



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:45 PM GMT

PDB ID : 1CA4  
Title : STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2)  
Authors : Park, Y.C.; Burkitt, V.; Villa, A.R.; Tong, L.; Wu, H.  
Deposited on : 1999-02-23  
Resolution : 2.20 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

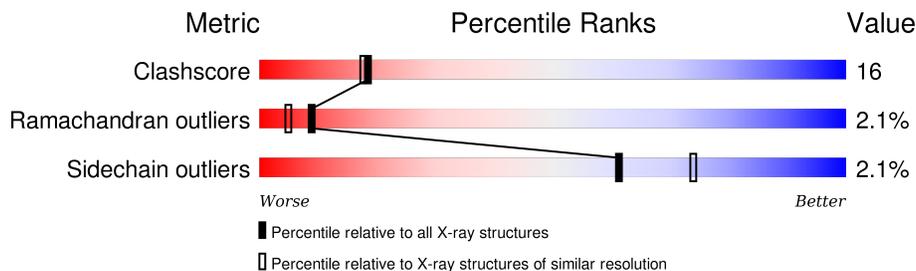
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	168	
1	B	168	
1	C	168	
1	D	168	
1	E	168	
1	F	168	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8435 atoms, of which 0 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 PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	168	1282	825	217	231	9	0	0	0
1	B	168	1282	825	217	231	9	0	0	0
1	C	168	1282	825	217	231	9	0	0	0
1	D	168	1282	825	217	231	9	0	0	0
1	E	168	1282	825	217	231	9	0	0	0
1	F	168	1282	825	217	231	9	0	0	0

- Molecule 2 is water.

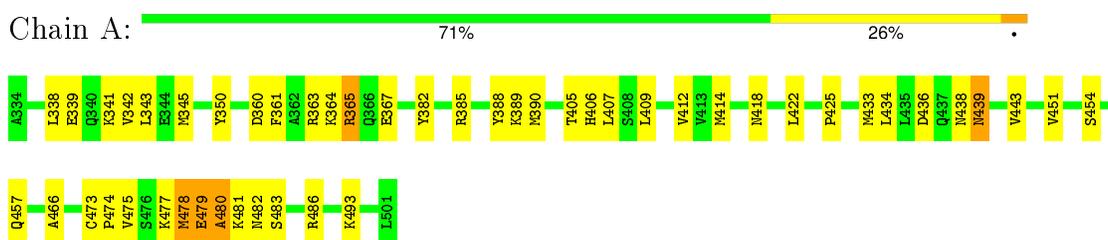
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	118	Total 118	O 118	0	0
2	B	136	Total 136	O 136	0	0
2	C	138	Total 138	O 138	0	0
2	D	90	Total 90	O 90	0	0
2	E	94	Total 94	O 94	0	0
2	F	167	Total 167	O 167	0	0

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

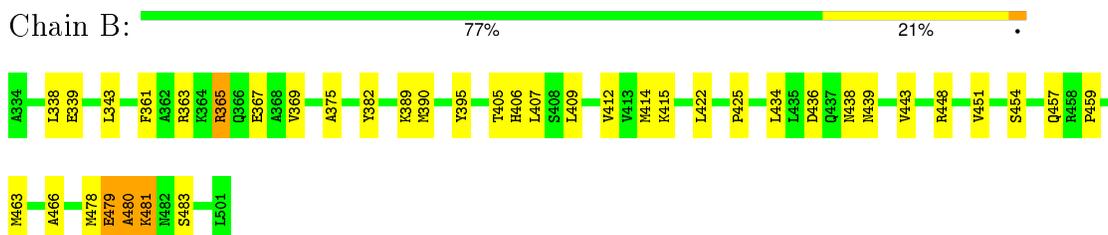
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

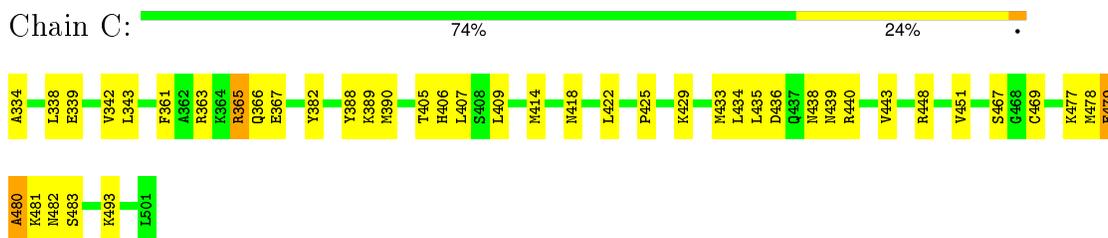
- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)



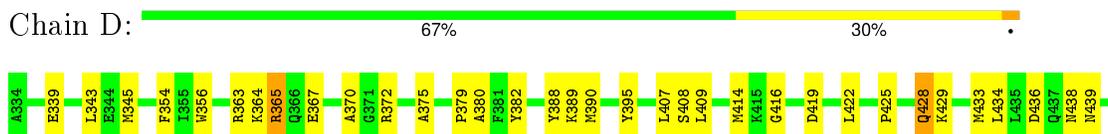
- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)



- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)



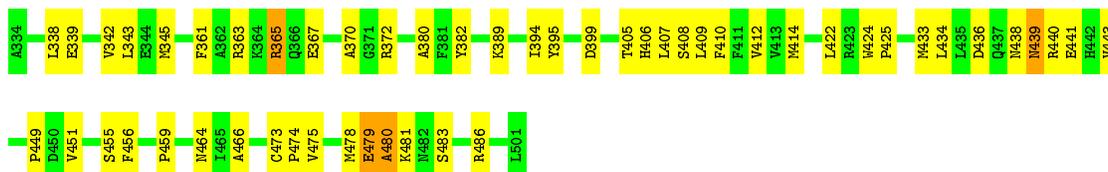
- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)





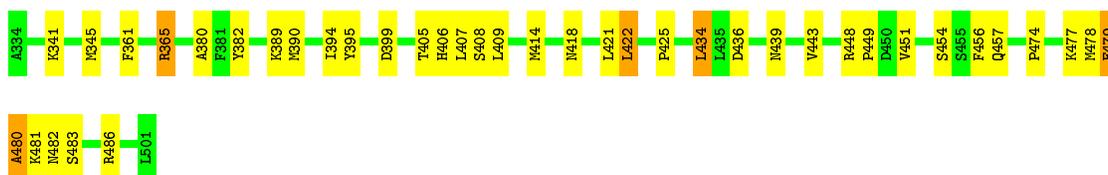
- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)

Chain E: 69% 29%



- Molecule 1: PROTEIN (TNF RECEPTOR ASSOCIATED FACTOR 2)

Chain F: 76% 21%



Chain F: 76% 21%



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.92Å 84.96Å 124.07Å 90.00° 118.60° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20	Depositor
% Data completeness (in resolution range)	92.7 (20.00-2.20)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.209 , 0.251	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8435	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

## 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	0.37	0/1312	0.67	0/1781
1	B	0.37	0/1312	0.67	0/1781
1	C	0.37	0/1312	0.68	0/1781
1	D	0.35	0/1312	0.65	0/1781
1	E	0.36	0/1312	0.66	0/1781
1	F	0.39	0/1312	0.68	1/1781 (0.1%)
All	All	0.37	0/7872	0.67	1/10686 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	434	LEU	N-CA-C	-5.18	97.02	111.00

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	1282	0	1242	39	0
1	B	1282	0	1242	36	0
1	C	1282	0	1242	39	0
1	D	1282	0	1242	45	0
1	E	1282	0	1242	43	0
1	F	1282	0	1242	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	118	0	0	0	0
2	B	136	0	0	3	0
2	C	138	0	0	4	0
2	D	90	0	0	0	0
2	E	94	0	0	3	0
2	F	167	0	0	5	0
All	All	8435	0	7452	235	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 16.

The worst 5 of 235 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:A:425:PRO:HG3	1:A:451:VAL:HG13	1.33	1.03
1:C:425:PRO:HG3	1:C:451:VAL:HG13	1.44	0.99
1:E:425:PRO:HG3	1:E:451:VAL:HG13	1.45	0.98
1:F:394:ILE:HD11	1:F:407:LEU:HD21	1.45	0.96
1:F:425:PRO:HG3	1:F:451:VAL:HG13	1.51	0.92

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	166/168 (99%)	155 (93%)	7 (4%)	4 (2%)	<b>7</b> <b>4</b>
1	B	166/168 (99%)	155 (93%)	8 (5%)	3 (2%)	<b>11</b> <b>7</b>
1	C	166/168 (99%)	155 (93%)	8 (5%)	3 (2%)	<b>11</b> <b>7</b>
1	D	166/168 (99%)	155 (93%)	8 (5%)	3 (2%)	<b>11</b> <b>7</b>
1	E	166/168 (99%)	154 (93%)	7 (4%)	5 (3%)	<b>5</b> <b>2</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	166/168 (99%)	155 (93%)	8 (5%)	3 (2%)	11	7
All	All	996/1008 (99%)	929 (93%)	46 (5%)	21 (2%)	9	5

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	GLU
1	A	481	LYS
1	B	479	GLU
1	B	480	ALA
1	B	481	LYS

### 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	132/144 (92%)	129 (98%)	3 (2%)	58	71
1	B	132/144 (92%)	129 (98%)	3 (2%)	58	71
1	C	132/144 (92%)	130 (98%)	2 (2%)	72	84
1	D	132/144 (92%)	129 (98%)	3 (2%)	58	71
1	E	132/144 (92%)	129 (98%)	3 (2%)	58	71
1	F	132/144 (92%)	129 (98%)	3 (2%)	58	71
All	All	792/864 (92%)	775 (98%)	17 (2%)	61	74

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	409	LEU
1	D	365	ARG
1	E	422	LEU
1	C	365	ARG
1	F	365	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	439	ASN
1	C	461	ASN
1	E	461	ASN
1	C	406	HIS
1	F	366	GLN

### 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 carbohydrates 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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers

EDS was not executed - this section will therefore be empty.