

# wwPDB X-ray Structure Validation Summary Report (i)

#### Aug 14, 2023 – 11:35 PM EDT

PDB ID : 1RF3

Title: Structurally Distinct Recognition Motifs in Lymphotoxin-B Receptor and

CD40 for TRAF-mediated Signaling

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Deposited on : 2003-11-07

Resolution : 3.50 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

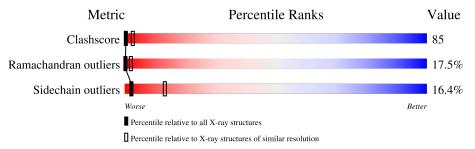
Validation Pipeline (wwPDB-VP) : 2.35

### 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	Similar resolution	
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$	
Clashscore	141614	1036 (3.58-3.42)	
Ramachandran outliers	138981	1005 (3.58-3.42)	
Sidechain outliers	138945	1006 (3.58-3.42)	

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 >=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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain				
1	A	200	16%	58%	20%		
2	В	24	21%	38%	38%	<del>.</del>	



## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1709 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 TNF receptor associated factor 3.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	192	Total 1531	C 979	N 259	O 282	S 11	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	505	LEU	-	expression tag	UNP Q13114
A	506	GLU	-	expression tag	UNP Q13114
A	507	HIS	-	expression tag	UNP Q13114
A	508	HIS	-	expression tag	UNP Q13114
A	509	HIS	-	expression tag	UNP Q13114
A	510	HIS	-	expression tag	UNP Q13114
A	511	HIS	=	expression tag	UNP Q13114
A	512	HIS	-	expression tag	UNP Q13114

• Molecule 2 is a protein called 24-residue peptide from Lymphotoxin-B Receptor.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	B	24	Total	С	N	О	0	0	0
	ט	24	178	111	28	39			

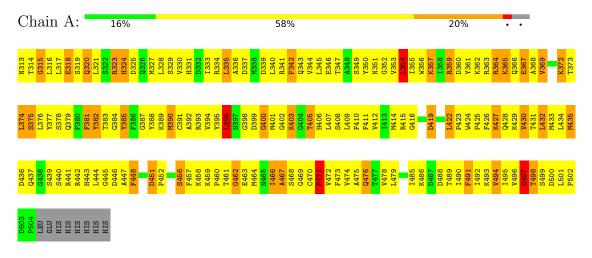


# 3 Residue-property plots (i)

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. 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. 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: TNF receptor associated factor 3



• Molecule 2: 24-residue peptide from Lymphotoxin-B Receptor







# 4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants	83.70Å 83.70Å 79.10Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	8.00 - 3.50	Depositor
% Data completeness	83.0 (8.00-3.50)	Depositor
(in resolution range)	09.0 (0.00 9.00)	Берозгог
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
Refinement program	CNS	Depositor
$R, R_{free}$	0.266 , $0.315$	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1709	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	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	ol Chain I		lengths	Bond	angles
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.46	0/1566	0.71	0/2113
2	В	0.48	0/186	0.76	0/254
All	All	0.47	0/1752	0.72	0/2367

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	1531	0	1526	266	0
2	В	178	0	158	36	0
All	All	1709	0	1684	290	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 85.

The worst 5 of 290 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:406:HIS:HA	1:A:476:GLN:HG2	1.32	1.11
1:A:323:ARG:HH11	1:A:323:ARG:HB3	1.21	1.02

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Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:A:399:ASP:HA	1:A:403:LYS:HD2	1.39	1.01
1:A:409:LEU:HD12	1:A:410:PHE:H	1.30	0.97
1:A:432:LEU:HA	1:A:494:VAL:HA	1.47	0.96

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	190/200~(95%)	125 (66%)	38 (20%)	27 (14%)	0 3
2	В	22/24~(92%)	8 (36%)	4 (18%)	10 (46%)	0 0
All	All	212/224 (95%)	133 (63%)	42 (20%)	37 (18%)	0 2

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	375	SER
1	A	385	TYR
1	A	439	SER
1	A	471	PRO
1	A	476	GLN

#### 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	Perce	ntiles
1	A	169/177 (96%)	141 (83%)	28 (17%)	2	13
2	В	20/20 (100%)	17 (85%)	3 (15%)	3	17
All	All	189/197 (96%)	158 (84%)	31 (16%)	2	13

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	390	MET
1	A	497	ASP
1	A	422	LEU
2	В	393	ASP
1	A	491	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	443	HIS
1	A	476	GLN
2	В	404	GLN
1	A	366	GLN
1	A	379	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 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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

#### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

#### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

