



# wwPDB X-ray Structure Validation Summary Report

Sep 26, 2023 – 02:58 PM EDT

PDB ID : 6CO1  
Title : Structure of human TIRR in complex with 53BP1 Tudor domains  
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Deposited on : 2018-03-10  
Resolution : 2.18 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp>

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>.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

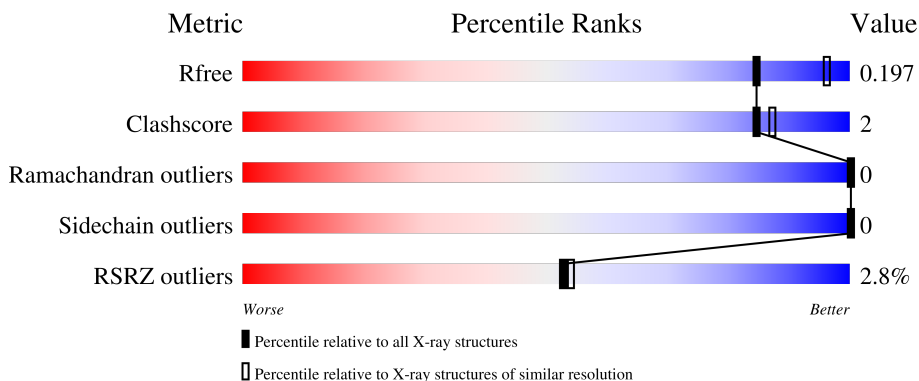
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.18 Å.

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.



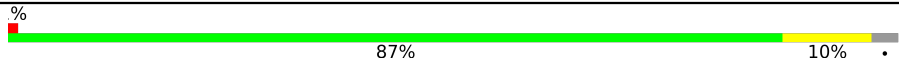
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	207	 2% 94% 5%
1	B	207	 3% 91% 5%
1	C	207	 5% 93%
1	D	207	 1% 93%
2	E	123	 3% 96%

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Mol	Chain	Length	Quality of chain
2	F	123	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into two segments: a green segment on the left labeled '87%' and a yellow segment on the right labeled '10%'. A small red square is at the beginning of the bar, and a small grey square is at the end. A '%' symbol is positioned above the start of the bar, and a '.' symbol is positioned below the end of the bar.</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18080 atoms, of which 8596 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tudor-interacting repair regulator protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	201	3310	1044	1672	298	286	10	24	14	0
1	B	200	3246	1024	1643	291	278	10	23	8	0
1	C	202	3304	1040	1678	298	278	10	0	8	0
1	D	201	3331	1050	1686	301	284	10	0	13	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	-	initiating methionine	UNP Q9BRJ7
B	5	MET	-	initiating methionine	UNP Q9BRJ7
C	5	MET	-	initiating methionine	UNP Q9BRJ7
D	5	MET	-	initiating methionine	UNP Q9BRJ7

- Molecule 2 is a protein called TP53-binding protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	E	120	1942	623	962	164	190	3	0	5	0
2	F	119	1927	619	955	161	189	3	0	5	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1481	GLY	-	expression tag	UNP Q12888
E	1482	HIS	-	expression tag	UNP Q12888
E	1483	MET	-	expression tag	UNP Q12888
F	1481	GLY	-	expression tag	UNP Q12888

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1482	HIS	-	expression tag	UNP Q12888
F	1483	MET	-	expression tag	UNP Q12888

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	224	Total O 224 224	0	0
3	B	191	Total O 191 191	0	0
3	C	164	Total O 164 164	0	0
3	D	204	Total O 204 204	0	0
3	E	116	Total O 116 116	0	0
3	F	121	Total O 121 121	0	0

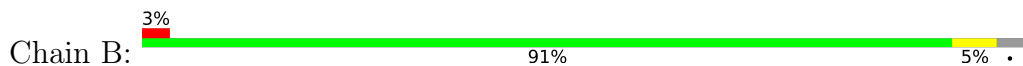
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

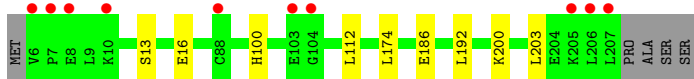
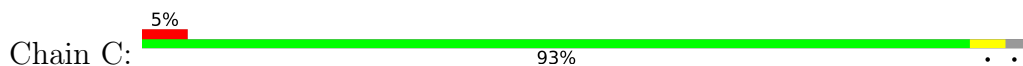
- Molecule 1: Tudor-interacting repair regulator protein



- Molecule 1: Tudor-interacting repair regulator protein



- Molecule 1: Tudor-interacting repair regulator protein




- Molecule 1: Tudor-interacting repair regulator protein



- Molecule 2: TP53-binding protein 1



- Molecule 2: TP53-binding protein 1

Chain F:  %  
87% 10%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.84Å 77.03Å 77.24Å 85.24° 86.07° 86.09°	Depositor
Resolution (Å)	38.31 – 2.18 46.63 – 2.18	Depositor EDS
% Data completeness (in resolution range)	99.5 (38.31-2.18) 98.9 (46.63-2.18)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 2.18Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.164 , 0.203 0.166 , 0.197	Depositor DCC
$R_{free}$ test set	1997 reflections (2.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.3	Xtrriage
Anisotropy	0.001	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 43.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.478 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	18080	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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 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	0.25	0/1723	0.42	0/2326
1	B	0.25	0/1667	0.42	0/2248
1	C	0.25	0/1692	0.41	0/2281
1	D	0.24	0/1721	0.41	0/2321
2	E	0.25	0/1017	0.43	0/1365
2	F	0.25	0/1009	0.44	0/1354
All	All	0.25	0/8829	0.42	0/11895

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1638	1672	1606	6	0
1	B	1603	1643	1603	13	0
1	C	1626	1678	1641	8	0
1	D	1645	1686	1637	8	0
2	E	980	962	949	1	0
2	F	972	955	939	9	0
3	A	224	0	0	2	0
3	B	191	0	0	0	0
3	C	164	0	0	2	0
3	D	204	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	116	0	0	0	0
3	F	121	0	0	0	0
All	All	9484	8596	8375	39	0

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 2.

The worst 5 of 39 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:MET:CE	1:B:187:LYS:HG2	2.03	0.89
1:B:183:MET:HE1	1:B:187:LYS:HG2	1.55	0.86
1:B:184:PRO:HD2	1:B:187:LYS:HD3	1.76	0.67
1:C:112:LEU:HB2	3:C:332:HOH:O	2.01	0.60
2:F:1494:LYS:NZ	2:F:1531:ASP:OD1	2.26	0.59

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	213/207 (103%)	204 (96%)	9 (4%)	0	100	100
1	B	206/207 (100%)	200 (97%)	6 (3%)	0	100	100
1	C	208/207 (100%)	201 (97%)	7 (3%)	0	100	100
1	D	211/207 (102%)	205 (97%)	6 (3%)	0	100	100
2	E	123/123 (100%)	121 (98%)	2 (2%)	0	100	100
2	F	122/123 (99%)	117 (96%)	5 (4%)	0	100	100
All	All	1083/1074 (101%)	1048 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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	179/172 (104%)	179 (100%)	0	100	100
1	B	173/172 (101%)	173 (100%)	0	100	100
1	C	176/172 (102%)	176 (100%)	0	100	100
1	D	178/172 (104%)	178 (100%)	0	100	100
2	E	106/103 (103%)	106 (100%)	0	100	100
2	F	105/103 (102%)	105 (100%)	0	100	100
All	All	917/894 (103%)	917 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	201/207 (97%)	-0.20	4 (1%) 65 66	9, 18, 43, 116	1 (0%)
1	B	200/207 (96%)	-0.02	7 (3%) 44 44	10, 22, 55, 85	0
1	C	202/207 (97%)	-0.03	10 (4%) 28 30	10, 21, 56, 113	0
1	D	201/207 (97%)	-0.15	3 (1%) 73 74	9, 18, 45, 90	0
2	E	120/123 (97%)	-0.07	4 (3%) 46 47	11, 23, 64, 119	0
2	F	119/123 (96%)	-0.12	1 (0%) 86 86	9, 25, 50, 76	0
All	All	1043/1074 (97%)	-0.10	29 (2%) 53 54	9, 20, 56, 119	1 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	206[A]	LEU	6.5
1	A	88	CYS	5.9
1	C	104	GLY	5.7
1	B	88	CYS	4.9
2	E	1550[A]	ASP	4.7

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.