



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2026 – 10:10 am BST

PDB ID : 9S3I / pdb\_00009s3i  
Title : Crystal structure of the human tumor necrosis factor receptor 1 extracellular domain at 1.64Å resolution  
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Deposited on : 2025-07-24  
Resolution : 1.64 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 4-5-2 with Phenix2.0  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

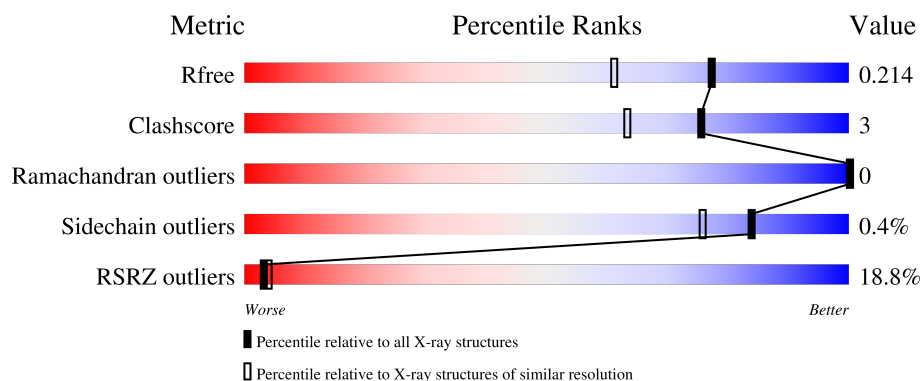
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.64 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))
$R_{free}$	180053	1141 (1.64-1.64)
Clashscore	190562	1171 (1.64-1.64)
Ramachandran outliers	187476	1151 (1.64-1.64)
Sidechain outliers	187428	1150 (1.64-1.64)
RSRZ outliers	180081	1141 (1.64-1.64)

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	164	<div> <div>10%</div> <div>72%</div> <div>5%</div> <div>23%</div> </div>
1	B	164	<div> <div>21%</div> <div>77%</div> <div>7%</div> <div>15%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4292 atoms, of which 1901 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 Tumor necrosis factor receptor superfamily member 1A, membrane form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	127	Total	C	H	N	O	S	0	2	0
			1902	595	907	183	197	20			
1	B	139	Total	C	H	N	O	S	0	2	0
			2088	658	994	201	214	21			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP P19438
A	10	PRO	-	expression tag	UNP P19438
B	9	GLY	-	expression tag	UNP P19438
B	10	PRO	-	expression tag	UNP P19438

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

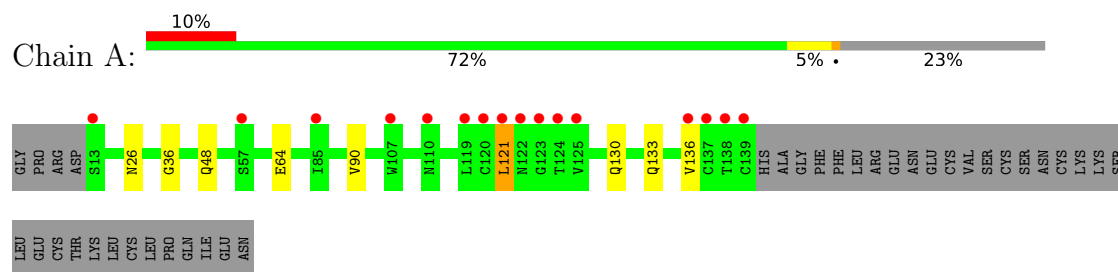
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	129	Total	O	0	1
			130	130		
3	B	135	Total	O	0	2
			137	137		

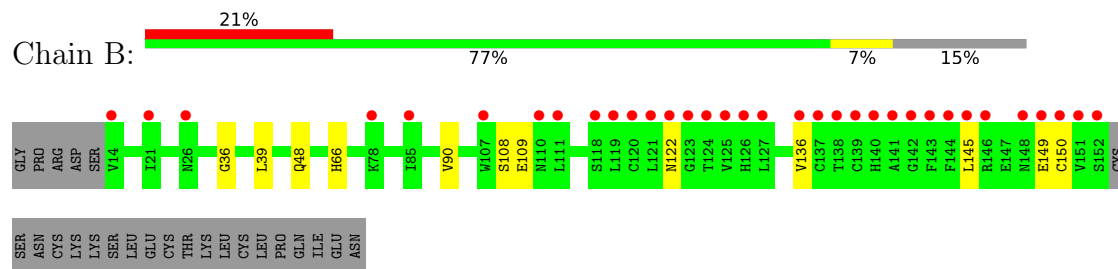
### 3 Residue-property plots [i](#)

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: Tumor necrosis factor receptor superfamily member 1A, membrane form



- Molecule 1: Tumor necrosis factor receptor superfamily member 1A, membrane form



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.22Å 69.22Å 185.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.72 – 1.64 27.72 – 1.64	Depositor EDS
% Data completeness (in resolution range)	100.0 (27.72-1.64) 100.0 (27.72-1.64)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.23 (at 1.64Å)	Xtriage
Refinement program	PHENIX v1.20.1_4487	Depositor
R, $R_{free}$	0.205 , 0.238 0.207 , 0.214	Depositor DCC
$R_{free}$ test set	2809 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.4	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.48 , 83.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4292	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.48	0/1021	0.66	0/1377
1	B	0.45	0/1123	0.64	0/1514
All	All	0.46	0/2144	0.65	0/2891

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

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	995	907	899	7	0
1	B	1094	994	986	7	0
2	A	15	0	0	0	0
2	B	20	0	0	0	0
3	A	130	0	0	2	0
3	B	137	0	0	0	0
All	All	2391	1901	1885	12	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 3.

All (12) 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:121:LEU:HD12	1:A:121:LEU:H	1.65	0.60
1:A:130:GLN:HB2	1:A:133:GLN:HB3	1.87	0.56
1:B:36:GLY:HA2	1:B:90:VAL:O	2.14	0.48
1:A:48:GLN:OE1	1:B:48:GLN:NE2	2.37	0.47
1:B:39:LEU:HD22	1:B:66:HIS:HB2	1.98	0.44
1:B:145:LEU:HA	1:B:149:GLU:O	2.18	0.44
1:B:122:ASN:O	1:B:150:CYS:SG	2.76	0.43
1:A:64:GLU:HG2	3:A:397[B]:HOH:O	2.16	0.43
1:A:136:VAL:HG11	1:B:136:VAL:HG11	2.02	0.42
1:B:108:SER:O	1:B:109:GLU:C	2.63	0.42
1:A:26:ASN:OD1	3:A:301:HOH:O	2.22	0.41
1:A:36:GLY:HA2	1:A:90:VAL:O	2.20	0.41

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	127/164 (77%)	124 (98%)	3 (2%)	0	100	100
1	B	139/164 (85%)	134 (96%)	5 (4%)	0	100	100
All	All	266/328 (81%)	258 (97%)	8 (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	120/152 (79%)	119 (99%)	1 (1%)	73	58
1	B	130/152 (86%)	130 (100%)	0	100	100
All	All	250/304 (82%)	249 (100%)	1 (0%)	84	76

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	LEU

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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	PO4	B	202	-	4,4,4	0.96	0	6,6,6	0.62	0
2	PO4	A	202	-	4,4,4	0.93	0	6,6,6	0.67	0
2	PO4	B	204	-	4,4,4	0.88	0	6,6,6	0.45	0
2	PO4	A	201	-	4,4,4	1.13	0	6,6,6	0.83	0
2	PO4	A	203	-	4,4,4	0.81	0	6,6,6	0.48	0
2	PO4	B	203	-	4,4,4	0.95	0	6,6,6	0.37	0
2	PO4	B	201	-	4,4,4	1.12	0	6,6,6	0.82	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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

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	127/164 (77%)	0.52	16 (12%) 8 9	17, 43, 99, 177	1 (0%)
1	B	139/164 (84%)	1.03	34 (24%) 2 2	18, 45, 154, 188	1 (0%)
All	All	266/328 (81%)	0.79	50 (18%) 3 4	17, 45, 147, 188	2 (0%)

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	145	LEU	7.4
1	B	143	PHE	7.4
1	B	152	SER	7.2
1	B	151	VAL	6.4
1	B	138	THR	6.4
1	B	144	PHE	6.1
1	B	121	LEU	5.9
1	B	14	VAL	5.7
1	A	121	LEU	5.5
1	B	125	VAL	5.4
1	A	139	CYS	4.8
1	B	110	ASN	4.3
1	B	140	HIS	4.1
1	B	150	CYS	4.0
1	B	124	THR	3.8
1	A	85	ILE	3.6
1	B	141	ALA	3.6
1	B	146	ARG	3.6
1	B	142	GLY	3.6
1	B	21	ILE	3.5
1	B	123	GLY	3.4
1	B	120	CYS	3.3
1	A	13	SER	3.2
1	A	138	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	122	ASN	3.2
1	B	122	ASN	3.2
1	B	139	CYS	3.2
1	A	124	THR	3.1
1	A	125	VAL	2.8
1	B	78	LYS	2.8
1	B	148	ASN	2.8
1	B	137	CYS	2.8
1	B	127	LEU	2.7
1	B	126	HIS	2.7
1	A	107	TRP	2.7
1	A	110	ASN	2.6
1	B	136	VAL	2.5
1	B	111	LEU	2.4
1	B	107	TRP	2.4
1	A	136	VAL	2.4
1	A	120	CYS	2.3
1	B	85	ILE	2.3
1	B	118	SER	2.3
1	A	119	LEU	2.2
1	A	137	CYS	2.2
1	B	149	GLU	2.1
1	B	119	LEU	2.1
1	B	26	ASN	2.0
1	A	123	GLY	2.0
1	A	57	SER	2.0

## 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 oligosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	B	204	5/5	0.79	0.23	39,40,50,57	5
2	PO4	B	201	5/5	0.83	0.22	23,52,56,57	5
2	PO4	A	201	5/5	0.86	0.22	24,45,51,54	5
2	PO4	A	203	5/5	0.86	0.15	50,55,64,73	5
2	PO4	B	202	5/5	0.88	0.17	53,54,60,71	5
2	PO4	A	202	5/5	0.89	0.14	49,51,58,60	5
2	PO4	B	203	5/5	0.92	0.16	40,49,58,62	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.