



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 19, 2022 – 11:38 AM EST

PDB ID : 1QBH  
Title : SOLUTION STRUCTURE OF A BACULOVIRAL INHIBITOR OF APOPTOSIS (IAP) REPEAT  
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Deposited on : 1999-04-20

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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 : 2.26  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.26

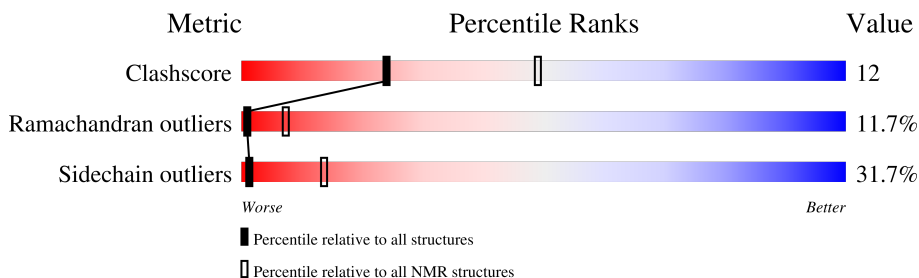
# 1 Overall quality at a glance

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  $\geq 3$ , 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	101	

## 2 Ensemble composition and analysis i

This entry contains 20 models. Model 6 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:271-A:299, A:304-A:309, A:321-A:352 (67)	0.23	6

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 and 1 single-model cluster was found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1595 atoms, of which 768 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1).

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	101	1594	524	768	144	149	9	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	263	GLY	-	SEE REMARK 999	UNP Q13490
A	264	SER	-	SEE REMARK 999	UNP Q13490
A	265	HIS	-	SEE REMARK 999	UNP Q13490

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

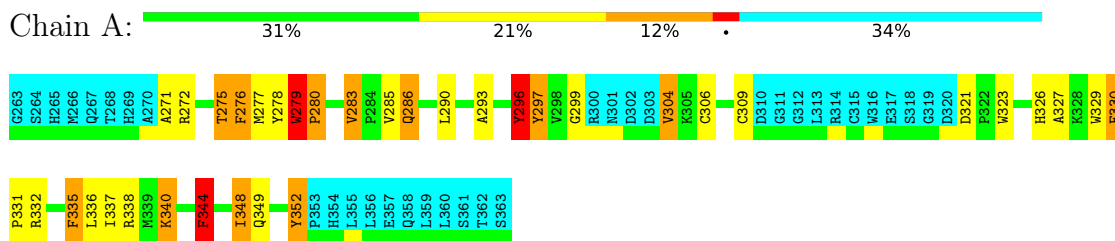
Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	1	1	1

## 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: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

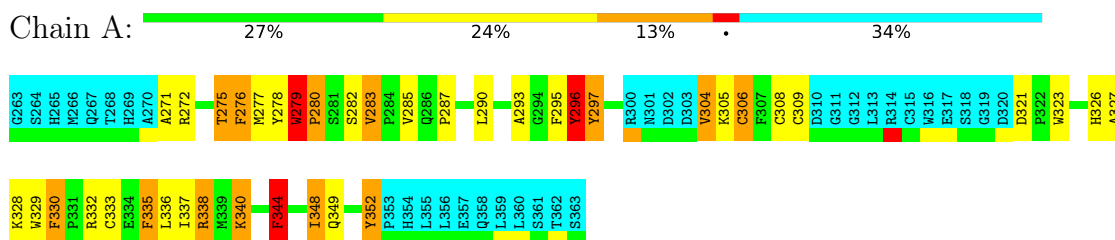


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

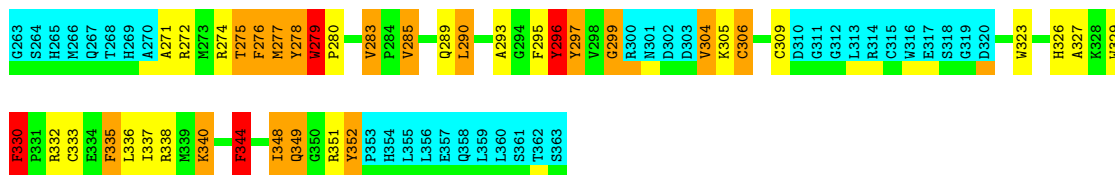
- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



#### 4.2.2 Score per residue for model 2

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

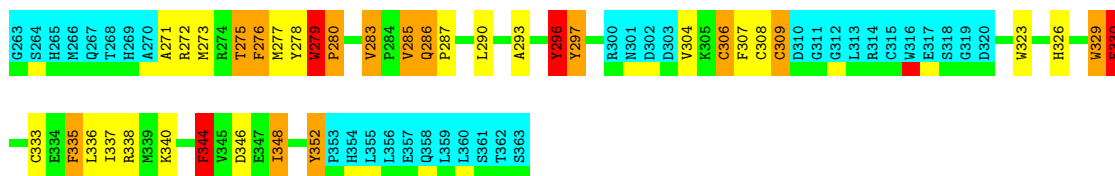




#### 4.2.3 Score per residue for model 3

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

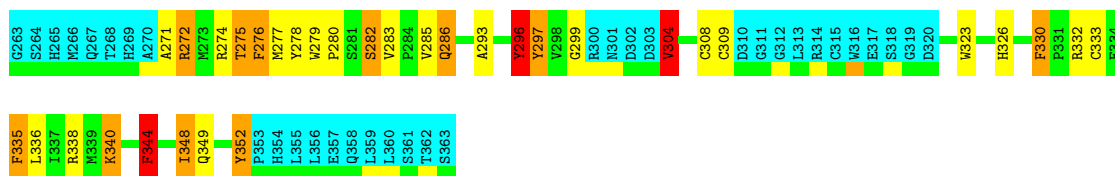
Chain A: 31% 19% 13% 34%



#### 4.2.4 Score per residue for model 4

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

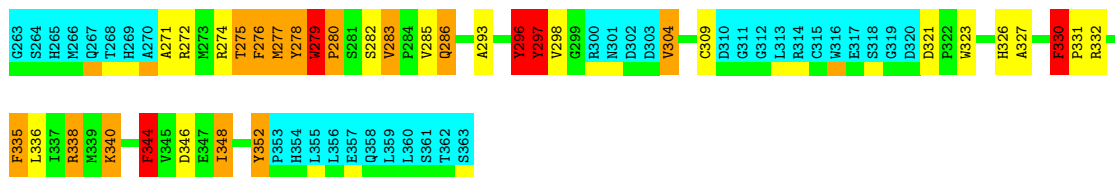
Chain A: 34% 19% 11% 34%



#### 4.2.5 Score per residue for model 5

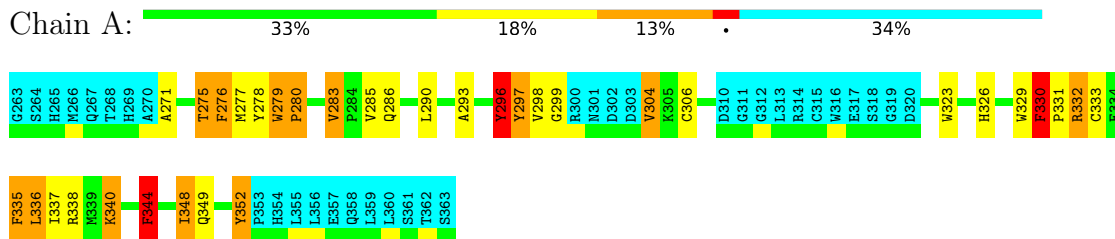
- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

Chain A: 33% 16% 13% 5% 34%



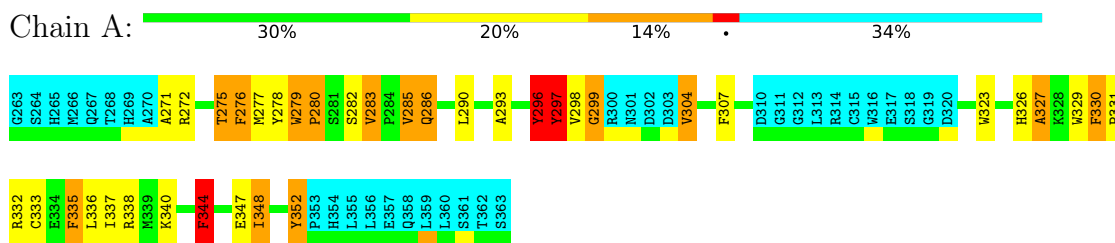
#### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



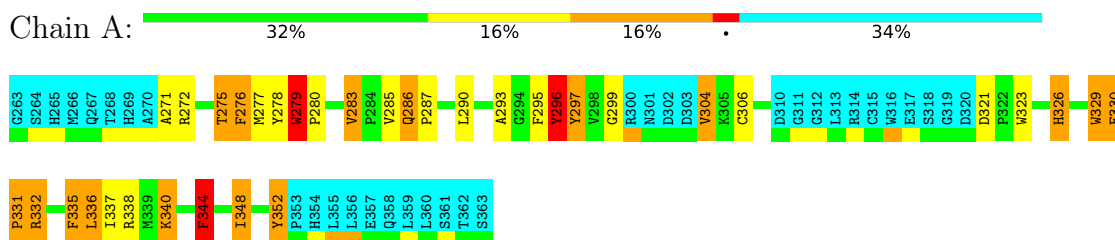
#### 4.2.7 Score per residue for model 7

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



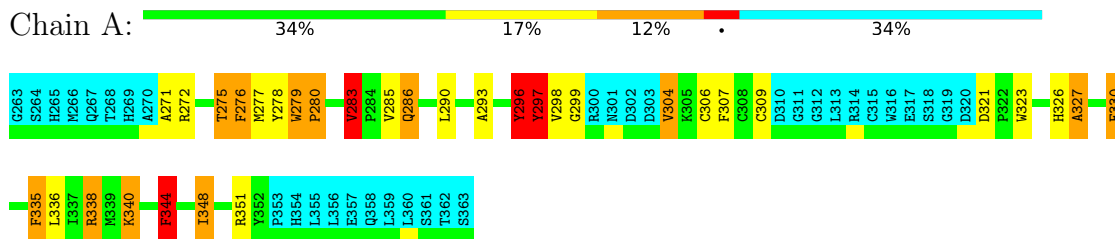
#### 4.2.8 Score per residue for model 8

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



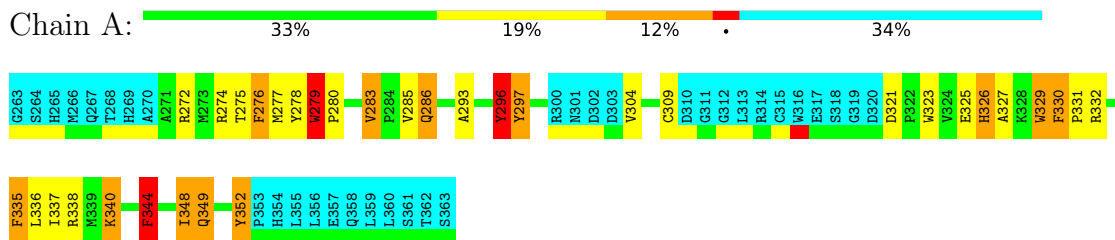
#### 4.2.9 Score per residue for model 9

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



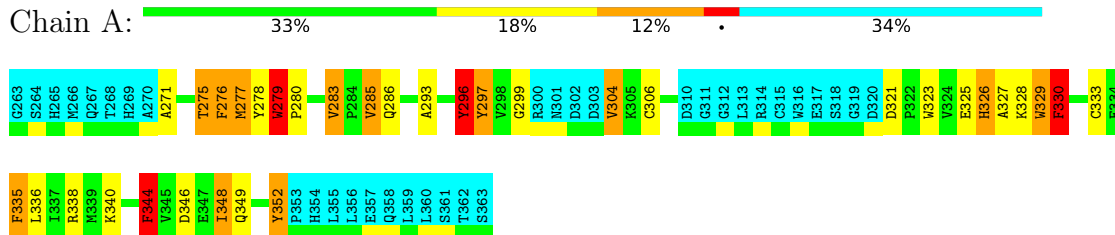
#### 4.2.10 Score per residue for model 10

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



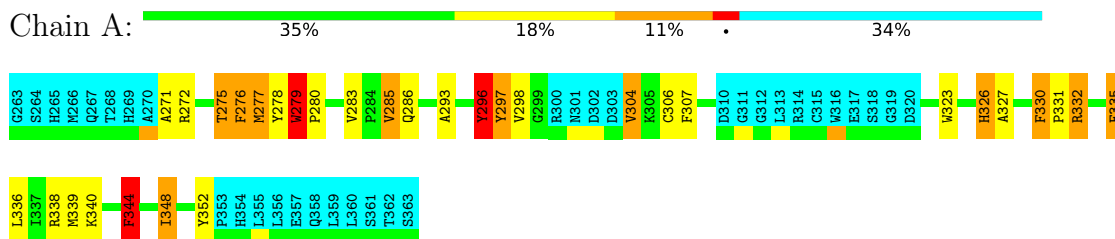
#### 4.2.11 Score per residue for model 11

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



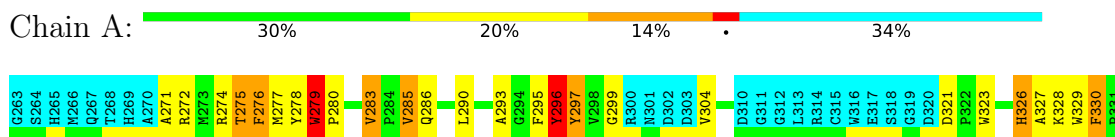
#### 4.2.12 Score per residue for model 12

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

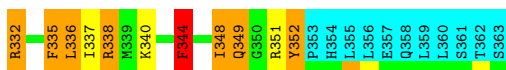


#### 4.2.13 Score per residue for model 13

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

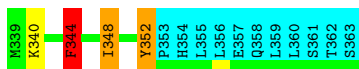
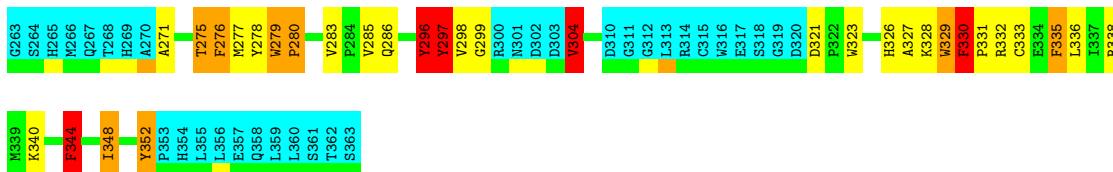
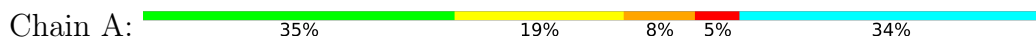






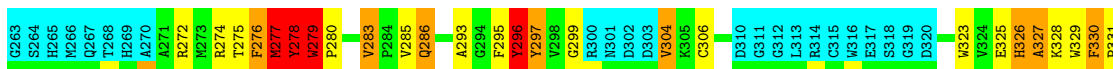
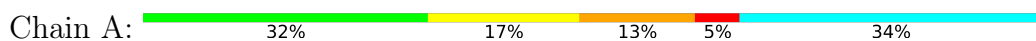
#### 4.2.14 Score per residue for model 14

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



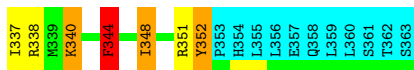
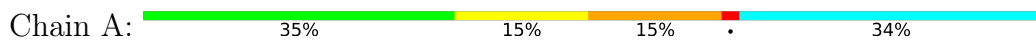
#### 4.2.15 Score per residue for model 15

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



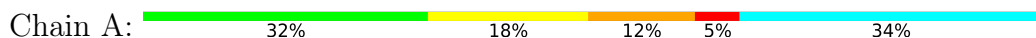
#### 4.2.16 Score per residue for model 16

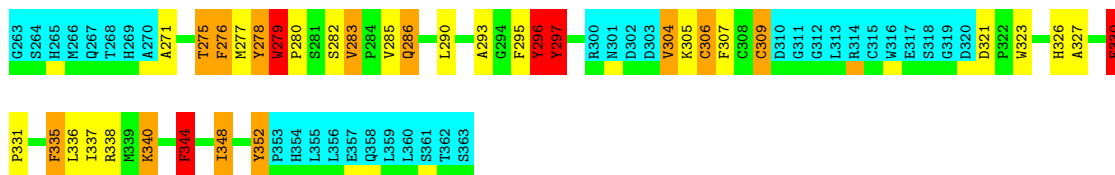
- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)



#### 4.2.17 Score per residue for model 17

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

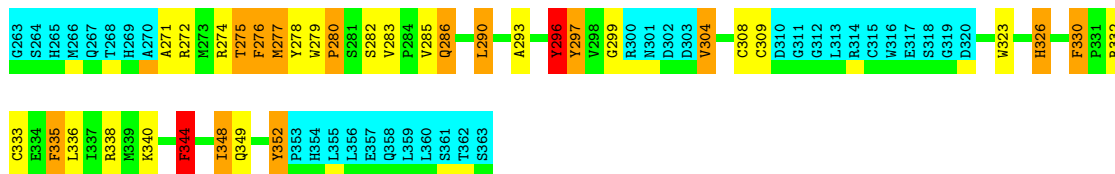




#### 4.2.18 Score per residue for model 18

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

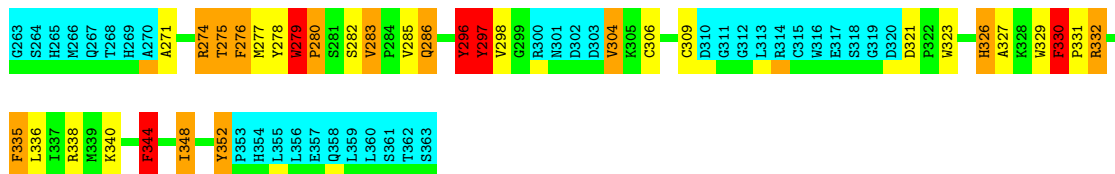
Chain A: 33% 19% 13% 34%



#### 4.2.19 Score per residue for model 19

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

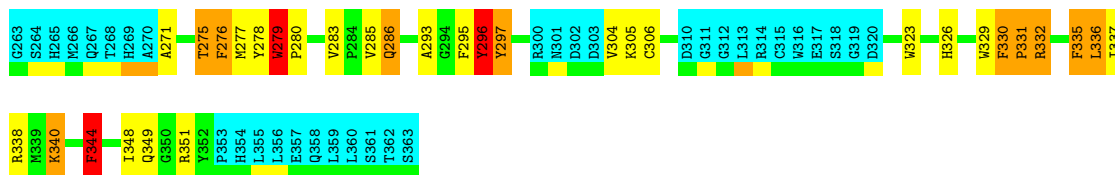
Chain A: 34% 16% 12% 5% 34%



#### 4.2.20 Score per residue for model 20

- Molecule 1: INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1)

Chain A: 35% 19% 10% 34%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS DISTANCE GEOMETRY SIMULATED ANNEALING MOLECULAR DYNAMICS*.

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *STRUCTURES WITH ACCEPTABLE COVALENT GEOMETRY, STRUCTURES WITH FAVORABLE NON- BOND ENERGY, 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
X-PLOR	refinement	3.851

No chemical shift data was provided.

## 6 Model quality i

### 6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	1.09±0.01	0±0/585 ( 0.0± 0.0%)	1.98±0.04	20±2/794 ( 2.5± 0.3%)
All	All	1.09	0/11700 ( 0.0%)	1.98	403/15880 ( 2.5%)

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	1.7±1.1
All	All	0	34

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	296	TYR	CB-CG-CD1	15.77	130.46	121.00	9	20
1	A	330	PHE	CB-CG-CD1	15.09	131.36	120.80	17	20
1	A	296	TYR	CB-CG-CD2	-13.45	112.93	121.00	14	20
1	A	297	TYR	CB-CG-CD1	12.93	128.76	121.00	13	20
1	A	335	PHE	CB-CG-CD1	12.12	129.28	120.80	12	20
1	A	297	TYR	CB-CG-CD2	-11.55	114.07	121.00	3	20
1	A	330	PHE	CB-CG-CD2	-11.25	112.92	120.80	5	20
1	A	276	PHE	CB-CG-CD1	10.69	128.28	120.80	10	20
1	A	335	PHE	CB-CG-CD2	-10.62	113.37	120.80	18	20
1	A	344	PHE	CB-CG-CD2	-9.49	114.16	120.80	19	20
1	A	344	PHE	CB-CG-CD1	9.21	127.25	120.80	19	20
1	A	352	TYR	CB-CG-CD2	-9.02	115.59	121.00	14	16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	352	TYR	CB-CG-CD1	8.46	126.08	121.00	14	16
1	A	286	GLN	N-CA-C	-8.44	88.22	111.00	20	17
1	A	276	PHE	CB-CG-CD2	-7.78	115.35	120.80	17	20
1	A	282	SER	N-CA-CB	7.15	121.23	110.50	4	1
1	A	283	VAL	CA-CB-CG1	6.56	120.74	110.90	15	12
1	A	327	ALA	CB-CA-C	6.46	119.79	110.10	2	2
1	A	333	CYS	N-CA-C	-6.43	93.63	111.00	4	8
1	A	297	TYR	CA-CB-CG	6.30	125.37	113.40	10	9
1	A	349	GLN	N-CA-CB	6.20	121.75	110.60	13	8
1	A	296	TYR	CB-CA-C	6.15	122.70	110.40	13	12
1	A	290	LEU	CB-CG-CD1	6.14	121.44	111.00	18	5
1	A	279	TRP	CA-CB-CG	6.10	125.29	113.70	20	8
1	A	274	ARG	NE-CZ-NH1	6.02	123.31	120.30	4	1
1	A	326	HIS	CA-CB-CG	5.96	123.74	113.60	19	9
1	A	277	MET	CA-CB-CG	5.88	123.30	113.30	15	3
1	A	309	CYS	CA-CB-SG	5.84	124.51	114.00	10	2
1	A	278	TYR	CB-CG-CD1	5.76	124.46	121.00	17	1
1	A	276	PHE	N-CA-CB	-5.65	100.43	110.60	16	8
1	A	332	ARG	N-CA-C	-5.64	95.77	111.00	16	4
1	A	295	PHE	CB-CA-C	-5.63	99.14	110.40	1	7
1	A	327	ALA	N-CA-CB	5.57	117.90	110.10	7	3
1	A	338	ARG	NE-CZ-NH2	-5.54	117.53	120.30	9	3
1	A	338	ARG	NE-CZ-NH1	5.33	122.96	120.30	1	1
1	A	272	ARG	NE-CZ-NH1	5.30	122.95	120.30	2	1
1	A	296	TYR	CA-CB-CG	5.17	123.22	113.40	9	1
1	A	274	ARG	NE-CZ-NH2	-5.13	117.74	120.30	4	1
1	A	306	CYS	CA-CB-SG	5.10	123.19	114.00	2	1
1	A	306	CYS	CB-CA-C	5.10	120.61	110.40	1	1
1	A	333	CYS	N-CA-CB	5.08	119.73	110.60	11	1
1	A	273	MET	CG-SD-CE	-5.05	92.11	100.20	3	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	279	TRP	Mainchain	12
1	A	272	ARG	Sidechain	8
1	A	332	ARG	Sidechain	5
1	A	274	ARG	Sidechain	5
1	A	351	ARG	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	338	ARG	Sidechain	1

## 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	563	532	532	13±2
All	All	11280	10640	10640	264

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:299:GLY:HA3	1:A:304:VAL:HG13	0.79	1.53	9	8
1:A:298:VAL:HG13	1:A:307:PHE:CD2	0.73	2.18	7	1
1:A:323:TRP:CZ3	1:A:336:LEU:HD21	0.66	2.25	14	20
1:A:323:TRP:HZ3	1:A:336:LEU:HD21	0.65	1.52	19	20
1:A:326:HIS:CE1	1:A:336:LEU:HD23	0.63	2.29	20	19
1:A:279:TRP:HE1	1:A:283:VAL:HG23	0.60	1.56	13	13
1:A:344:PHE:CE1	1:A:348:ILE:HG13	0.57	2.34	9	16
1:A:348:ILE:HD12	1:A:352:TYR:CE2	0.56	2.36	13	15
1:A:336:LEU:HD11	1:A:340:LYS:HE3	0.56	1.77	2	2
1:A:299:GLY:HA3	1:A:304:VAL:HG12	0.55	1.78	14	3
1:A:293:ALA:O	1:A:326:HIS:CD2	0.54	2.61	18	18
1:A:279:TRP:HB2	1:A:280:PRO:HD3	0.51	1.83	6	10
1:A:323:TRP:HB3	1:A:344:PHE:CZ	0.50	2.42	9	20
1:A:323:TRP:HB3	1:A:344:PHE:CE2	0.49	2.42	4	20
1:A:287:PRO:HA	1:A:290:LEU:HD13	0.49	1.84	8	2
1:A:271:ALA:O	1:A:275:THR:HG22	0.49	2.07	12	18
1:A:297:TYR:CE1	1:A:298:VAL:HG22	0.48	2.43	5	4
1:A:299:GLY:CA	1:A:304:VAL:HG13	0.48	2.37	2	1
1:A:326:HIS:CE1	1:A:330:PHE:CD2	0.48	3.01	17	8
1:A:277:MET:HG2	1:A:278:TYR:CD1	0.47	2.44	2	2
1:A:340:LYS:HG3	1:A:344:PHE:CD2	0.45	2.46	5	12
1:A:275:THR:HG23	1:A:297:TYR:HA	0.45	1.88	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:298:VAL:HA	1:A:307:PHE:CZ	0.44	2.47	7	1
1:A:348:ILE:HD12	1:A:352:TYR:CZ	0.44	2.47	7	1
1:A:283:VAL:HG21	1:A:290:LEU:CD2	0.43	2.43	6	4
1:A:279:TRP:HZ2	1:A:290:LEU:HD23	0.43	1.74	7	1
1:A:306:CYS:SG	1:A:307:PHE:N	0.43	2.90	3	2
1:A:286:GLN:O	1:A:290:LEU:HD13	0.43	2.14	18	1
1:A:326:HIS:CE1	1:A:330:PHE:CE2	0.42	3.07	14	3
1:A:283:VAL:HG11	1:A:296:TYR:HD2	0.42	1.75	1	1
1:A:325:GLU:HG3	1:A:329:TRP:CH2	0.41	2.50	11	1
1:A:297:TYR:CD1	1:A:298:VAL:HG22	0.41	2.50	9	1
1:A:277:MET:HG3	1:A:278:TYR:CD1	0.41	2.50	15	1
1:A:326:HIS:O	1:A:326:HIS:ND1	0.41	2.48	4	4
1:A:298:VAL:HA	1:A:307:PHE:CE2	0.41	2.51	9	2
1:A:297:TYR:C	1:A:297:TYR:CD1	0.41	2.93	5	2
1:A:306:CYS:HB3	1:A:309:CYS:HB2	0.41	1.93	3	1
1:A:325:GLU:HB2	1:A:329:TRP:CH2	0.41	2.51	10	1
1:A:297:TYR:CD1	1:A:297:TYR:C	0.41	2.94	9	2
1:A:287:PRO:HB3	1:A:296:TYR:CD2	0.40	2.51	1	1
1:A:279:TRP:CB	1:A:280:PRO:HD3	0.40	2.47	3	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	67/101 (66%)	45±2 (67±3%)	14±2 (21±3%)	8±2 (12±2%)	<b>1</b>   <b>7</b>
All	All	1340/2020 (66%)	904 (67%)	279 (21%)	157 (12%)	<b>1</b>   <b>7</b>

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	277	MET	20
1	A	280	PRO	20
1	A	285	VAL	20

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Mol	Chain	Res	Type	Models (Total)
1	A	296	TYR	20
1	A	304	VAL	15
1	A	306	CYS	12
1	A	331	PRO	12
1	A	327	ALA	11
1	A	279	TRP	10
1	A	344	PHE	7
1	A	282	SER	5
1	A	299	GLY	2
1	A	278	TYR	1
1	A	337	ILE	1
1	A	309	CYS	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	59/88 (67%)	40±2 (68±3%)	19±2 (32±3%)	1	14
All	All	1180/1760 (67%)	806 (68%)	374 (32%)	1	14

All 36 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	275	THR	20
1	A	276	PHE	20
1	A	278	TYR	20
1	A	296	TYR	20
1	A	297	TYR	20
1	A	330	PHE	20
1	A	335	PHE	20
1	A	338	ARG	20
1	A	340	LYS	20
1	A	344	PHE	20
1	A	348	ILE	20
1	A	279	TRP	18
1	A	332	ARG	14

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Mol	Chain	Res	Type	Models (Total)
1	A	329	TRP	13
1	A	286	GLN	13
1	A	304	VAL	12
1	A	337	ILE	12
1	A	321	ASP	11
1	A	283	VAL	8
1	A	309	CYS	8
1	A	328	LYS	5
1	A	272	ARG	5
1	A	336	LEU	5
1	A	305	LYS	4
1	A	308	CYS	4
1	A	349	GLN	4
1	A	346	ASP	3
1	A	282	SER	3
1	A	351	ARG	3
1	A	274	ARG	3
1	A	289	GLN	1
1	A	298	VAL	1
1	A	347	GLU	1
1	A	277	MET	1
1	A	339	MET	1
1	A	325	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

## 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