.77	3	5
1:A:155:LEU:HD12	1:A:160:LYS:HD3	0.55	1.77	9	1
1:A:154:THR:HG23	1:A:155:LEU:N	0.55	2.16	1	1
1:A:167:SER:HB3	1:A:177:ILE:HD11	0.55	1.77	3	1
1:A:131:LEU:HD21	1:A:149:TYR:CD2	0.55	2.37	9	1
1:A:46:ALA:HB3	1:A:150:SER:N	0.55	2.17	8	9
1:A:62:LEU:HD23	1:A:181:PRO:CG	0.55	2.32	3	1
1:A:172:LEU:HD22	1:A:176:ASP:HB2	0.55	1.79	5	1
1:A:40:LEU:CG	1:A:77:LEU:HD23	0.55	2.31	3	1
1:A:69:VAL:CG2	1:A:79:LEU:HD12	0.55	2.32	7	2
1:A:77:LEU:N	1:A:77:LEU:HD12	0.55	2.16	6	1
1:A:177:ILE:HD12	1:A:177:ILE:N	0.55	2.17	8	1
1:A:30:VAL:HG13	1:A:121:VAL:HA	0.54	1.80	1	1
1:A:167:SER:CB	1:A:177:ILE:HD11	0.54	2.32	10	3
1:A:115:ILE:N	1:A:115:ILE:HD12	0.54	2.17	2	1
1:A:48:LEU:HD13	1:A:180:LEU:HD12	0.53	1.78	6	1
1:A:124:ASN:N	1:A:129:ALA:HB2	0.53	2.18	2	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:PHE:CD2	1:A:77:LEU:HD11	0.53	2.38	5	1
1:A:118:VAL:HG12	1:A:133:SER:HA	0.53	1.80	2	2
1:A:172:LEU:HD11	1:A:176:ASP:CB	0.53	2.32	6	1
1:A:36:GLN:HB2	1:A:77:LEU:HD21	0.53	1.79	3	1
1:A:118:VAL:HG23	1:A:132:PHE:O	0.53	2.03	8	2
1:A:46:ALA:O	1:A:47:GLY:O	0.53	2.26	4	9
1:A:59:LYS:HG3	1:A:178:VAL:HG21	0.53	1.80	2	1
1:A:69:VAL:HA	1:A:79:LEU:HA	0.52	1.81	5	10
1:A:157:ASP:O	1:A:161:GLU:N	0.52	2.42	9	10
1:A:96:LEU:HD23	1:A:105:TYR:CD2	0.52	2.39	6	1
1:A:76:GLY:C	1:A:77:LEU:HD13	0.52	2.25	8	1
1:A:124:ASN:H	1:A:129:ALA:HB2	0.52	1.64	2	1
1:A:84:LEU:O	1:A:84:LEU:HD23	0.52	2.05	7	2
1:A:148:LEU:HD22	1:A:163:PHE:CG	0.52	2.39	3	2
1:A:155:LEU:HD11	1:A:179:PHE:HB3	0.51	1.80	1	1
1:A:96:LEU:HD11	1:A:105:TYR:HB3	0.51	1.82	7	2
1:A:163:PHE:CD1	1:A:177:ILE:HD13	0.51	2.41	6	1
1:A:154:THR:O	1:A:154:THR:HG23	0.51	2.06	4	2
1:A:167:SER:O	1:A:171:GLY:N	0.51	2.43	8	2
1:A:49:ALA:HB2	1:A:163:PHE:CE2	0.51	2.41	4	1
1:A:66:LYS:O	1:A:81:SER:HA	0.50	2.06	5	10
1:A:82:THR:HG22	1:A:91:THR:HA	0.50	1.84	9	8
1:A:106:THR:HG22	1:A:117:SER:HB3	0.50	1.82	7	1
1:A:79:LEU:HD21	1:A:107:TYR:HE1	0.50	1.65	3	1
1:A:49:ALA:HB2	1:A:163:PHE:HE2	0.50	1.66	4	1
1:A:39:PHE:CD2	1:A:105:TYR:CZ	0.50	3.00	4	1
1:A:130:LEU:N	1:A:130:LEU:HD12	0.50	2.22	4	1
1:A:121:VAL:HG11	1:A:130:LEU:HD22	0.50	1.83	6	1
1:A:47:GLY:N	1:A:148:LEU:O	0.49	2.45	3	10
1:A:48:LEU:CD1	1:A:180:LEU:HD12	0.49	2.36	4	1
1:A:67:THR:HG21	1:A:79:LEU:HD13	0.49	1.84	9	4
1:A:155:LEU:O	1:A:155:LEU:HG	0.49	2.07	7	2
1:A:69:VAL:HG11	1:A:77:LEU:HD12	0.49	1.84	10	1
1:A:69:VAL:HG22	1:A:79:LEU:CD1	0.49	2.37	7	2
1:A:48:LEU:HB2	1:A:180:LEU:HD11	0.49	1.84	7	1
1:A:64:MET:O	1:A:83:PHE:CB	0.49	2.61	10	10
1:A:177:ILE:N	1:A:177:ILE:HD13	0.48	2.23	7	1
1:A:96:LEU:HD21	1:A:105:TYR:CG	0.48	2.44	5	1
1:A:129:ALA:O	1:A:148:LEU:HD12	0.48	2.08	4	1
1:A:38:LYS:HD2	1:A:123:ALA:HB2	0.48	1.86	2	1
1:A:65:ALA:CA	1:A:83:PHE:HB3	0.48	2.39	10	10

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:THR:HG22	1:A:79:LEU:CD2	0.48	2.38	8	2
1:A:62:LEU:HD22	1:A:181:PRO:HD2	0.48	1.84	9	1
1:A:121:VAL:HG13	1:A:122:GLU:N	0.48	2.23	6	2
1:A:85:ARG:N	1:A:88:GLN:O	0.48	2.45	4	1
1:A:155:LEU:HG	1:A:155:LEU:O	0.48	2.09	8	3
1:A:34:PHE:CE2	1:A:120:VAL:HG13	0.47	2.44	3	1
1:A:65:ALA:HA	1:A:83:PHE:CA	0.47	2.39	3	10
1:A:155:LEU:HD12	1:A:179:PHE:CD2	0.47	2.45	7	1
1:A:42:ARG:HG3	1:A:68:VAL:HG22	0.47	1.87	2	2
1:A:128:TYR:HD2	1:A:148:LEU:HD11	0.47	1.70	4	1
1:A:48:LEU:HD22	1:A:178:VAL:HB	0.47	1.86	5	1
1:A:38:LYS:CE	1:A:120:VAL:HG11	0.47	2.40	8	1
1:A:167:SER:OG	1:A:177:ILE:HD11	0.47	2.10	2	2
1:A:40:LEU:HD22	1:A:71:PRO:HD3	0.47	1.85	10	1
1:A:55:PHE:CD1	1:A:56:ARG:N	0.47	2.82	6	1
1:A:137:LYS:CE	1:A:143:PHE:CD1	0.47	2.98	9	1
1:A:128:TYR:CE2	1:A:130:LEU:HD11	0.47	2.45	4	1
1:A:155:LEU:CD1	1:A:179:PHE:CD2	0.46	2.99	7	1
1:A:64:MET:O	1:A:64:MET:HE2	0.46	2.11	4	1
1:A:46:ALA:HB3	1:A:149:TYR:CA	0.46	2.39	5	5
1:A:165:THR:O	1:A:169:ALA:HB2	0.46	2.10	6	2
1:A:49:ALA:HB3	1:A:146:ALA:HB3	0.46	1.87	6	1
1:A:84:LEU:HD23	1:A:84:LEU:O	0.46	2.10	8	1
1:A:77:LEU:HB2	1:A:96:LEU:HD21	0.46	1.86	2	1
1:A:79:LEU:HD21	1:A:96:LEU:CD1	0.46	2.36	4	1
1:A:65:ALA:CB	1:A:83:PHE:HB3	0.46	2.41	1	6
1:A:80:THR:HG23	1:A:92:LYS:O	0.46	2.11	1	1
1:A:131:LEU:HD21	1:A:149:TYR:HD2	0.45	1.71	9	1
1:A:76:GLY:O	1:A:77:LEU:HD13	0.45	2.12	4	1
1:A:160:LYS:CG	1:A:179:PHE:CD1	0.45	2.99	9	1
1:A:84:LEU:C	1:A:84:LEU:HD23	0.45	2.31	7	1
1:A:128:TYR:CG	1:A:159:LEU:HD21	0.45	2.47	1	1
1:A:130:LEU:HG	1:A:148:LEU:HD12	0.45	1.88	5	1
1:A:34:PHE:CE2	1:A:105:TYR:CE1	0.45	3.05	8	1
1:A:161:GLU:HA	1:A:164:THR:HG22	0.45	1.88	10	2
1:A:163:PHE:CD2	1:A:177:ILE:CG2	0.45	3.00	7	1
1:A:96:LEU:HD12	1:A:106:THR:O	0.45	2.12	10	1
1:A:96:LEU:HD22	1:A:105:TYR:HB3	0.45	1.88	9	1
1:A:130:LEU:HD23	1:A:148:LEU:HD13	0.45	1.89	1	1
1:A:163:PHE:CE2	1:A:177:ILE:CG2	0.45	3.00	7	1
1:A:62:LEU:HD23	1:A:181:PRO:HG3	0.44	1.87	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:LEU:H	1:A:155:LEU:HD23	0.44	1.73	4	1
1:A:48:LEU:CD2	1:A:180:LEU:HD11	0.44	2.37	9	1
1:A:79:LEU:HD11	1:A:94:MET:HG3	0.44	1.89	4	1
1:A:155:LEU:HD12	1:A:179:PHE:HE1	0.44	1.71	4	1
1:A:47:GLY:O	1:A:48:LEU:HD12	0.44	2.12	3	1
1:A:39:PHE:CD2	1:A:40:LEU:HD23	0.44	2.48	1	1
1:A:65:ALA:HB2	1:A:83:PHE:HD2	0.44	1.73	9	2
1:A:136:THR:O	1:A:141:GLN:N	0.44	2.51	7	2
1:A:52:SER:O	1:A:53:SER:CB	0.43	2.66	6	1
1:A:62:LEU:HD23	1:A:181:PRO:HB3	0.43	1.89	4	1
1:A:82:THR:CG2	1:A:91:THR:HG22	0.43	2.43	9	2
1:A:62:LEU:HD11	1:A:181:PRO:CG	0.43	2.43	1	1
1:A:176:ASP:C	1:A:177:ILE:HD13	0.43	2.33	7	1
1:A:133:SER:N	1:A:145:MET:O	0.43	2.50	10	4
1:A:48:LEU:HD12	1:A:180:LEU:HD11	0.43	1.91	5	1
1:A:68:VAL:C	1:A:79:LEU:HA	0.43	2.34	3	5
1:A:30:VAL:HG21	1:A:104:HIS:NE2	0.43	2.29	8	1
1:A:34:PHE:CD1	1:A:34:PHE:O	0.43	2.71	2	1
1:A:173:THR:O	1:A:177:ILE:HD12	0.43	2.14	9	1
1:A:79:LEU:HD21	1:A:107:TYR:CE1	0.43	2.46	3	1
1:A:130:LEU:HD22	1:A:132:PHE:CZ	0.43	2.49	5	1
1:A:39:PHE:CE1	1:A:77:LEU:HD22	0.43	2.48	10	1
1:A:120:VAL:HG22	1:A:131:LEU:CD1	0.42	2.42	4	1
1:A:82:THR:CG2	1:A:91:THR:CG2	0.42	2.97	10	3
1:A:155:LEU:HD11	1:A:180:LEU:O	0.42	2.13	8	1
1:A:155:LEU:CD1	1:A:179:PHE:CE2	0.42	3.03	7	1
1:A:130:LEU:HD12	1:A:148:LEU:CD1	0.42	2.44	6	1
1:A:47:GLY:HA3	1:A:148:LEU:HB3	0.42	1.92	7	6
1:A:77:LEU:CD2	1:A:77:LEU:N	0.42	2.80	8	1
1:A:133:SER:O	1:A:145:MET:N	0.42	2.53	3	3
1:A:128:TYR:N	1:A:128:TYR:CD1	0.42	2.86	7	1
1:A:121:VAL:HB	1:A:130:LEU:HD22	0.42	1.90	3	1
1:A:67:THR:HA	1:A:80:THR:O	0.42	2.14	2	1
1:A:65:ALA:HA	1:A:83:PHE:HA	0.42	1.91	3	1
1:A:38:LYS:HE3	1:A:123:ALA:HB2	0.41	1.92	10	1
1:A:63:TYR:CD1	1:A:63:TYR:O	0.41	2.73	9	1
1:A:49:ALA:HB3	1:A:146:ALA:O	0.41	2.14	4	1
1:A:63:TYR:O	1:A:180:LEU:HD21	0.41	2.16	4	1
1:A:61:VAL:C	1:A:62:LEU:HD12	0.41	2.36	3	1
1:A:36:GLN:O	1:A:40:LEU:HD23	0.41	2.15	9	1
1:A:67:THR:CG2	1:A:79:LEU:CD1	0.41	2.98	6	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:160:LYS:CD	1:A:179:PHE:CD2	0.41	3.03	7	1
1:A:123:ALA:O	1:A:125:TYR:N	0.41	2.53	10	2
1:A:59:LYS:HE2	1:A:178:VAL:HG11	0.41	1.92	8	1
1:A:131:LEU:HD11	1:A:149:TYR:HE2	0.41	1.76	9	1
1:A:44:TYR:O	1:A:46:ALA:N	0.41	2.54	1	2
1:A:42:ARG:HA	1:A:68:VAL:HG22	0.41	1.92	3	1
1:A:61:VAL:HB	1:A:63:TYR:CZ	0.41	2.50	3	1
1:A:96:LEU:HD21	1:A:105:TYR:HD2	0.41	1.74	3	1
1:A:42:ARG:HD3	1:A:68:VAL:HG21	0.41	1.92	5	1
1:A:39:PHE:CE1	1:A:77:LEU:HD21	0.41	2.50	1	1
1:A:41:GLY:O	1:A:43:TRP:CD1	0.41	2.74	4	1
1:A:130:LEU:HA	1:A:148:LEU:HD12	0.41	1.93	10	1
1:A:163:PHE:CD1	1:A:177:ILE:HG21	0.41	2.50	10	1
1:A:160:LYS:HG3	1:A:179:PHE:CD1	0.41	2.51	9	1
1:A:107:TYR:CE2	1:A:109:SER:OG	0.41	2.74	6	1
1:A:44:TYR:CE1	1:A:45:SER:O	0.40	2.74	10	1
1:A:40:LEU:HA	1:A:69:VAL:O	0.40	2.16	1	1
1:A:34:PHE:CE1	1:A:120:VAL:CG2	0.40	3.03	7	1
1:A:124:ASN:O	1:A:126:ASP:N	0.40	2.51	8	1
1:A:116:HIS:CD2	1:A:134:ARG:O	0.40	2.74	5	1
1:A:72:SER:N	1:A:76:GLY:O	0.40	2.55	4	1
1:A:45:SER:O	1:A:180:LEU:HD13	0.40	2.17	4	1
1:A:62:LEU:HD23	1:A:181:PRO:HG2	0.40	1.93	3	1
1:A:136:THR:O	1:A:137:LYS:O	0.40	2.39	5	1
1:A:120:VAL:HG13	1:A:131:LEU:HD23	0.40	1.91	2	1
1:A:63:TYR:O	1:A:63:TYR:CD1	0.40	2.75	2	1
1:A:43:TRP:N	1:A:67:THR:O	0.40	2.54	6	1
1:A:132:PHE:CZ	1:A:146:ALA:HB2	0.40	2.50	2	1
1:A:118:VAL:HG12	1:A:133:SER:CA	0.40	2.47	10	1
1:A:156:LYS:C	1:A:158:GLU:N	0.40	2.75	1	1
1:A:132:PHE:CD1	1:A:145:MET:O	0.40	2.75	6	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	153/167 (92%)	136±3 (89±2%)	11±2 (7±2%)	7±1 (4±1%)	6	30
All	All	1530/1670 (92%)	1356 (89%)	107 (7%)	67 (4%)	6	30

All 18 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	47	GLY	10
1	A	62	LEU	10
1	A	142	ASP	8
1	A	33	ASN	6
1	A	137	LYS	6
1	A	127	GLU	5
1	A	45	SER	4
1	A	124	ASN	4
1	A	138	GLY	2
1	A	75	GLY	2
1	A	171	GLY	2
1	A	181	PRO	2
1	A	113	GLY	1
1	A	182	GLN	1
1	A	32	PRO	1
1	A	172	LEU	1
1	A	111	HIS	1
1	A	125	TYR	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	131/143 (92%)	92±3 (70±3%)	39±3 (30±3%)	2	18
All	All	1310/1430 (92%)	922 (70%)	388 (30%)	2	18

All 103 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	82	THR	10
1	A	173	THR	10
1	A	91	THR	10
1	A	67	THR	9
1	A	137	LYS	8
1	A	77	LEU	7
1	A	133	SER	7
1	A	85	ARG	7
1	A	134	ARG	7
1	A	147	THR	6
1	A	34	PHE	6
1	A	56	ARG	6
1	A	145	MET	6
1	A	162	LYS	6
1	A	89	CYS	6
1	A	88	GLN	6
1	A	54	TRP	6
1	A	35	GLN	5
1	A	62	LEU	5
1	A	38	LYS	5
1	A	66	LYS	5
1	A	33	ASN	5
1	A	31	GLN	5
1	A	81	SER	5
1	A	155	LEU	5
1	A	157	ASP	5
1	A	59	LYS	5
1	A	40	LEU	5
1	A	141	GLN	5
1	A	158	GLU	5
1	A	64	MET	5
1	A	112	SER	4
1	A	152	THR	4
1	A	182	GLN	4
1	A	86	LYS	4
1	A	156	LYS	4
1	A	153	GLN	4
1	A	90	GLU	4
1	A	142	ASP	4
1	A	150	SER	4
1	A	108	SER	4
1	A	151	ARG	4
1	A	79	LEU	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	50	SER	4
1	A	160	LYS	4
1	A	154	THR	4
1	A	144	ARG	4
1	A	119	SER	4
1	A	111	HIS	4
1	A	167	SER	4
1	A	122	GLU	4
1	A	51	ASN	3
1	A	48	LEU	3
1	A	180	LEU	3
1	A	117	SER	3
1	A	161	GLU	3
1	A	92	LYS	3
1	A	96	LEU	3
1	A	53	SER	3
1	A	178	VAL	3
1	A	72	SER	3
1	A	130	LEU	3
1	A	58	LYS	3
1	A	61	VAL	3
1	A	131	LEU	3
1	A	159	LEU	3
1	A	176	ASP	3
1	A	57	GLU	3
1	A	174	GLU	3
1	A	78	ASN	3
1	A	74	GLU	3
1	A	37	ASP	3
1	A	170	GLN	3
1	A	172	LEU	2
1	A	87	ASN	2
1	A	109	SER	2
1	A	114	SER	2
1	A	42	ARG	2
1	A	168	LYS	2
1	A	52	SER	2
1	A	127	GLU	2
1	A	179	PHE	2
1	A	125	TYR	2
1	A	94	MET	2
1	A	116	HIS	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	124	ASN	2
1	A	132	PHE	2
1	A	163	PHE	2
1	A	126	ASP	2
1	A	39	PHE	2
1	A	55	PHE	2
1	A	164	THR	2
1	A	106	THR	1
1	A	84	LEU	1
1	A	104	HIS	1
1	A	45	SER	1
1	A	177	ILE	1
1	A	44	TYR	1
1	A	128	TYR	1
1	A	36	GLN	1
1	A	63	TYR	1
1	A	69	VAL	1
1	A	105	TYR	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 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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 70% for the well-defined parts and 70% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 11062

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	1471
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	162	0.05 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	149	-0.04 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	153	-0.47 ± 0.35	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 70%, i.e. 1308 atoms were assigned a chemical shift out of a possible 1874. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	579/751 (77%)	290/299 (97%)	148/306 (48%)	141/146 (97%)
Sidechain	653/938 (70%)	383/554 (69%)	261/341 (77%)	9/43 (21%)

Continued on next page...

Continued from previous page...

	Total	^1H	^{13}C	^{15}N
Aromatic	76/185 (41%)	49/97 (51%)	25/80 (31%)	2/8 (25%)
Overall	1308/1874 (70%)	722/950 (76%)	434/727 (60%)	152/197 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 70%, i.e. 1422 atoms were assigned a chemical shift out of a possible 2029. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	631/819 (77%)	316/326 (97%)	162/334 (49%)	153/159 (96%)
Sidechain	713/1017 (70%)	421/601 (70%)	282/370 (76%)	10/46 (22%)
Aromatic	78/193 (40%)	50/101 (50%)	26/82 (32%)	2/10 (20%)
Overall	1422/2029 (70%)	787/1028 (77%)	470/786 (60%)	165/215 (77%)

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.

Random coil index (RCI) for chain A:

