



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 07:33 PM UTC

PDB ID : 5HP0 / pdb_00005hp0
BMRB ID : 30003
Title : Solution Structure of TAZ2-p53AD2
Authors : Krois, A.S.; Ferreon, J.C.; Martinez-Yamout, M.A.; Dyson, H.J.; Wright, P.E.
Deposited on : 2016-01-19

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A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

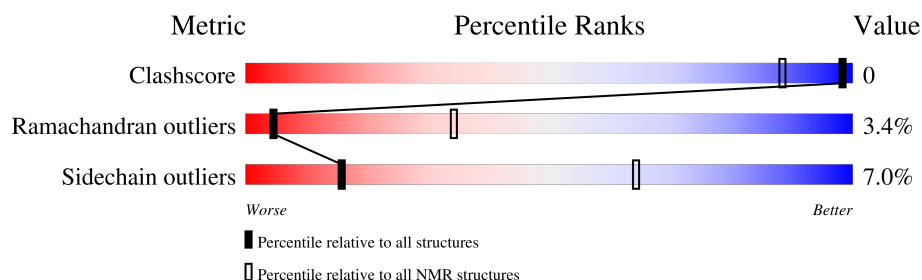
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 84%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	122	

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 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:1768-A:1809, A:1813-A:1851, A:3043-A:3053 (92)	0.25	11

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 2 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1880 atoms, of which 932 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CREB-binding protein, Cellular tumor antigen p53 fusion protein.

Mol	Chain	Residues	Atoms						Trace
1	A	122	Total	C	H	N	O	S	0
			1877	573	932	182	174	16	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2001	GLY	-	linker	UNP P45481
A	2002	SER	-	linker	UNP P45481
A	2003	GLY	-	linker	UNP P45481
A	2004	SER	-	linker	UNP P45481
A	2005	GLY	-	linker	UNP P45481

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

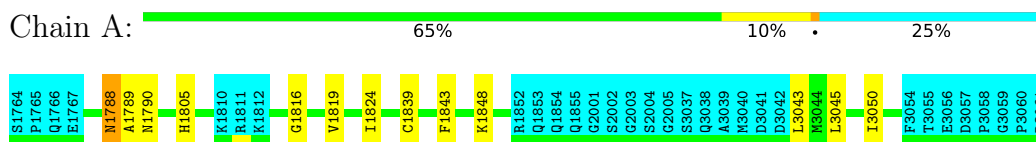
Mol	Chain	Residues	Atoms	
2	A	3	Total	Zn
			3	3

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: CREB-binding protein,Cellular tumor antigen p53 fusion protein

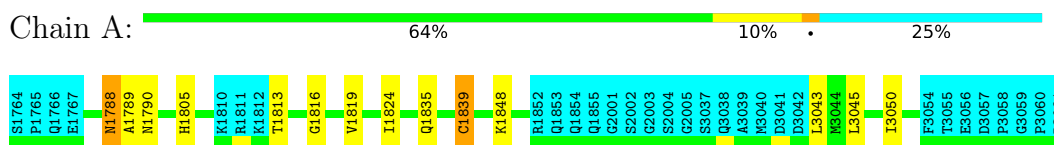


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

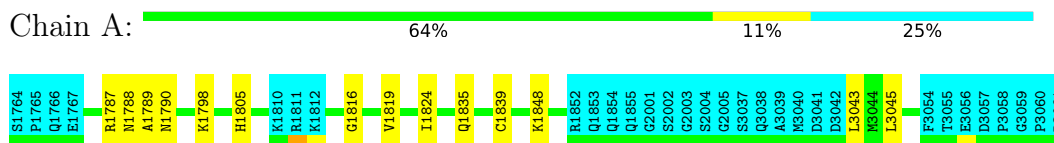
4.2.1 Score per residue for model 1

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



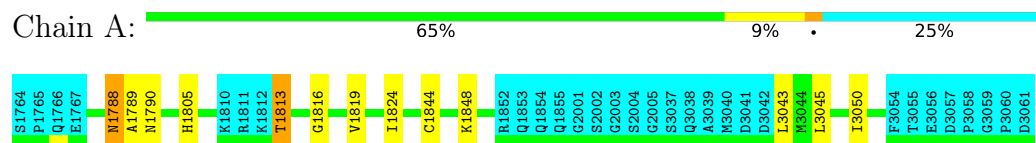
4.2.2 Score per residue for model 2

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



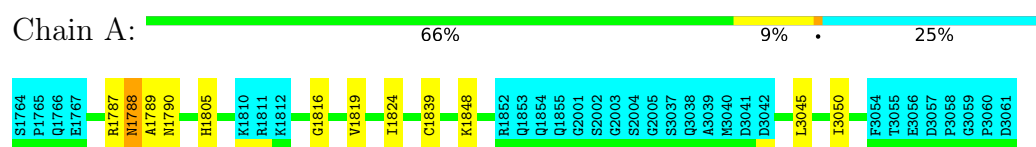
4.2.3 Score per residue for model 3

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



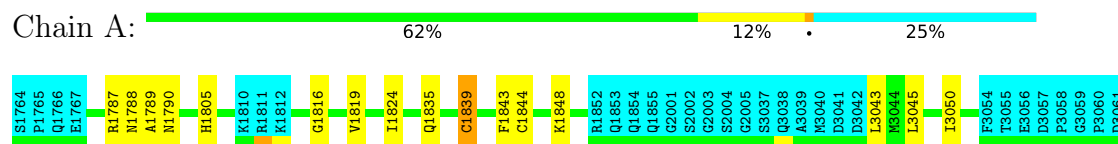
4.2.4 Score per residue for model 4

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



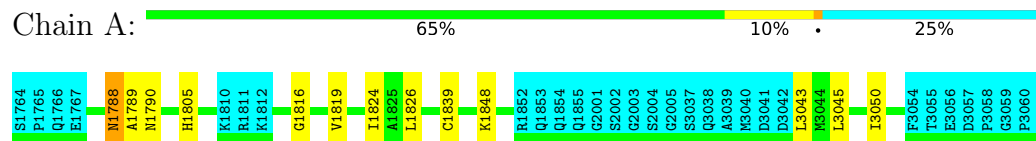
4.2.5 Score per residue for model 5

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



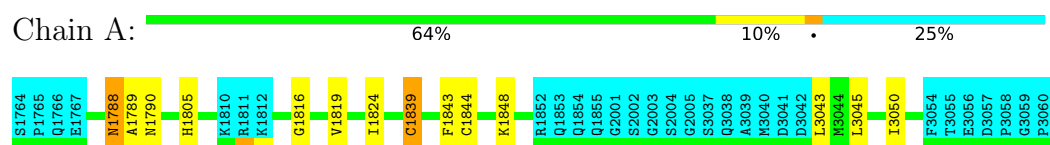
4.2.6 Score per residue for model 6

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



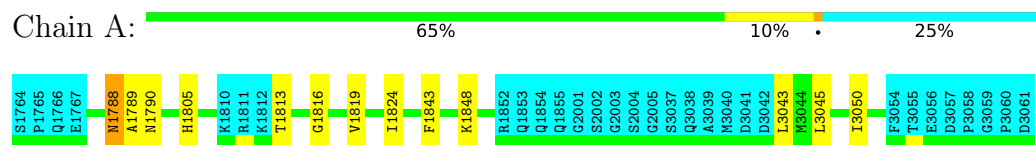
4.2.7 Score per residue for model 7

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



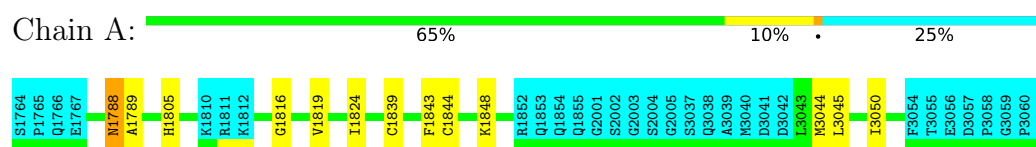
4.2.8 Score per residue for model 8

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



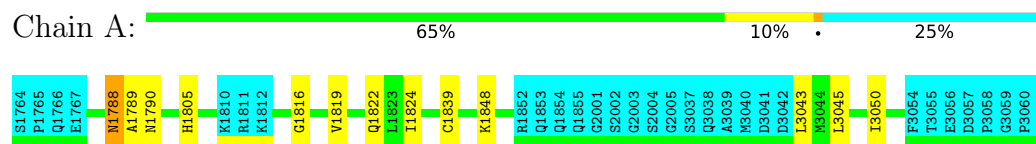
4.2.9 Score per residue for model 9

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



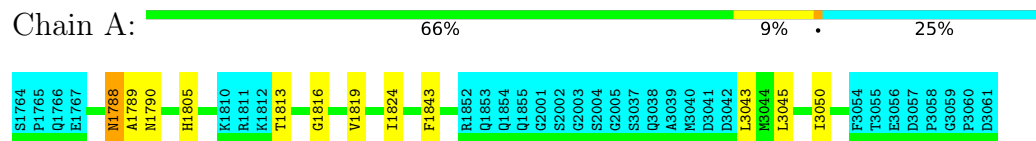
4.2.10 Score per residue for model 10

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



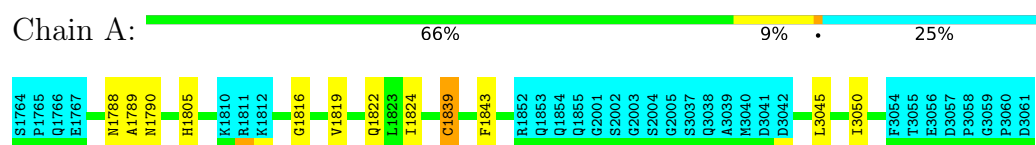
4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



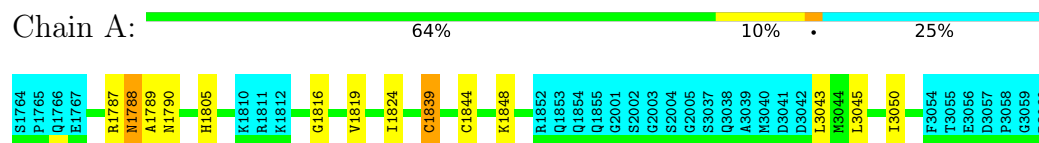
4.2.12 Score per residue for model 12

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



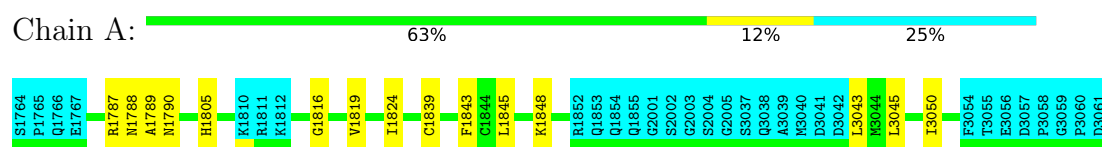
4.2.13 Score per residue for model 13

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



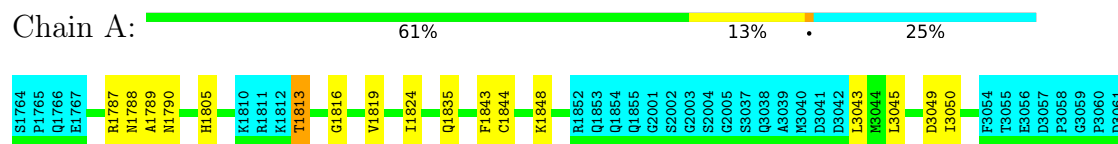
4.2.14 Score per residue for model 14

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



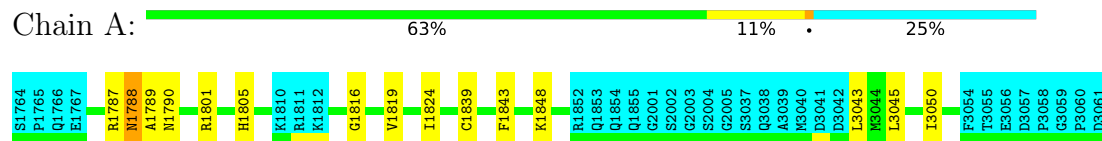
4.2.15 Score per residue for model 15

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



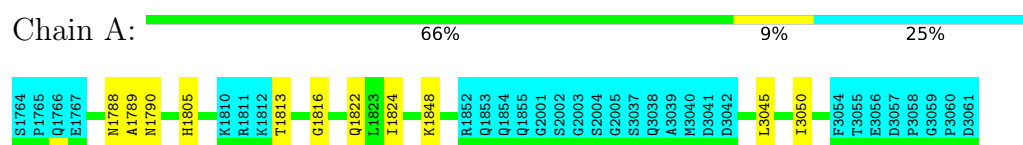
4.2.16 Score per residue for model 16

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



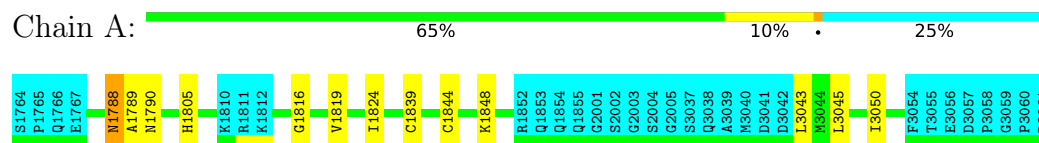
4.2.17 Score per residue for model 17

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



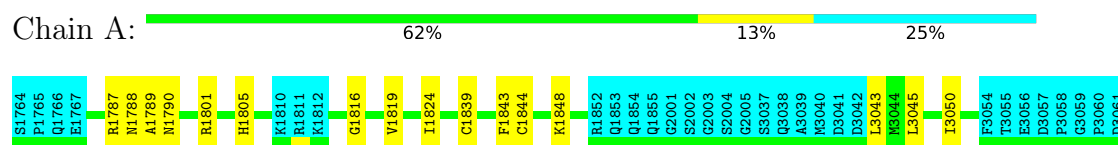
4.2.18 Score per residue for model 18

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



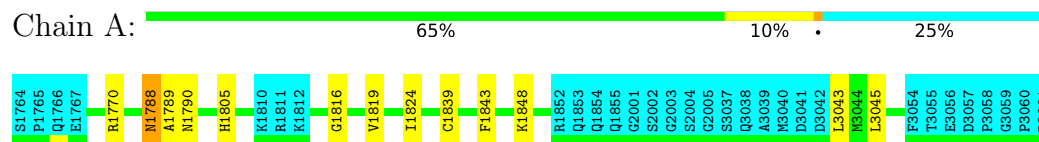
4.2.19 Score per residue for model 19

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



4.2.20 Score per residue for model 20

- Molecule 1: CREB-binding protein,Cellular tumor antigen p53 fusion protein



5 Refinement protocol and experimental data overview

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

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 calculation	2.1
Amber	refinement	12

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1329
Number of shifts mapped to atoms	1329
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

6 Model quality

6.1 Standard geometry

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	0.87±0.01	0±0/732 (0.0± 0.0%)	1.58±0.02	6±2/986 (0.7± 0.2%)
All	All	0.87	0/14640 (0.0%)	1.58	130/19720 (0.7%)

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	1.0±0.0
All	All	0	20

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	1790	ASN	CA-C-N	6.03	129.68	120.82	4	19
1	A	1790	ASN	C-N-CA	6.03	129.68	120.82	4	19
1	A	1788	ASN	CA-C-N	5.87	132.75	121.54	3	20
1	A	1788	ASN	C-N-CA	5.87	132.75	121.54	3	20
1	A	1843	PHE	CA-CB-CG	5.87	119.67	113.80	11	11
1	A	1787	ARG	NE-CZ-NH2	5.57	124.21	119.20	13	8
1	A	1839	CYS	CA-C-N	5.39	125.21	119.28	10	13
1	A	1839	CYS	C-N-CA	5.39	125.21	119.28	10	13
1	A	1813	THR	CA-C-N	5.30	127.64	120.38	15	2
1	A	1813	THR	C-N-CA	5.30	127.64	120.38	15	2
1	A	1801	ARG	NE-CZ-NH2	5.27	123.94	119.20	19	2
1	A	1822	GLN	OE1-CD-NE2	-5.04	117.56	122.60	12	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	1805	HIS	Sidechain	20

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	718	729	727	0±0
All	All	14420	14580	14540	8

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:1844:CYS:SG	1:A:1848:LYS:HE2	0.44	2.52	19	8

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	92/122 (75%)	84±1 (92±1%)	5±1 (5±1%)	3±1 (3±1%)	4	34
All	All	1840/2440 (75%)	1685 (92%)	93 (5%)	62 (3%)	4	34

All 5 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	1789	ALA	20
1	A	1816	GLY	20
1	A	3043	LEU	15
1	A	1813	THR	6
1	A	3044	MET	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	85/110 (77%)	79±1 (93±1%)	6±1 (7±1%)	16	64
All	All	1700/2200 (77%)	1581 (93%)	119 (7%)	16	64

All 15 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	1824	ILE	20
1	A	3045	LEU	20
1	A	1819	VAL	19
1	A	3050	ILE	18
1	A	1788	ASN	13
1	A	1848	LYS	10
1	A	1839	CYS	7
1	A	1835	GLN	4
1	A	1822	GLN	2
1	A	1798	LYS	1
1	A	1826	LEU	1
1	A	1845	LEU	1
1	A	3049	ASP	1
1	A	3043	LEU	1
1	A	1770	ARG	1

6.3.3 RNA ⓘ

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *p53ad2_corrected_shifts.str*

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	1329
Number of shifts mapped to atoms	1329
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	118	-0.38 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	111	0.33 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	105	-0.48 ± 0.31	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 84%, i.e. 1056 atoms were assigned a chemical shift out of a possible 1258. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	352/453 (78%)	178/182 (98%)	91/184 (49%)	83/87 (95%)
Sidechain	659/737 (89%)	451/478 (94%)	196/223 (88%)	12/36 (33%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	45/68 (66%)	25/35 (71%)	19/25 (76%)	1/8 (12%)
Overall	1056/1258 (84%)	654/695 (94%)	306/432 (71%)	96/131 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 82%, i.e. 1328 atoms were assigned a chemical shift out of a possible 1620. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	453/601 (75%)	230/243 (95%)	118/244 (48%)	105/114 (92%)
Sidechain	822/941 (87%)	561/604 (93%)	245/288 (85%)	16/49 (33%)
Aromatic	53/78 (68%)	30/40 (75%)	22/30 (73%)	1/8 (12%)
Overall	1328/1620 (82%)	821/887 (93%)	385/562 (69%)	122/171 (71%)

7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	1806	THR	HG1	5.52	0.08 – 2.19	20.8
1	A	1816	GLY	N	128.64	91.59 – 127.52	5.3

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

