



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 28, 2026 – 02:27 AM UTC

PDB ID : 1TBA / pdb_00001tba
Title : SOLUTION STRUCTURE OF A TBP-TAFII230 COMPLEX: PROTEIN MIMICRY OF THE MINOR GROOVE SURFACE OF THE TATA BOX UNWOUND BY TBP, NMR, 25 STRUCTURES
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Deposited on : 1998-08-16

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 ⓘ 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

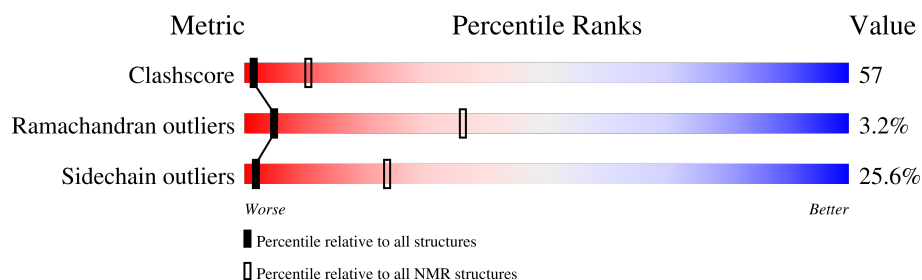
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

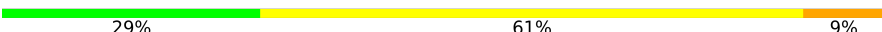
The overall completeness of chemical shifts assignment was not calculated.

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	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	67	
2	B	180	

2 Ensemble composition and analysis

This entry contains 25 models. Model 3 is the overall representative, medoid model (most similar to other models).

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:18-A:35, A:50-A:74, B:63-B:240 (221)	0.77	3

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 4 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 5, 7, 9, 10, 16, 18, 24
2	6, 8, 11, 14, 15, 17, 22, 23, 25
3	20, 21
Single-model clusters	4; 12; 13; 19

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3881 atoms, of which 1974 are hydrogens and 0 are deuteriums.

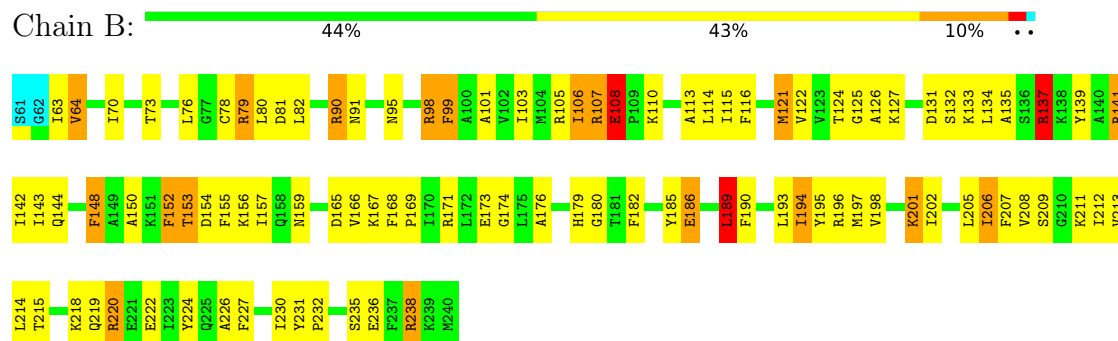
- Molecule 1 is a protein called TRANSCRIPTION INITIATION FACTOR IID 230K CHAIN.

Mol	Chain	Residues	Atoms						Trace
1	A	67	Total	C	H	N	O	S	0
			969	299	478	82	109	1	

- Molecule 2 is a protein called TRANSCRIPTION INITIATION FACTOR TFIID.

Mol	Chain	Residues	Atoms						Trace
2	B	180	Total	C	H	N	O	S	0
			2912	921	1496	242	247	6	

- Molecule 2: TRANSCRIPTION INITIATION FACTOR TFIID



5 Refinement protocol and experimental data overview ⓘ

Of the ? calculated structures, 25 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
X-PLOR	refinement	3.851

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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	1.46±0.02	0±0/326 (0.0± 0.1%)	1.60±0.02	1±1/439 (0.1± 0.2%)
2	B	1.44±0.01	0±0/1433 (0.0± 0.0%)	1.62±0.01	8±2/1929 (0.4± 0.1%)
All	All	1.45	6/43975 (0.0%)	1.62	210/59200 (0.4%)

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	1.9±0.3
2	B	0.0±0.0	10.4±0.9
All	All	0	306

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
1	A	27	ASN	C-N	-6.79	1.29	1.33	15	3
2	B	192	GLY	N-CA	5.55	1.49	1.44	6	2
2	B	168	PHE	N-CA	5.04	1.49	1.46	20	1

5 of 35 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
2	B	106	ILE	N-CA-CB	-6.52	105.15	112.45	13	8
2	B	63	ILE	N-CA-CB	-6.31	105.02	112.40	21	3
2	B	123	VAL	N-CA-CB	-6.22	105.25	112.34	14	8
2	B	206	ILE	N-CA-CB	-6.17	105.01	112.35	19	10
2	B	190	PHE	N-CA-CB	-6.14	105.50	111.27	5	1

There are no chirality outliers.

5 of 13 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	B	238	ARG	Sidechain	25
1	A	53	ARG	Sidechain	24
2	B	90	ARG	Sidechain	24
2	B	141	ARG	Sidechain	24
2	B	171	ARG	Sidechain	24

6.2 Too-close contacts

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	325	341	341	117±13
2	B	1406	1486	1486	113±16
All	All	43275	45675	45675	5030

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 57.

5 of 1704 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:ILE:HD11	1:A:74:LEU:HD12	1.11	1.13	1	18
2:B:76:LEU:HD22	2:B:150:ALA:HB1	1.11	1.15	10	21
2:B:99:PHE:CE2	2:B:101:ALA:HB3	1.09	1.83	17	12
1:A:18:LEU:HD21	1:A:20:LEU:HD21	1.09	1.18	1	23
1:A:74:LEU:HD11	2:B:101:ALA:HB2	1.05	1.26	11	13

6.3 Torsion angles

6.3.1 Protein backbone

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	43/67 (64%)	30±2 (70±4%)	9±2 (20±5%)	4±1 (10±3%)	1	9
2	B	177/180 (98%)	158±4 (89±2%)	16±3 (9±2%)	3±1 (2±1%)	11	57
All	All	5500/6175 (89%)	4709 (86%)	616 (11%)	175 (3%)	5	36

5 of 28 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	27	ASN	25
1	A	30	SER	24
1	A	72	ILE	18
2	B	64	VAL	17
1	A	63	GLY	15

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	37/52 (71%)	23±2 (61±5%)	14±2 (39±5%)	0	6
2	B	151/152 (99%)	117±5 (78±3%)	34±5 (22±3%)	2	29
All	All	4700/5100 (92%)	3499 (74%)	1201 (26%)	2	23

5 of 136 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	18	LEU	25
1	A	28	ILE	22
1	A	53	ARG	22
1	A	33	ARG	20
2	B	114	LEU	19

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](#)

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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided