wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1TTV
Title	:	NMR Structure of a Complex Between MDM2 and a Small Molecule Inhibitor
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This is a wwPDB NMR Structure Validation Summary 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

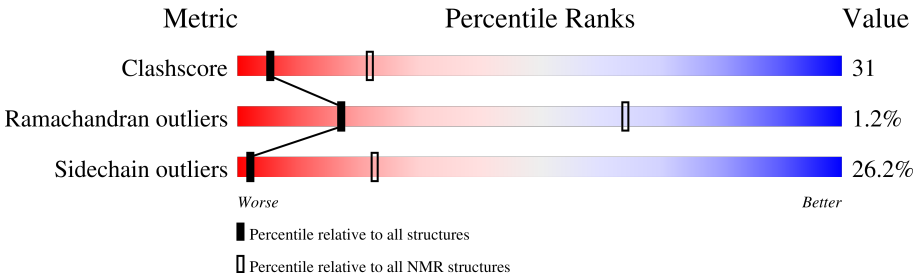
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	107	39% 29% 8% 23%

2 Ensemble composition and analysis (i)

This entry contains 18 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 4 as representative, based on the following criterion: *fewest violations*.

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:23-A:104 (82)	0.20	13

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 5 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1772 atoms, of which 885 are hydrogens and 0 are deuteriums.

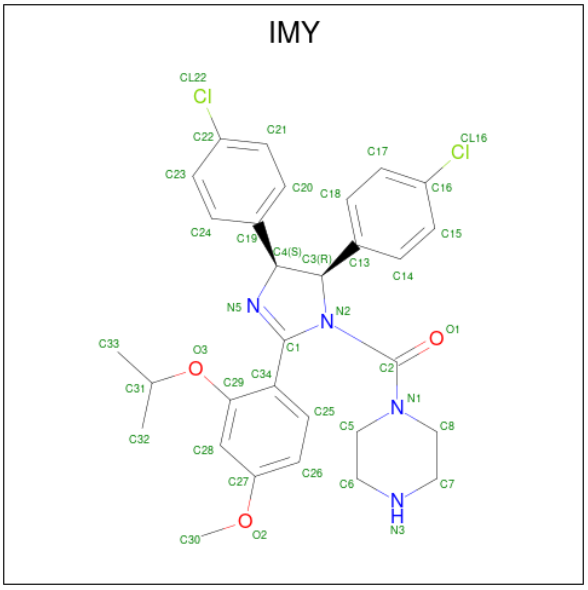
- Molecule 1 is a protein called Ubiquitin-protein ligase E3 Mdm2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	107	1718	541	862	147	164	4	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	LEU	ILE	engineered mutation	UNP P56273
A	92	HIS	PRO	engineered mutation	UNP P56273
A	95	ILE	LEU	engineered mutation	UNP P56273

- Molecule 2 is 1-{[4,5-BIS(4-CHLOROPHENYL)-2-(2-ISOPROPOXY-4-METHOXYPHENYL)-4,5-DIHYDRO-1H-IMIDAZOL-1-YL]CARBONYL}PIPERAZINE (three-letter code: IMY) (formula: $C_{30}H_{32}Cl_2N_4O_3$).



Mol	Chain	Residues	Atoms					
			Total	C	Cl	H	N	O
2	A	1	54	25	2	23	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

Chain A: 39% 29% 8% 23%

N13 H14 I15 S16 T17 S18 D19 Q20 E21 K22 L23 V24 Q25 L29 L30 L33 L34 K35 S36 A39 Q40 K41 E42 T43 F44 T45 M46 K47 E48 V49 L50 Y51 H52 L53 Y56 I57 K60 Q61 L62 K66 Q67 Q68 H69 H72 C73 D76 P77 L78 G79 E80 L81

V89 R94 I95 L103 V104 S105 A106 N107 V108 K109 E110 S111 S112 E113 D114 I115 F116 G117 N118 V119

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 13. Colouring as in section 4.1 above.

- Molecule 1: Ubiquitin-protein ligase E3 Mdm2

Chain A: 40% 29% 7% 23%

N13 H14 I15 S16 T17 S18 D19 Q20 E21 K22 L23 V24 T27 P28 L29 L30 L31 S32 L33 S36 A39 Q40 K41 E42 T43 F44 T45 M46 K47 E48 V49 L50 Y51 H52 L53 Y56 I57 Q61 L62 E65 K66 Q67 Q68 H69 H72 C73 D76 E80 L81 S88

V89 I95 N102 L103 V104 S105 A106 N107 V108 K109 E110 S111 S112 E113 D114 I115 F116 G117 N118 V119

5 Refinement protocol and experimental data overview (i)

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

Of the 42 calculated structures, 18 were deposited, based on the following criterion: *structures with acceptable covalent geometry,structures with the least restraint violations*.

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

Software name	Classification	Version
CNX	structure solution	2000.1
CNX	refinement	2000.1

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: IMY

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	665	685	681	41±5
2	A	31	23	23	17±5
All	All	12528	12744	12672	788

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 31.

5 of 220 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:96:TYR:CE2	2:A:120:IMY:CL22	1.39	2.11	2	1
1:A:69:HIS:HB3	2:A:120:IMY:C30	1.32	1.55	5	14
1:A:68:GLN:O	2:A:120:IMY:H332	1.26	1.26	14	6
1:A:50:LEU:CD1	2:A:120:IMY:H21	1.24	1.61	17	1
1:A:68:GLN:O	2:A:120:IMY:C33	1.17	1.91	14	2

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	82/107 (77%)	72±1 (88±2%)	9±1 (11±1%)	1±1 (1±1%)	17 64
All	All	1476/1926 (77%)	1302 (88%)	156 (11%)	18 (1%)	17 64

All 4 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	41	LYS	11
1	A	104	VAL	5
1	A	66	LYS	1
1	A	86	GLU	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	74/97 (76%)	55±3 (74±3%)	19±3 (26±3%)	2 23
All	All	1332/1746 (76%)	983 (74%)	349 (26%)	2 23

5 of 40 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	36	SER	18
1	A	41	LYS	18
1	A	43	THR	18
1	A	73	CYS	18
1	A	46	MET	17

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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	IMY	A	120	-	34,34,43	1.09±0.01	2±0 (5±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	IMY	A	120	-	42,48,61	1.24±0.01	2±0 (4±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means

no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IMY	A	120	-	-	0±0,18,30,50	0±0,4,4,5

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	120	IMY	C3-N2	3.16	1.50	1.46	9	18
2	A	120	IMY	C1-N5	2.75	1.33	1.29	8	18

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

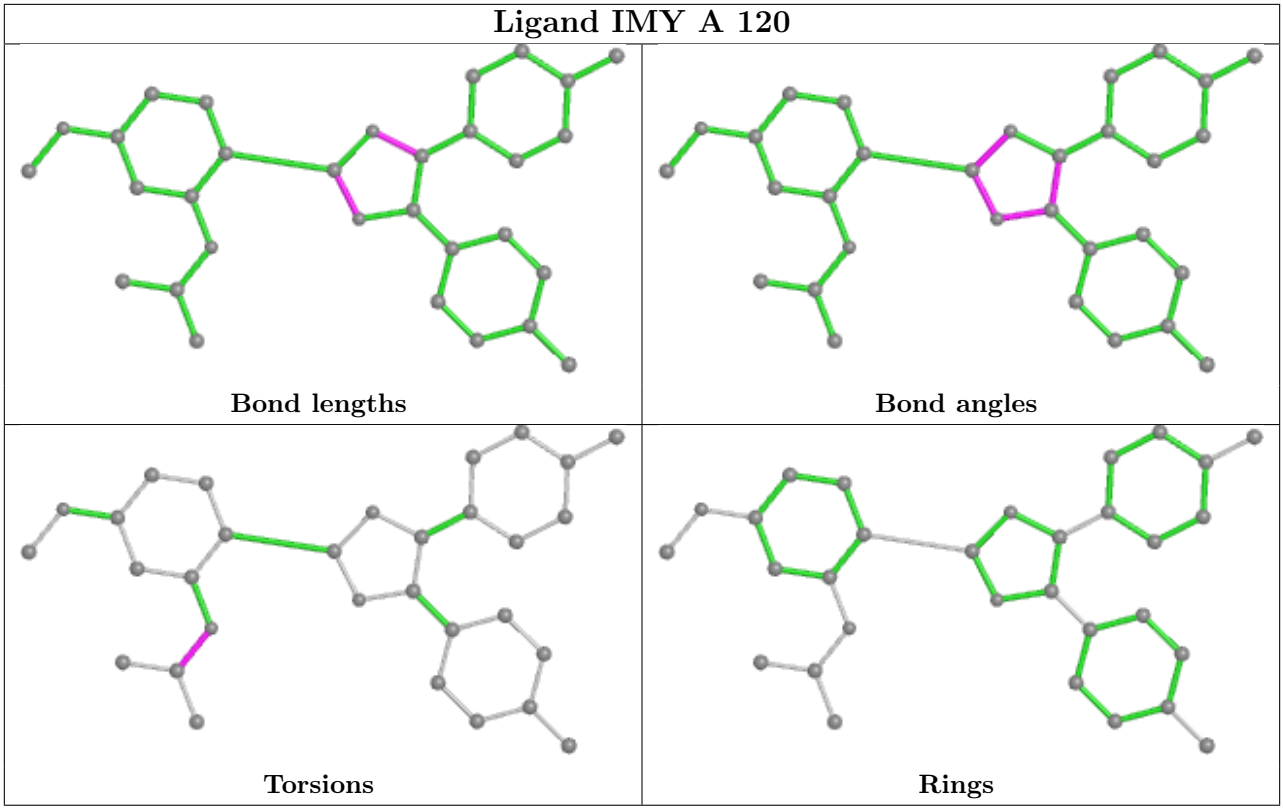
Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	120	IMY	N2-C1-N5	5.22	112.51	116.71	17	18
2	A	120	IMY	C3-C4-N5	3.97	101.13	104.75	16	18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 (i)

No chemical shift data were provided