



Full wwPDB NMR Structure Validation Report ⓘ

Oct 17, 2021 – 02:00 AM EDT

PDB ID : 100L
Title : THE STRUCTURE OF BCL-W REVEALS A ROLE FOR THE C-
TERMINAL RESIDUES IN MODULATING BIOLOGICAL ACTIVITY
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C.L.
Deposited on : 2003-02-22

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 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)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.23.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

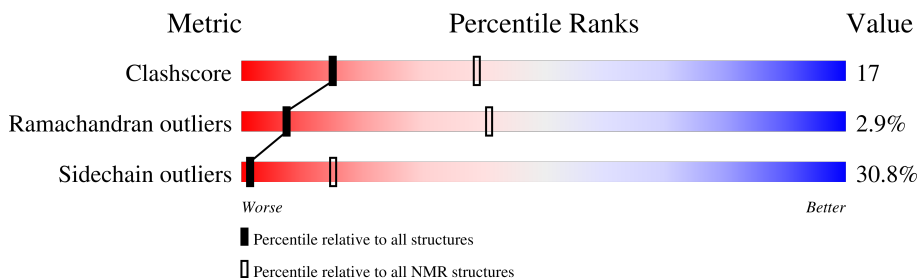
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment 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	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	188	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:8-A:180 (173)	0.22	2

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 4 clusters and 6 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2804 atoms, of which 1376 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Apoptosis regulator Bcl-W.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	188	2804	901	1376	253	268	6	0

There are 6 discrepancies between the modelled and reference sequences:

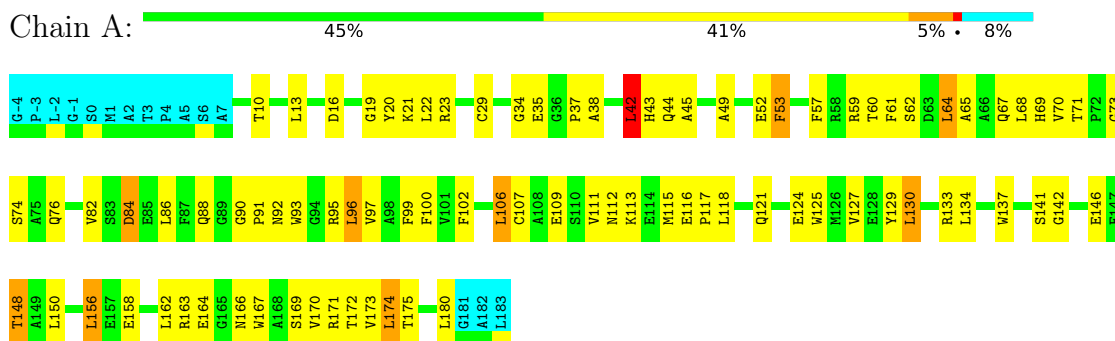
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	cloning artifact	UNP Q92843
A	-3	PRO	-	cloning artifact	UNP Q92843
A	-2	LEU	-	cloning artifact	UNP Q92843
A	-1	GLY	-	cloning artifact	UNP Q92843
A	0	SER	-	cloning artifact	UNP Q92843
A	128	GLU	ALA	engineered mutation	UNP Q92843

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: Apoptosis regulator Bcl-W

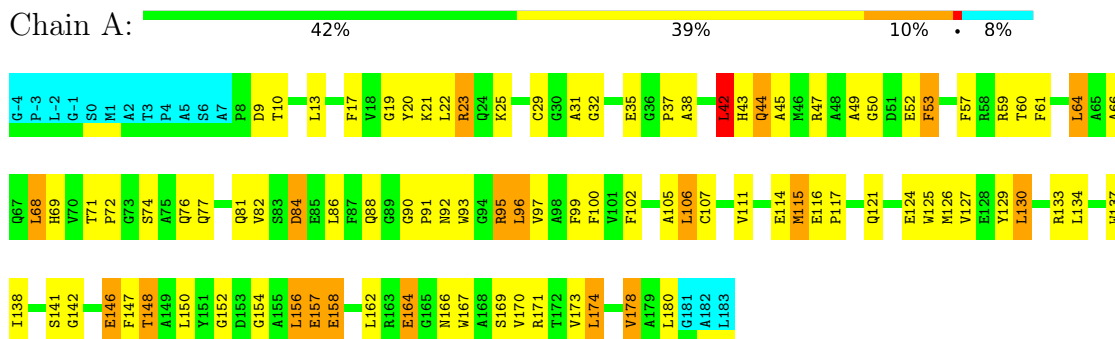


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

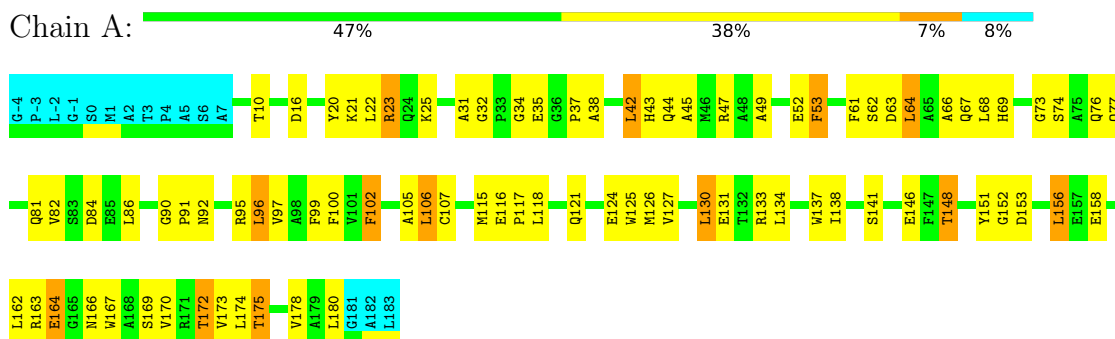
4.2.1 Score per residue for model 1

- Molecule 1: Apoptosis regulator Bcl-W



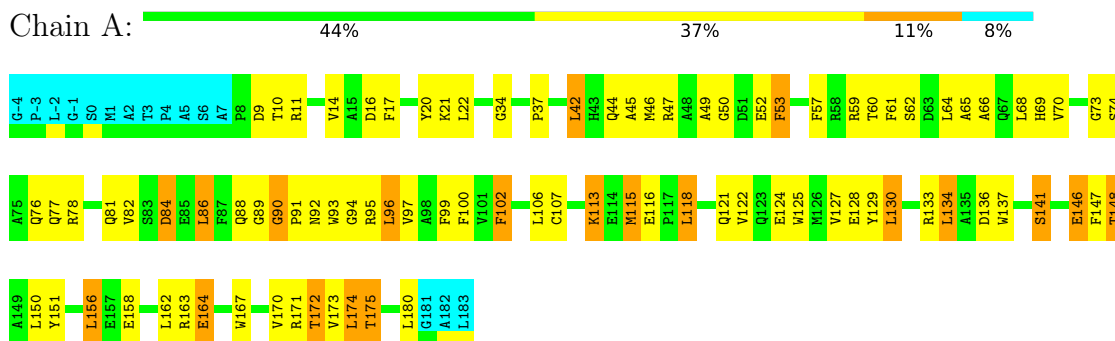
4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Apoptosis regulator Bcl-W



4.2.3 Score per residue for model 3

- Molecule 1: Apoptosis regulator Bcl-W



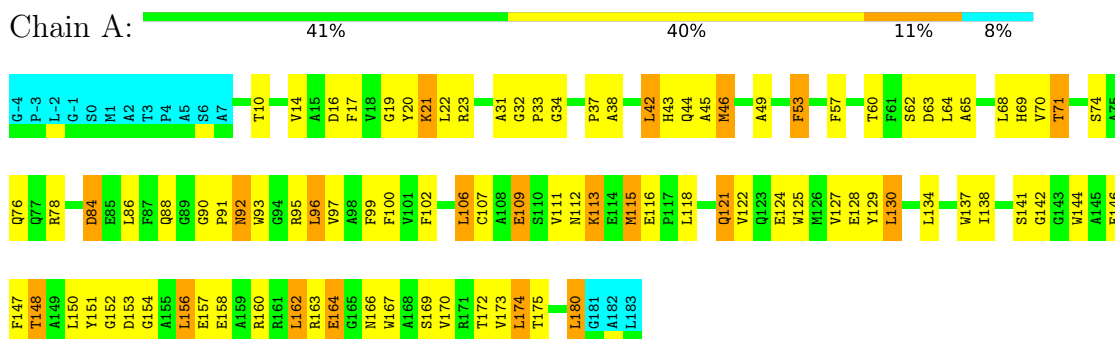
4.2.4 Score per residue for model 4

- Molecule 1: Apoptosis regulator Bcl-W



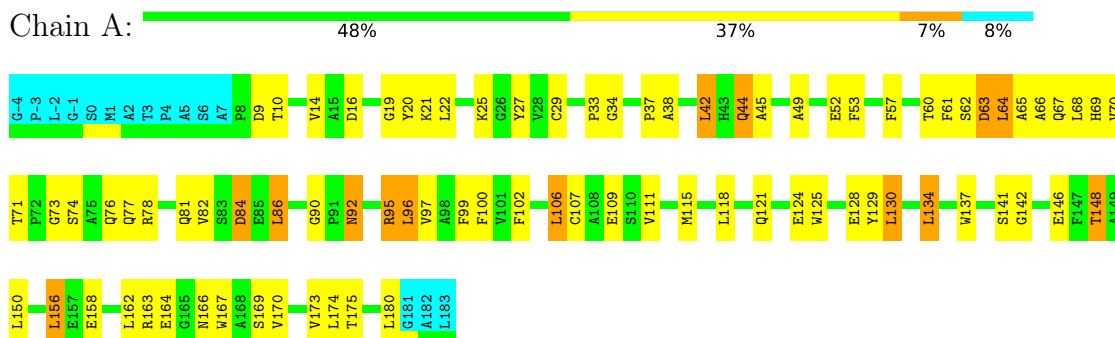
4.2.5 Score per residue for model 5

- Molecule 1: Apoptosis regulator Bcl-W



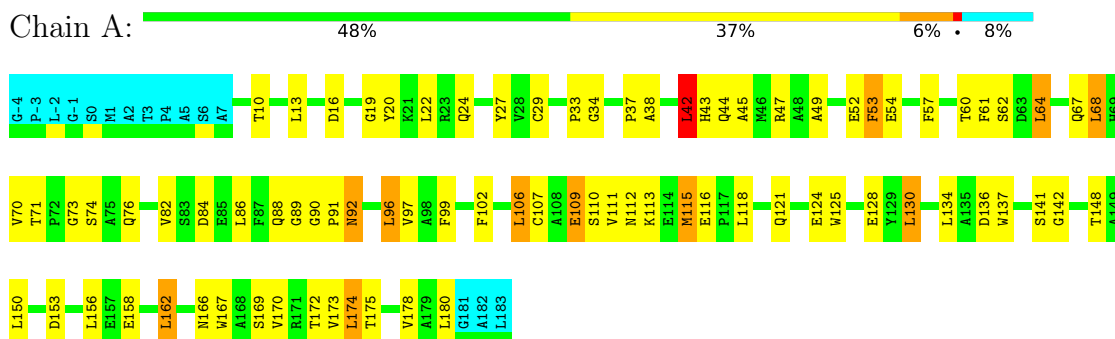
4.2.6 Score per residue for model 6

- Molecule 1: Apoptosis regulator Bcl-W



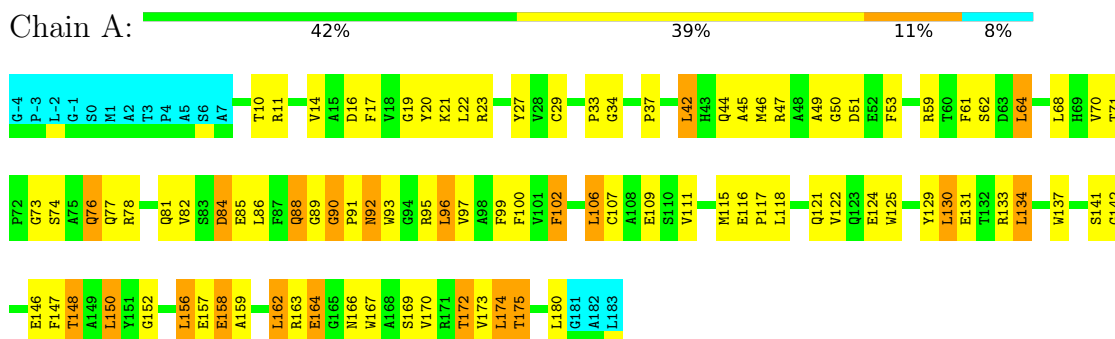
4.2.7 Score per residue for model 7

- Molecule 1: Apoptosis regulator Bcl-W



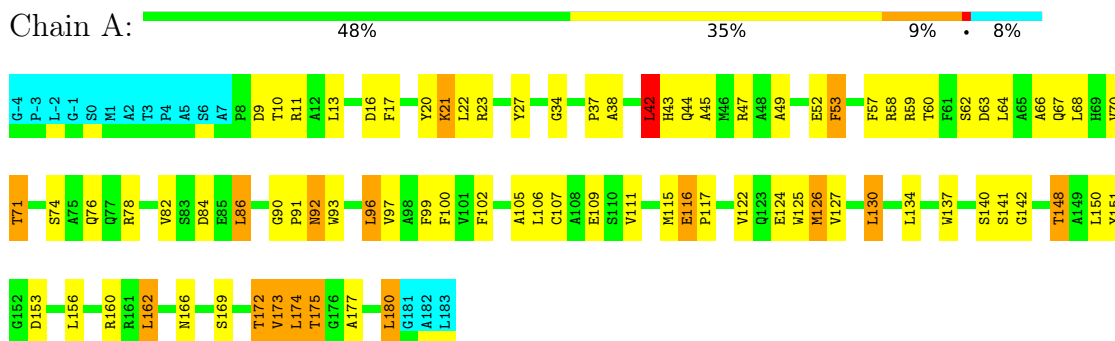
4.2.8 Score per residue for model 8

- Molecule 1: Apoptosis regulator Bcl-W



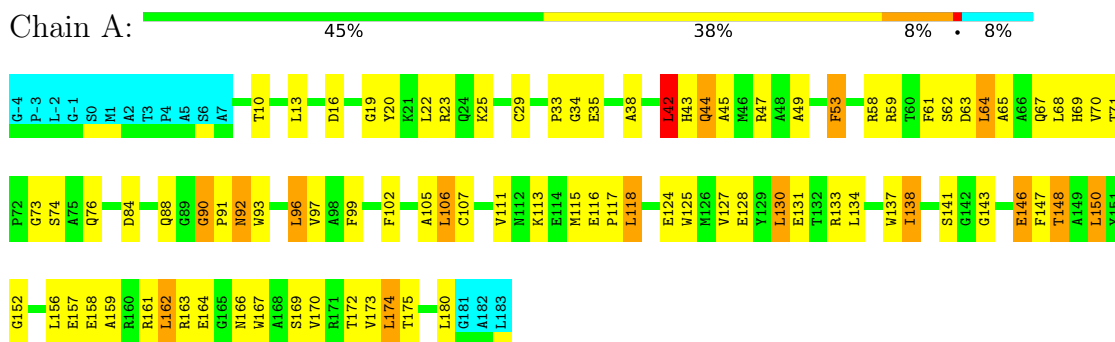
4.2.9 Score per residue for model 9

- Molecule 1: Apoptosis regulator Bcl-W



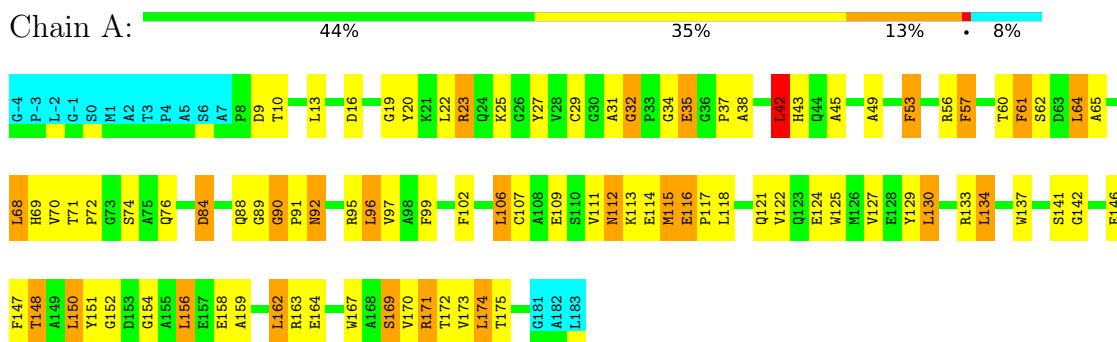
4.2.10 Score per residue for model 10

- Molecule 1: Apoptosis regulator Bcl-W



4.2.11 Score per residue for model 11

- Molecule 1: Apoptosis regulator Bcl-W



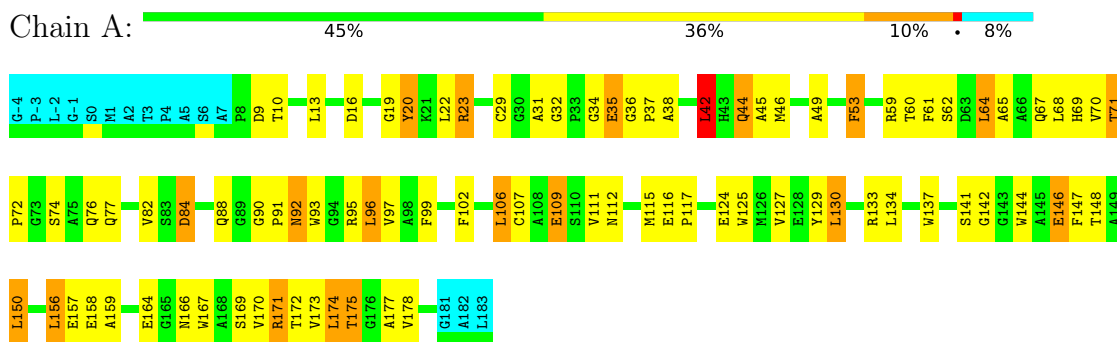
4.2.12 Score per residue for model 12

- Molecule 1: Apoptosis regulator Bcl-W



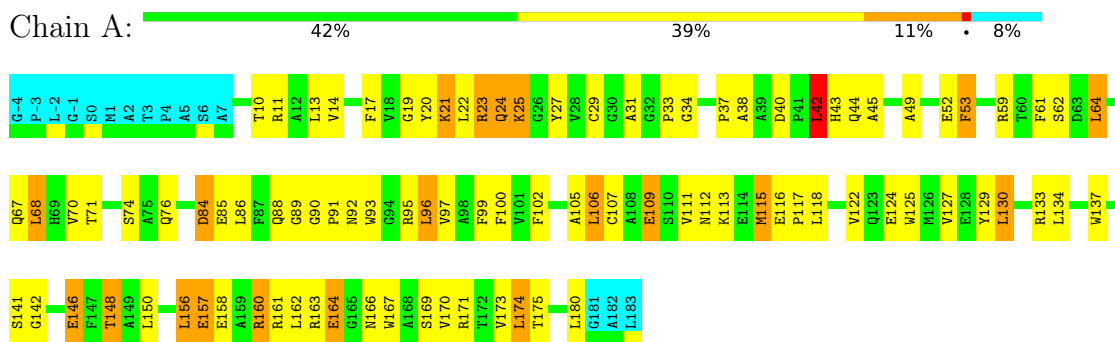
4.2.13 Score per residue for model 13

- Molecule 1: Apoptosis regulator Bcl-W



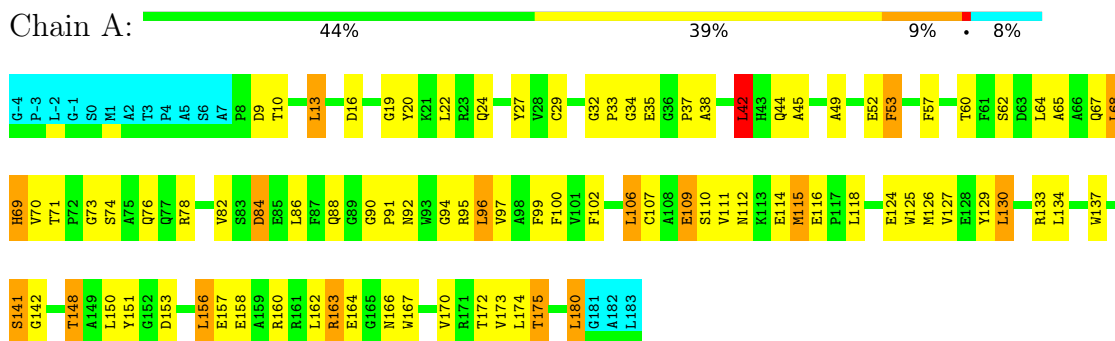
4.2.14 Score per residue for model 14

- Molecule 1: Apoptosis regulator Bcl-W



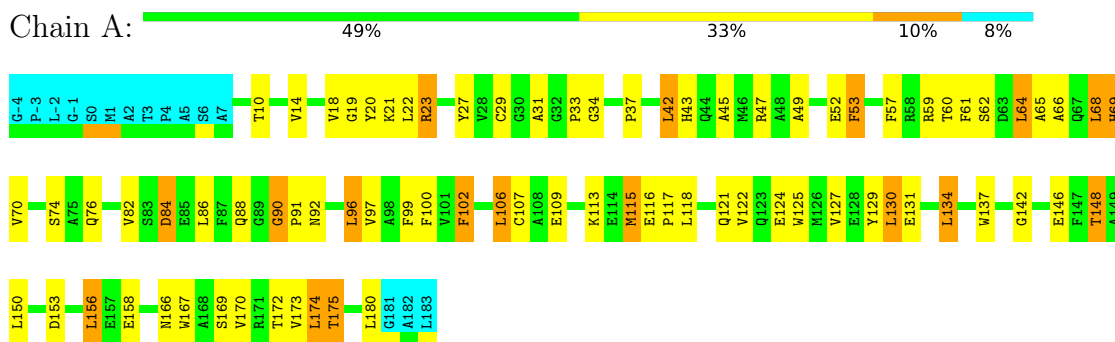
4.2.15 Score per residue for model 15

- Molecule 1: Apoptosis regulator Bcl-W



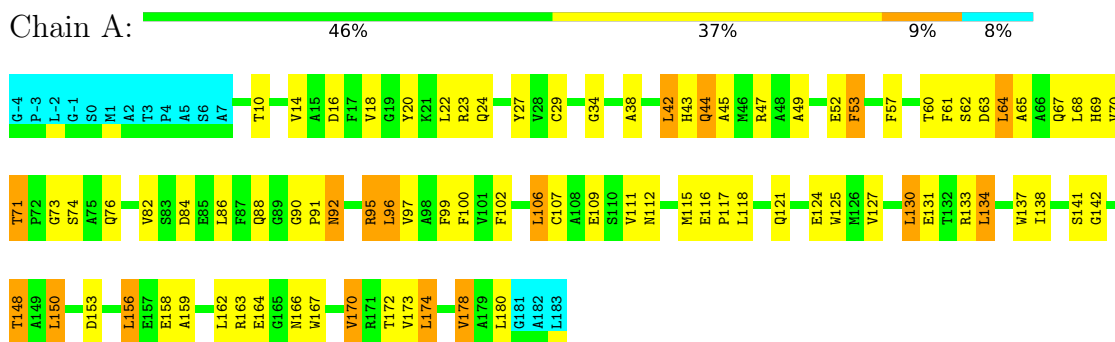
4.2.16 Score per residue for model 16

- Molecule 1: Apoptosis regulator Bcl-W



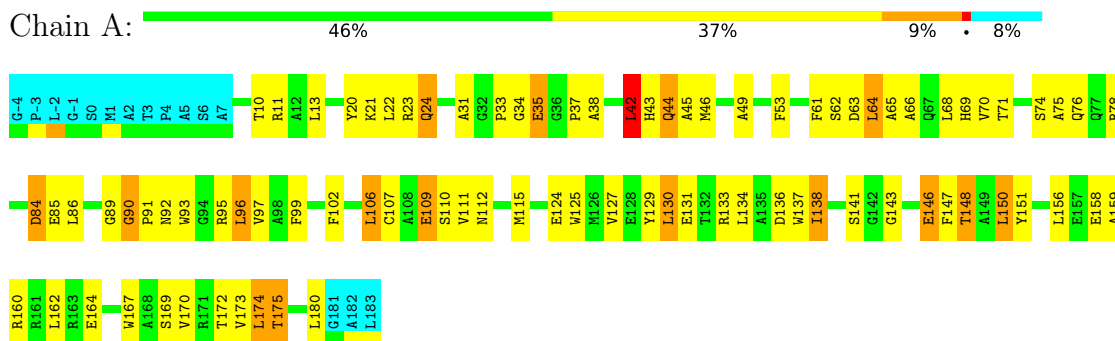
4.2.17 Score per residue for model 17

- Molecule 1: Apoptosis regulator Bcl-W



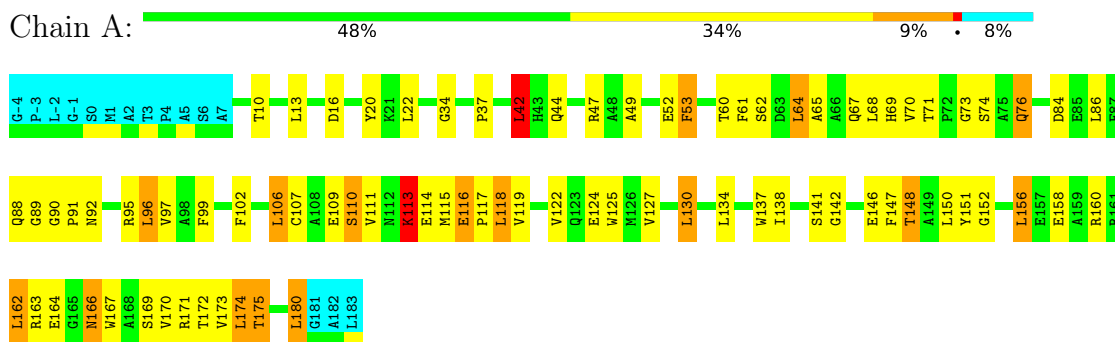
4.2.18 Score per residue for model 18

- Molecule 1: Apoptosis regulator Bcl-W



4.2.19 Score per residue for model 19

- Molecule 1: Apoptosis regulator Bcl-W



4.2.20 Score per residue for model 20

- Molecule 1: Apoptosis regulator Bcl-W



5 Refinement protocol and experimental data overview

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

Of the 256 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with the least restraint violations, structures with the lowest energy, target function*.

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

Software name	Classification	Version
DYANA	structure solution	1.5
CNS	refinement	1.1

No chemical shift data was provided.

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	1338	1283	1280	44±4
All	All	26760	25660	25600	872

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 17.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:167:TRP:HA	1:A:170:VAL:HG22	0.85	1.48	8	12
1:A:130:LEU:HA	1:A:134:LEU:HB2	0.83	1.48	3	20
1:A:61:PHE:HA	1:A:64:LEU:HD22	0.83	1.49	13	15
1:A:173:VAL:HG13	1:A:174:LEU:HG	0.81	1.52	17	18
1:A:63:ASP:HB3	1:A:180:LEU:HB3	0.81	1.52	18	2
1:A:78:ARG:HB3	1:A:180:LEU:HD11	0.79	1.53	5	1
1:A:38:ALA:HB1	1:A:44:GLN:HA	0.79	1.54	10	8
1:A:45:ALA:HB2	1:A:148:THR:HA	0.77	1.57	15	19
1:A:92:ASN:HA	1:A:137:TRP:CZ2	0.74	2.17	19	20
1:A:49:ALA:HB1	1:A:97:VAL:HG22	0.74	1.57	19	20
1:A:156:LEU:HD12	1:A:158:GLU:HB2	0.70	1.61	4	15
1:A:53:PHE:HB2	1:A:97:VAL:HG11	0.70	1.61	5	17
1:A:172:THR:HA	1:A:175:THR:HG23	0.70	1.62	13	11
1:A:82:VAL:HG11	1:A:180:LEU:HG	0.70	1.64	17	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:167:TRP:HA	1:A:170:VAL:CG2	0.69	2.17	3	17
1:A:150:LEU:HA	1:A:159:ALA:HB1	0.69	1.65	11	6
1:A:92:ASN:HB2	1:A:170:VAL:HG21	0.68	1.66	17	1
1:A:96:LEU:HA	1:A:99:PHE:HD2	0.68	1.48	15	20
1:A:49:ALA:HB2	1:A:147:PHE:HZ	0.66	1.50	10	8
1:A:20:TYR:HA	1:A:34:GLY:HA3	0.66	1.67	19	19
1:A:113:LYS:HB3	1:A:115:MET:SD	0.65	2.32	5	2
1:A:64:LEU:HG	1:A:106:LEU:HA	0.65	1.67	5	17
1:A:124:GLU:HA	1:A:127:VAL:HG12	0.63	1.70	12	16
1:A:23:ARG:HD2	1:A:31:ALA:HA	0.63	1.70	14	8
1:A:82:VAL:HG11	1:A:180:LEU:HD22	0.62	1.72	15	1
1:A:92:ASN:HB2	1:A:170:VAL:HG11	0.62	1.72	14	8
1:A:38:ALA:HB1	1:A:44:GLN:CA	0.62	2.24	1	7
1:A:164:GLU:HA	1:A:167:TRP:CD1	0.61	2.29	11	10
1:A:116:GLU:HB3	1:A:117:PRO:HD3	0.61	1.70	11	1
1:A:76:GLN:HB3	1:A:125:TRP:CZ2	0.61	2.30	4	20
1:A:59:ARG:HH21	1:A:178:VAL:HG11	0.61	1.54	12	1
1:A:49:ALA:HA	1:A:163:ARG:HH22	0.60	1.56	3	6
1:A:91:PRO:HG2	1:A:137:TRP:CD1	0.59	2.32	7	18
1:A:159:ALA:O	1:A:163:ARG:HG2	0.59	1.98	4	2
1:A:22:LEU:HD21	1:A:107:CYS:HB3	0.58	1.74	12	16
1:A:92:ASN:HA	1:A:137:TRP:CH2	0.57	2.33	12	20
1:A:157:GLU:HA	1:A:160:ARG:HD2	0.57	1.74	5	2
1:A:166:ASN:O	1:A:170:VAL:HG22	0.57	1.99	15	11
1:A:63:ASP:HB3	1:A:180:LEU:HB2	0.57	1.76	17	5
1:A:19:GLY:HA3	1:A:33:PRO:HB2	0.57	1.74	15	8
1:A:82:VAL:HG11	1:A:102:PHE:CE2	0.57	2.35	3	2
1:A:116:GLU:HB2	1:A:117:PRO:HD3	0.57	1.77	13	11
1:A:65:ALA:O	1:A:69:HIS:HB3	0.56	1.98	19	2
1:A:127:VAL:O	1:A:131:GLU:HG2	0.56	1.99	17	1
1:A:77:GLN:O	1:A:81:GLN:HG2	0.56	1.99	1	5
1:A:84:ASP:HA	1:A:129:TYR:OH	0.56	2.01	18	12
1:A:95:ARG:HD2	1:A:174:LEU:HD12	0.56	1.77	3	1
1:A:13:LEU:HB2	1:A:42:LEU:HD13	0.56	1.77	1	10
1:A:109:GLU:HA	1:A:112:ASN:ND2	0.56	2.16	12	9
1:A:93:TRP:CZ2	1:A:146:GLU:HG2	0.55	2.36	3	5
1:A:20:TYR:CA	1:A:34:GLY:HA3	0.55	2.32	3	10
1:A:164:GLU:HA	1:A:167:TRP:NE1	0.55	2.16	4	8
1:A:167:TRP:CE3	1:A:171:ARG:HD3	0.55	2.36	4	2
1:A:167:TRP:HA	1:A:170:VAL:HG12	0.55	1.79	17	1
1:A:93:TRP:HA	1:A:96:LEU:HB2	0.55	1.79	4	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:GLY:H	1:A:118:LEU:HD21	0.54	1.63	12	11
1:A:95:ARG:HH11	1:A:170:VAL:HB	0.54	1.61	6	1
1:A:167:TRP:O	1:A:171:ARG:HB2	0.54	2.02	12	1
1:A:95:ARG:HH11	1:A:174:LEU:HB2	0.53	1.63	5	5
1:A:82:VAL:HG12	1:A:86:LEU:HD12	0.53	1.81	3	1
1:A:151:TYR:CE1	1:A:160:ARG:HA	0.53	2.39	19	3
1:A:49:ALA:HB2	1:A:147:PHE:CZ	0.53	2.37	10	6
1:A:100:PHE:HA	1:A:126:MET:SD	0.52	2.44	4	4
1:A:67:GLN:HE22	1:A:106:LEU:HD11	0.52	1.64	20	8
1:A:67:GLN:HG2	1:A:78:ARG:HD3	0.52	1.81	12	3
1:A:67:GLN:NE2	1:A:180:LEU:HG	0.52	2.20	9	1
1:A:38:ALA:HA	1:A:43:HIS:HB3	0.52	1.82	5	9
1:A:107:CYS:O	1:A:111:VAL:HG23	0.52	2.04	11	17
1:A:162:LEU:O	1:A:166:ASN:HB2	0.51	2.05	2	9
1:A:86:LEU:HG	1:A:95:ARG:HH11	0.51	1.65	20	1
1:A:138:ILE:HG23	1:A:143:GLY:HA2	0.51	1.83	10	2
1:A:166:ASN:O	1:A:170:VAL:HB	0.51	2.06	13	2
1:A:64:LEU:HD21	1:A:105:ALA:HB1	0.50	1.81	14	4
1:A:75:ALA:HA	1:A:78:ARG:HD2	0.50	1.81	18	1
1:A:158:GLU:O	1:A:162:LEU:HB2	0.50	2.05	7	2
1:A:76:GLN:HB3	1:A:125:TRP:CE2	0.50	2.41	19	19
1:A:172:THR:HA	1:A:175:THR:OG1	0.49	2.06	12	1
1:A:46:MET:HE3	1:A:144:TRP:CZ3	0.49	2.42	13	1
1:A:173:VAL:CG1	1:A:174:LEU:HG	0.49	2.35	7	13
1:A:158:GLU:OE1	1:A:161:ARG:HD2	0.49	2.07	14	1
1:A:14:VAL:HA	1:A:100:PHE:HE2	0.49	1.68	12	9
1:A:121:GLN:HA	1:A:124:GLU:HG2	0.49	1.85	17	8
1:A:38:ALA:CB	1:A:44:GLN:HA	0.48	2.33	18	3
1:A:86:LEU:HG	1:A:174:LEU:HD22	0.48	1.85	6	1
1:A:94:GLY:HA3	1:A:167:TRP:HB3	0.48	1.85	15	4
1:A:148:THR:O	1:A:152:GLY:HA3	0.48	2.09	19	8
1:A:169:SER:O	1:A:173:VAL:HB	0.48	2.08	11	1
1:A:65:ALA:O	1:A:69:HIS:HB2	0.48	2.09	12	11
1:A:70:VAL:HG13	1:A:71:THR:H	0.48	1.67	13	4
1:A:150:LEU:HD22	1:A:163:ARG:HB3	0.48	1.86	15	2
1:A:95:ARG:HE	1:A:171:ARG:HA	0.47	1.67	3	1
1:A:157:GLU:O	1:A:161:ARG:HG2	0.47	2.09	10	1
1:A:32:GLY:O	1:A:35:GLU:HB3	0.47	2.09	11	1
1:A:68:LEU:HG	1:A:115:MET:SD	0.47	2.49	14	6
1:A:95:ARG:NH1	1:A:174:LEU:HB2	0.47	2.25	14	4
1:A:118:LEU:O	1:A:122:VAL:HG23	0.47	2.10	3	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:GLU:HA	1:A:112:ASN:HD21	0.47	1.69	17	7
1:A:22:LEU:HD11	1:A:107:CYS:HB2	0.47	1.86	20	7
1:A:13:LEU:HD11	1:A:46:MET:HE2	0.47	1.87	13	1
1:A:117:PRO:O	1:A:121:GLN:HG2	0.47	2.10	1	1
1:A:38:ALA:HB1	1:A:44:GLN:HB2	0.47	1.87	15	2
1:A:95:ARG:HD3	1:A:171:ARG:HG2	0.47	1.86	12	1
1:A:90:GLY:H	1:A:91:PRO:HD3	0.46	1.70	8	4
1:A:124:GLU:O	1:A:128:GLU:HB2	0.46	2.09	7	1
1:A:96:LEU:HA	1:A:99:PHE:CD2	0.46	2.46	12	8
1:A:61:PHE:HA	1:A:64:LEU:CD1	0.46	2.40	4	2
1:A:59:ARG:HD3	1:A:63:ASP:OD1	0.46	2.10	4	1
1:A:72:PRO:HB3	1:A:115:MET:SD	0.46	2.50	11	1
1:A:49:ALA:HA	1:A:151:TYR:CE1	0.46	2.45	9	2
1:A:63:ASP:HB3	1:A:180:LEU:CB	0.46	2.41	17	1
1:A:61:PHE:HA	1:A:64:LEU:HD12	0.46	1.88	4	1
1:A:156:LEU:CD1	1:A:158:GLU:HB2	0.46	2.41	13	4
1:A:102:PHE:O	1:A:106:LEU:HB2	0.45	2.11	16	4
1:A:92:ASN:HB3	1:A:170:VAL:HG21	0.45	1.87	4	2
1:A:90:GLY:N	1:A:91:PRO:HD3	0.45	2.26	3	2
1:A:122:VAL:HG22	1:A:125:TRP:CZ3	0.45	2.46	14	7
1:A:154:GLY:O	1:A:156:LEU:HD23	0.45	2.12	1	3
1:A:126:MET:HG2	1:A:127:VAL:N	0.45	2.26	9	1
1:A:49:ALA:HA	1:A:163:ARG:HH12	0.45	1.71	11	1
1:A:109:GLU:HA	1:A:112:ASN:HD22	0.45	1.71	11	1
1:A:53:PHE:HB2	1:A:97:VAL:CG1	0.45	2.42	3	1
1:A:116:GLU:N	1:A:117:PRO:HD2	0.45	2.27	9	1
1:A:157:GLU:HA	1:A:160:ARG:HG2	0.45	1.86	14	1
1:A:86:LEU:HD12	1:A:177:ALA:HB1	0.45	1.88	9	1
1:A:23:ARG:HA	1:A:27:TYR:O	0.45	2.12	9	3
1:A:17:PHE:HZ	1:A:50:GLY:HA3	0.44	1.72	3	4
1:A:16:ASP:HB2	1:A:43:HIS:CE1	0.44	2.47	9	1
1:A:102:PHE:CE2	1:A:180:LEU:HD11	0.44	2.47	8	2
1:A:64:LEU:HD12	1:A:106:LEU:HD12	0.44	1.90	15	1
1:A:167:TRP:HA	1:A:170:VAL:HG23	0.44	1.89	4	2
1:A:121:GLN:HB3	1:A:125:TRP:CE2	0.44	2.47	16	3
1:A:17:PHE:O	1:A:21:LYS:HB2	0.44	2.13	4	4
1:A:78:ARG:HB3	1:A:180:LEU:CD1	0.44	2.37	5	1
1:A:85:GLU:HA	1:A:88:GLN:NE2	0.43	2.28	8	1
1:A:57:PHE:HB3	1:A:60:THR:HB	0.43	1.89	11	1
1:A:160:ARG:HG3	1:A:161:ARG:N	0.43	2.28	14	1
1:A:32:GLY:CA	1:A:35:GLU:HG3	0.43	2.43	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:GLY:O	1:A:23:ARG:HB2	0.43	2.14	13	4
1:A:113:LYS:O	1:A:114:GLU:HG3	0.43	2.14	19	1
1:A:151:TYR:CD1	1:A:163:ARG:HD3	0.43	2.48	11	1
1:A:23:ARG:HD2	1:A:32:GLY:H	0.43	1.73	1	1
1:A:157:GLU:HG3	1:A:158:GLU:N	0.43	2.28	1	1
1:A:82:VAL:HG13	1:A:177:ALA:O	0.43	2.14	13	1
1:A:130:LEU:HG	1:A:134:LEU:HG	0.43	1.90	9	1
1:A:22:LEU:HB3	1:A:27:TYR:HB2	0.42	1.92	6	2
1:A:110:SER:HB3	1:A:119:VAL:HG22	0.42	1.91	19	1
1:A:137:TRP:HE3	1:A:138:ILE:HG13	0.42	1.74	1	3
1:A:170:VAL:O	1:A:173:VAL:HG12	0.42	2.13	4	1
1:A:137:TRP:O	1:A:141:SER:HB2	0.42	2.14	15	2
1:A:35:GLU:HG3	1:A:36:GLY:N	0.42	2.30	13	1
1:A:23:ARG:HG3	1:A:31:ALA:HA	0.42	1.91	5	2
1:A:130:LEU:CA	1:A:134:LEU:HB2	0.42	2.38	7	3
1:A:70:VAL:HG22	1:A:71:THR:OG1	0.42	2.15	13	1
1:A:64:LEU:HD11	1:A:105:ALA:HB1	0.42	1.91	9	1
1:A:24:GLN:HB3	1:A:25:LYS:HD3	0.42	1.90	14	1
1:A:18:VAL:O	1:A:22:LEU:HD13	0.42	2.15	17	2
1:A:93:TRP:CE3	1:A:147:PHE:HB2	0.41	2.50	13	2
1:A:46:MET:HE3	1:A:144:TRP:HZ3	0.41	1.74	13	1
1:A:82:VAL:HG23	1:A:177:ALA:HB1	0.41	1.92	4	1
1:A:53:PHE:CZ	1:A:171:ARG:HD2	0.41	2.51	11	1
1:A:49:ALA:HA	1:A:163:ARG:NH2	0.41	2.30	19	1
1:A:22:LEU:HD11	1:A:107:CYS:CB	0.41	2.46	13	1
1:A:70:VAL:HG22	1:A:71:THR:HG22	0.41	1.92	18	1
1:A:40:ASP:HB2	1:A:43:HIS:HB2	0.41	1.90	20	1
1:A:95:ARG:HA	1:A:95:ARG:HD2	0.41	1.50	17	2
1:A:46:MET:CE	1:A:144:TRP:HZ3	0.41	2.28	5	1
1:A:17:PHE:CD2	1:A:100:PHE:HB3	0.41	2.51	9	1
1:A:138:ILE:HD13	1:A:144:TRP:CZ2	0.41	2.51	12	1
1:A:116:GLU:H	1:A:116:GLU:HG3	0.41	1.43	20	1
1:A:91:PRO:HG2	1:A:137:TRP:CG	0.41	2.50	7	5
1:A:146:GLU:HG3	1:A:150:LEU:HD12	0.41	1.93	13	1
1:A:167:TRP:HE3	1:A:171:ARG:HD3	0.41	1.76	13	1
1:A:164:GLU:HG3	1:A:167:TRP:HE1	0.41	1.76	8	1
1:A:23:ARG:HD2	1:A:35:GLU:OE2	0.41	2.15	10	2
1:A:92:ASN:HB3	1:A:166:ASN:OD1	0.40	2.16	6	1
1:A:82:VAL:CG1	1:A:180:LEU:HD13	0.40	2.46	9	1
1:A:40:ASP:HB2	1:A:43:HIS:CG	0.40	2.51	14	1
1:A:21:LYS:O	1:A:24:GLN:HG2	0.40	2.17	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:GLN:HG3	1:A:180:LEU:HB3	0.40	1.94	19	1
1:A:19:GLY:CA	1:A:33:PRO:HB2	0.40	2.46	14	1
1:A:13:LEU:HD13	1:A:42:LEU:HD13	0.40	1.94	18	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	173/188 (92%)	151±2 (87±1%)	17±2 (10±1%)	5±1 (3±1%)	7	41
All	All	3460/3760 (92%)	3022 (87%)	339 (10%)	99 (3%)	7	41

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	42	LEU	20
1	A	90	GLY	20
1	A	37	PRO	18
1	A	142	GLY	16
1	A	89	GLY	9
1	A	32	GLY	5
1	A	72	PRO	2
1	A	178	VAL	2
1	A	115	MET	2
1	A	175	THR	1
1	A	114	GLU	1
1	A	116	GLU	1
1	A	33	PRO	1
1	A	113	LYS	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	131/139 (94%)	91±4 (69±3%)	40±4 (31±3%)	1	15
All	All	2620/2780 (94%)	1812 (69%)	808 (31%)	1	15

All 91 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	10	THR	20
1	A	42	LEU	20
1	A	68	LEU	20
1	A	96	LEU	20
1	A	106	LEU	20
1	A	130	LEU	20
1	A	156	LEU	20
1	A	74	SER	19
1	A	84	ASP	19
1	A	102	PHE	19
1	A	53	PHE	18
1	A	115	MET	18
1	A	141	SER	18
1	A	148	THR	18
1	A	62	SER	18
1	A	174	LEU	17
1	A	146	GLU	16
1	A	169	SER	16
1	A	175	THR	16
1	A	71	THR	15
1	A	86	LEU	15
1	A	150	LEU	15
1	A	29	CYS	14
1	A	60	THR	14
1	A	64	LEU	14
1	A	133	ARG	14
1	A	16	ASP	14
1	A	57	PHE	13
1	A	88	GLN	13
1	A	162	LEU	13
1	A	21	LYS	12
1	A	44	GLN	12
1	A	70	VAL	12

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Mol	Chain	Res	Type	Models (Total)
1	A	109	GLU	12
1	A	52	GLU	11
1	A	164	GLU	11
1	A	172	THR	11
1	A	47	ARG	10
1	A	153	ASP	10
1	A	59	ARG	9
1	A	113	LYS	9
1	A	92	ASN	9
1	A	9	ASP	8
1	A	25	LYS	8
1	A	95	ARG	8
1	A	171	ARG	7
1	A	116	GLU	7
1	A	134	LEU	7
1	A	23	ARG	6
1	A	35	GLU	6
1	A	178	VAL	6
1	A	131	GLU	6
1	A	163	ARG	6
1	A	11	ARG	6
1	A	180	LEU	6
1	A	69	HIS	5
1	A	24	GLN	5
1	A	27	TYR	5
1	A	110	SER	5
1	A	157	GLU	4
1	A	158	GLU	4
1	A	138	ILE	4
1	A	46	MET	4
1	A	118	LEU	4
1	A	128	GLU	4
1	A	78	ARG	3
1	A	136	ASP	3
1	A	43	HIS	3
1	A	20	TYR	2
1	A	114	GLU	2
1	A	77	GLN	2
1	A	151	TYR	2
1	A	63	ASP	2
1	A	121	GLN	2
1	A	173	VAL	2

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Mol	Chain	Res	Type	Models (Total)
1	A	76	GLN	2
1	A	58	ARG	2
1	A	160	ARG	2
1	A	85	GLU	2
1	A	81	GLN	1
1	A	54	GLU	1
1	A	51	ASP	1
1	A	126	MET	1
1	A	140	SER	1
1	A	56	ARG	1
1	A	61	PHE	1
1	A	112	ASN	1
1	A	13	LEU	1
1	A	170	VAL	1
1	A	166	ASN	1
1	A	28	VAL	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

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided