



Full wwPDB NMR Structure Validation Report ⓘ

Mar 3, 2022 – 07:49 AM EST

PDB ID : 2HDP
Title : Solution Structure of Hdm2 RING Finger Domain
Authors : Kostic, M.; Matt, T.; Yamout-Martinez, M.; Dyson, H.J.; Wright, P.E.
Deposited on : 2006-06-20

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

We welcome your comments at validation@mail.wwpdb.org
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 : 2.27
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

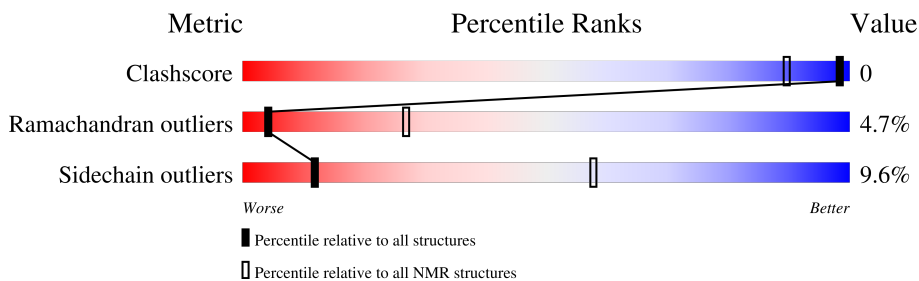
1 Overall quality at a glance

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	63	79% 8% 13%
1	B	63	81% 6% 13%

2 Ensemble composition and analysis i

This entry contains 20 models. Model 18 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:437-A:491, B:437-B:491 (110)	0.69	18

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 5 clusters and 7 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1998 atoms, of which 1028 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ubiquitin-protein ligase E3 Mdm2.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	63	997	309	514	89	76	9	0
1	B	63	997	309	514	89	76	9	0

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

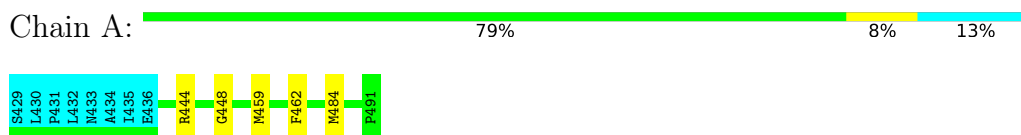
Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2
2	B	2	2	2

4 Residue-property plots [i](#)

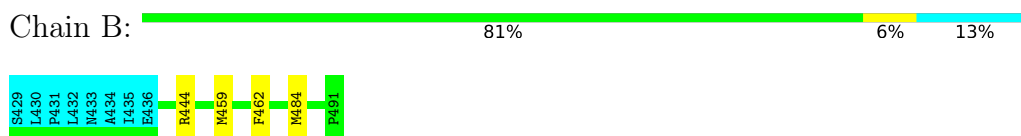
4.1 Average score per residue in the NMR ensemble

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: Ubiquitin-protein ligase E3 Mdm2



- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

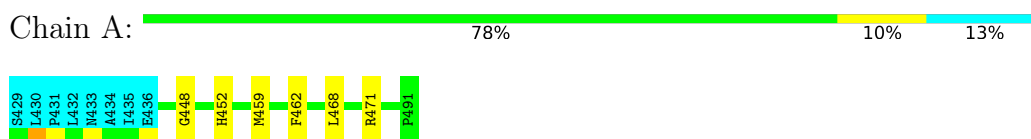


4.2 Scores per residue for each member of the ensemble

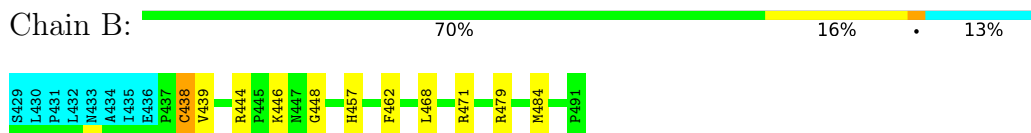
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

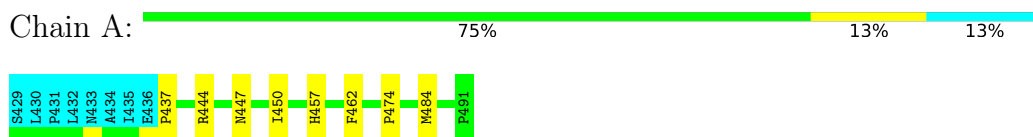


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

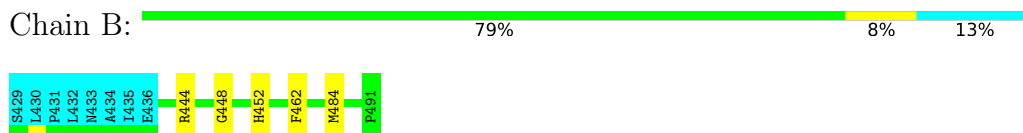


4.2.2 Score per residue for model 2

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

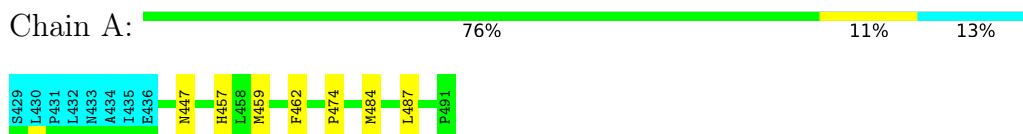


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

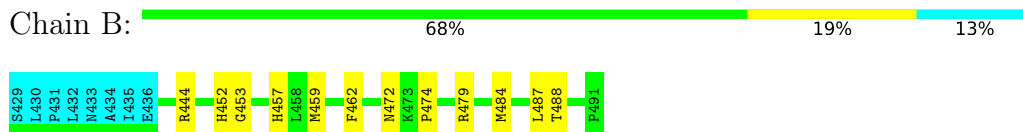


4.2.3 Score per residue for model 3

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

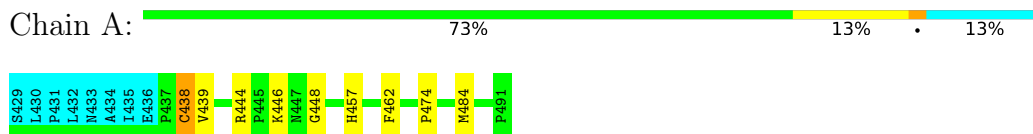


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

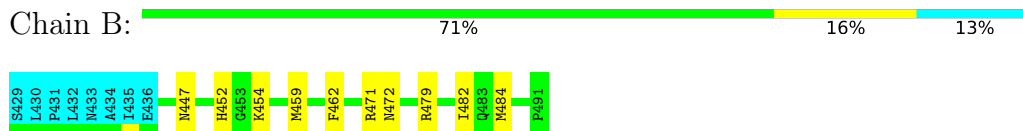


4.2.4 Score per residue for model 4

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

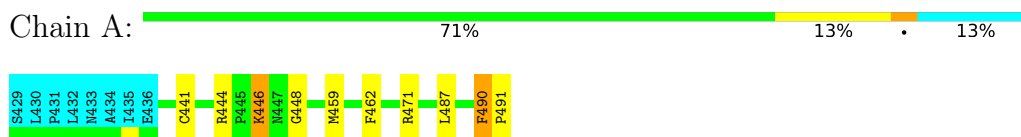


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

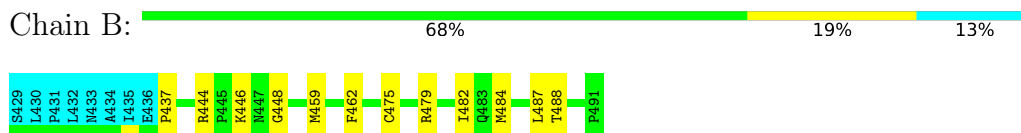


4.2.5 Score per residue for model 5

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

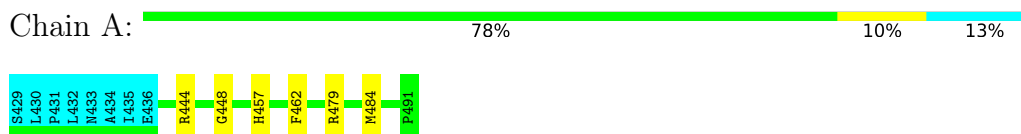


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

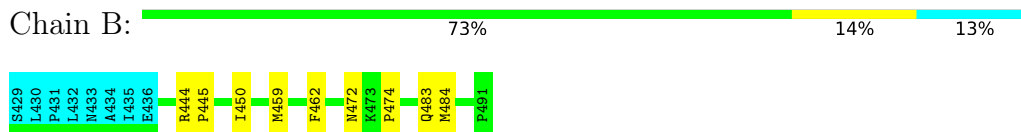


4.2.6 Score per residue for model 6

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

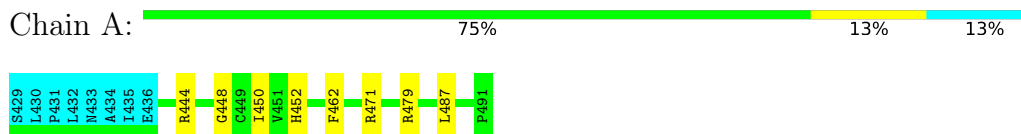


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

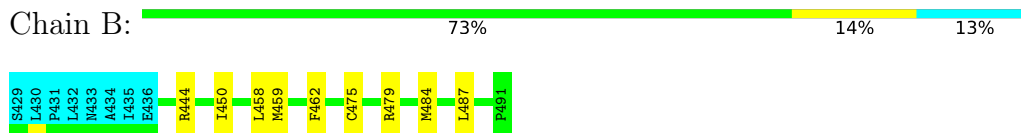


4.2.7 Score per residue for model 7

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

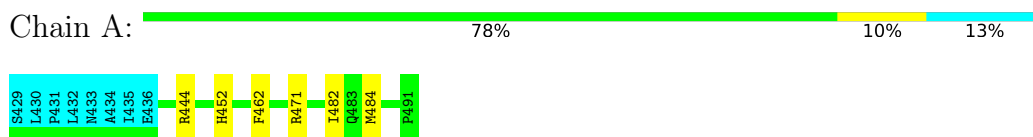


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

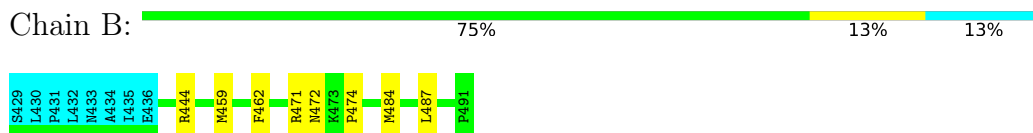


4.2.8 Score per residue for model 8

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

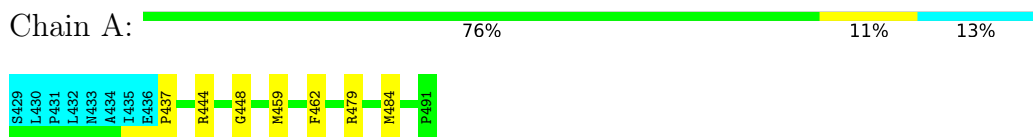


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

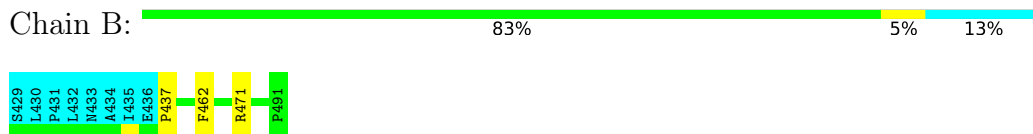


4.2.9 Score per residue for model 9

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

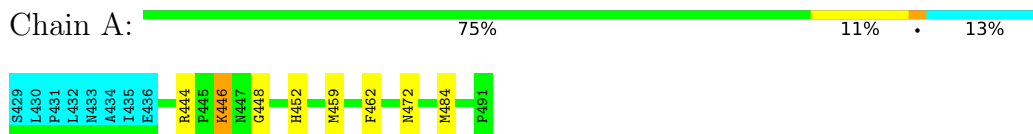


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

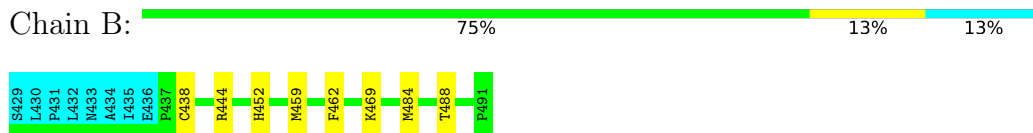


4.2.10 Score per residue for model 10

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

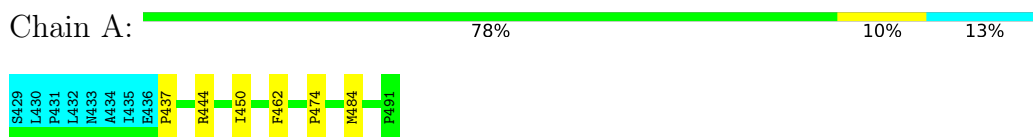


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

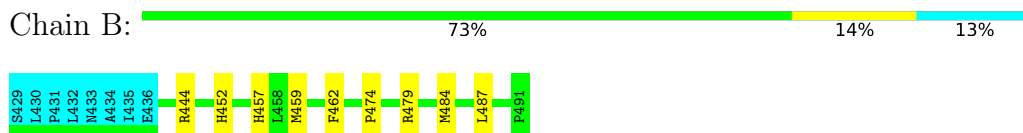


4.2.11 Score per residue for model 11

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

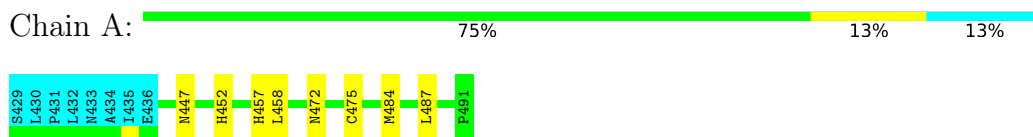


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

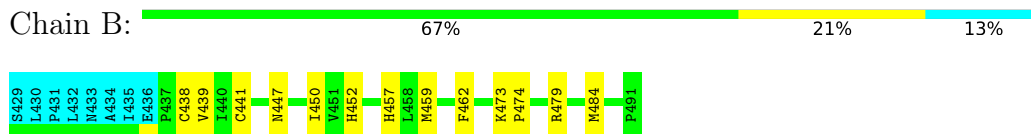


4.2.12 Score per residue for model 12

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

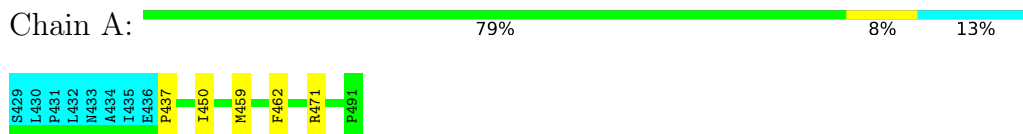


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

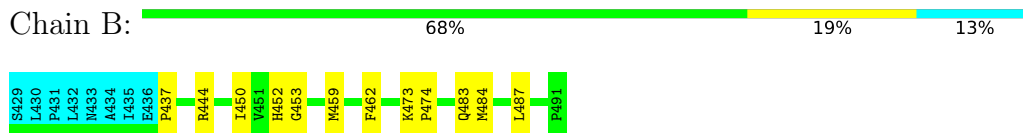


4.2.13 Score per residue for model 13

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

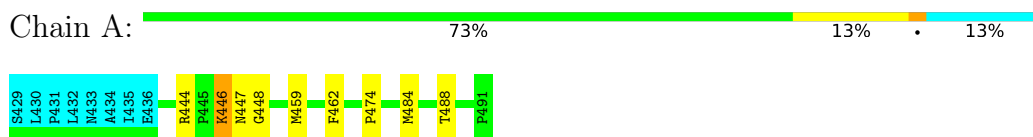


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

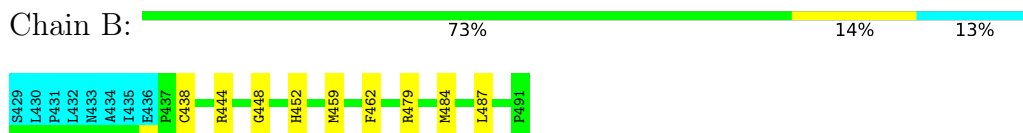


4.2.14 Score per residue for model 14

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

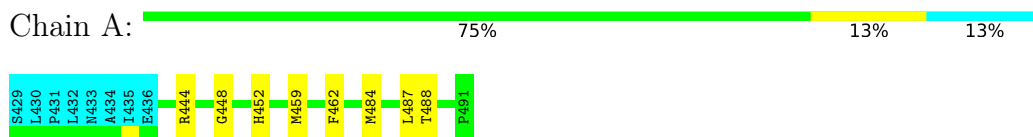


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

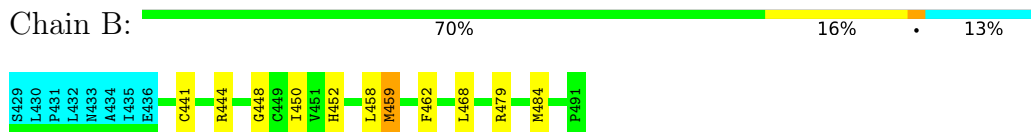


4.2.15 Score per residue for model 15

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

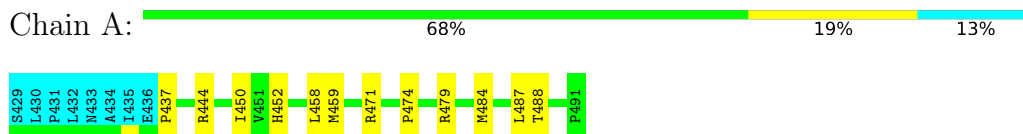


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

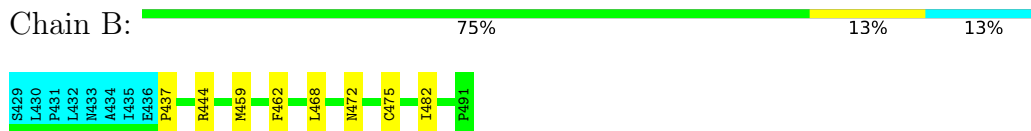


4.2.16 Score per residue for model 16

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

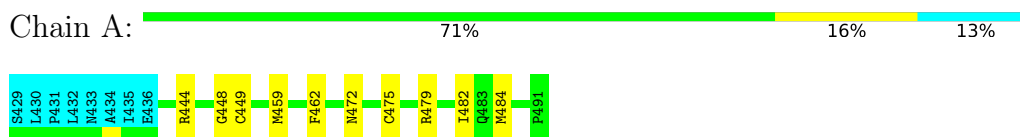


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

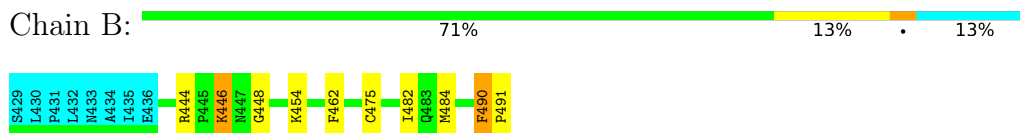


4.2.17 Score per residue for model 17

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

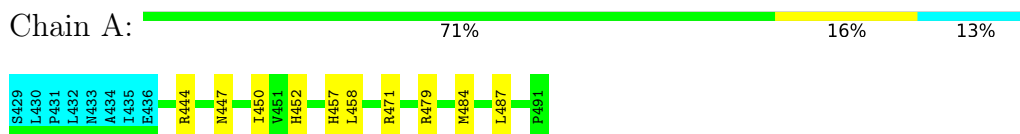


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

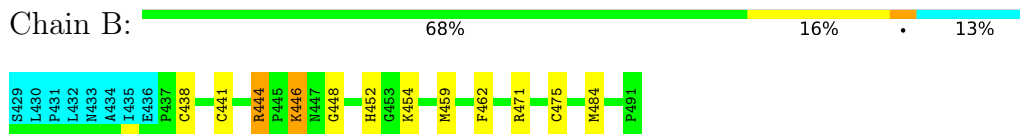


4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

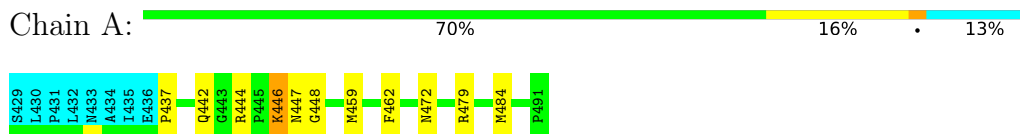


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

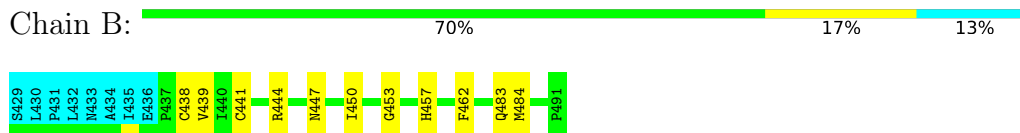


4.2.19 Score per residue for model 19

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

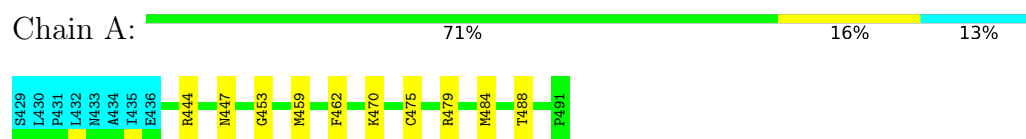


- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

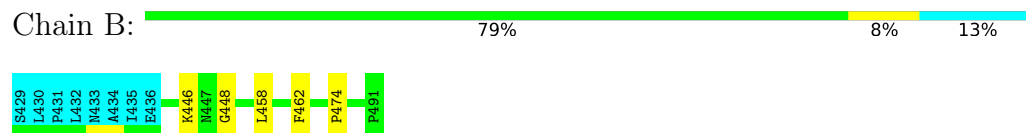


4.2.20 Score per residue for model 20

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2



- Molecule 1: Ubiquitin-protein ligase E3 Mdm2



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 20 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
CYANA	structure solution	2.1
Amber	refinement	8

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	0.66±0.01	0±0/434 (0.0± 0.0%)	1.10±0.03	2±1/582 (0.3± 0.1%)
1	B	0.66±0.01	0±0/434 (0.0± 0.0%)	1.10±0.03	2±1/582 (0.3± 0.1%)
All	All	0.66	0/17360 (0.0%)	1.10	61/23280 (0.3%)

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	B	0.0±0.0	0.1±0.3
All	All	0	2

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	471	ARG	NE-CZ-NH1	7.01	123.80	120.30	18	7
1	B	444	ARG	NE-CZ-NH1	7.00	123.80	120.30	18	15
1	A	444	ARG	NE-CZ-NH1	6.78	123.69	120.30	19	16
1	B	479	ARG	NE-CZ-NH1	5.92	123.26	120.30	5	8
1	A	479	ARG	NE-CZ-NH1	5.85	123.22	120.30	20	8
1	B	444	ARG	NE-CZ-NH2	-5.72	117.44	120.30	18	1
1	B	471	ARG	NE-CZ-NH1	5.71	123.16	120.30	1	5
1	B	444	ARG	CD-NE-CZ	5.25	130.95	123.60	8	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	B	444	ARG	Sidechain	2

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	424	452	452	0±0
1	B	424	452	452	0±0
All	All	17040	18080	18080	6

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:490:PHE:H	1:A:491:PRO:CD	0.43	2.27	5	1
1:B:438:CYS:SG	1:B:439:VAL:N	0.41	2.93	19	3
1:B:490:PHE:H	1:B:491:PRO:CD	0.41	2.28	17	1
1:A:438:CYS:SG	1:A:439:VAL:N	0.41	2.93	4	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	54/63 (86%)	44±2 (81±3%)	8±2 (14±3%)	2±1 (4±2%)	4	29
1	B	54/63 (86%)	43±2 (80±3%)	8±2 (15±3%)	3±1 (5±2%)	4	24
All	All	2160/2520 (86%)	1743 (81%)	315 (15%)	102 (5%)	4	27

All 23 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	459	MET	14
1	A	459	MET	12
1	A	448	GLY	11
1	B	448	GLY	8
1	B	474	PRO	7
1	A	437	PRO	6
1	A	474	PRO	6
1	B	446	LYS	5
1	A	446	LYS	5
1	B	437	PRO	4
1	B	475	CYS	4
1	B	441	CYS	4
1	B	453	GLY	3
1	A	475	CYS	3
1	B	438	CYS	2
1	A	438	CYS	1
1	A	441	CYS	1
1	A	490	PHE	1
1	B	445	PRO	1
1	B	472	ASN	1
1	B	479	ARG	1
1	B	490	PHE	1
1	A	453	GLY	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	49/56 (88%)	45±1 (91±3%)	4±1 (9±3%)	13	60
1	B	49/56 (88%)	44±2 (90±3%)	5±2 (10±3%)	11	56
All	All	1960/2240 (88%)	1772 (90%)	188 (10%)	12	58

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	B	462	PHE	20
1	A	462	PHE	17

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Mol	Chain	Res	Type	Models (Total)
1	B	484	MET	17
1	A	484	MET	16
1	B	452	HIS	10
1	A	452	HIS	8
1	A	447	ASN	7
1	A	487	LEU	7
1	B	487	LEU	7
1	A	450	ILE	6
1	A	457	HIS	6
1	B	450	ILE	6
1	B	457	HIS	5
1	B	472	ASN	4
1	B	482	ILE	4
1	A	446	LYS	4
1	A	472	ASN	4
1	A	488	THR	4
1	B	468	LEU	3
1	B	488	THR	3
1	B	447	ASN	3
1	B	454	LYS	3
1	B	483	GLN	3
1	B	458	LEU	3
1	A	458	LEU	3
1	A	482	ILE	2
1	B	438	CYS	2
1	B	473	LYS	2
1	B	446	LYS	2
1	A	468	LEU	1
1	B	475	CYS	1
1	B	469	LYS	1
1	B	459	MET	1
1	A	449	CYS	1
1	A	442	GLN	1
1	A	470	LYS	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 4 ligands modelled in this entry, 4 are 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