



# Full wwPDB X-ray Structure Validation Report ⓘ

May 5, 2025 – 10:09 AM EDT

PDB ID : 1TBE / pdb\_00001tbe  
Title : STRUCTURE OF TETRAUBIQUITIN SHOWS HOW MULTIUBIQUITIN CHAINS CAN BE FORMED  
Authors : Cook, W.J.; Jeffrey, L.C.; Kasperek, E.; Pickart, C.M.  
Deposited on : 1993-10-14  
Resolution : 2.40 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

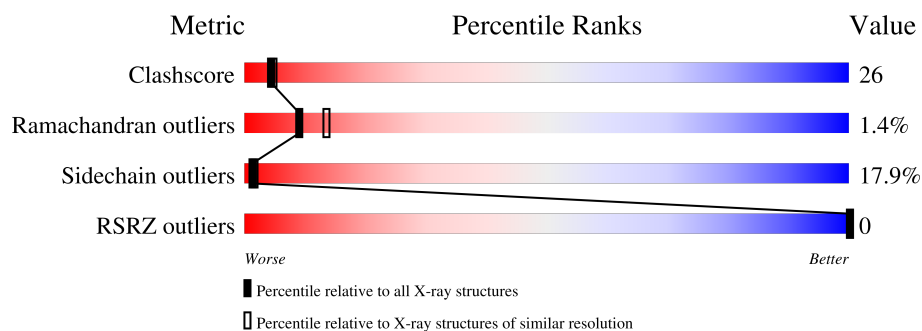
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

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	76	
1	B	76	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1175 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.

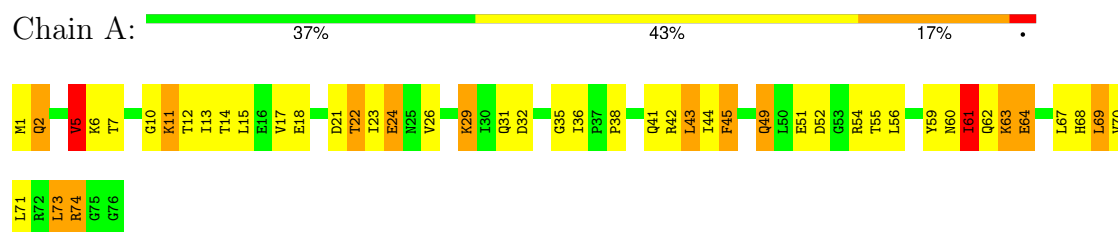
- Molecule 1 is a protein called TETRAUBIQUITIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	76	Total	C	N	O	S	0	0	0
			601	378	105	117	1			
1	B	72	Total	C	N	O	S	0	0	0
			574	362	98	113	1			

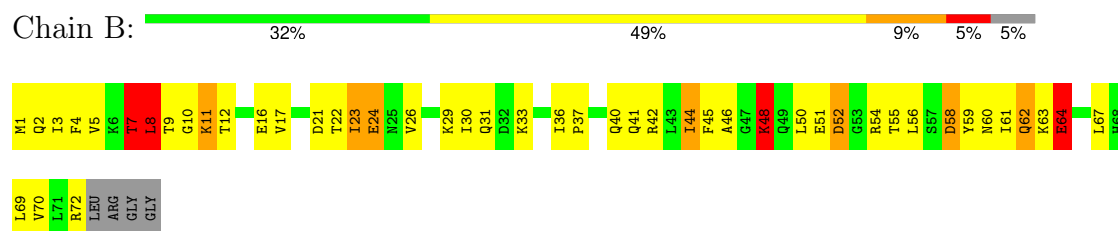
### 3 Residue-property plots [i](#)

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: TETRAUBIQUITIN



#### • Molecule 1: TETRAUBIQUITIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	24.10Å 57.00Å 47.00Å 90.00° 94.06° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.40 46.88 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.40) 76.7 (46.88-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.184 , (Not available) 0.178 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.3	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 76.8	EDS
L-test for twinning <sup>1</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	1175	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</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

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	1.18	0/607	2.15	22/816 (2.7%)
1	B	1.16	0/580	2.26	29/781 (3.7%)
All	All	1.17	0/1187	2.21	51/1597 (3.2%)

There are no bond length outliers.

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	52	ASP	CA-CB-CG	10.68	123.28	112.60
1	A	51	GLU	CA-C-N	10.25	134.43	120.38
1	A	51	GLU	C-N-CA	10.25	134.43	120.38
1	B	58	ASP	CA-CB-CG	10.19	122.79	112.60
1	B	37	PRO	O-C-N	8.77	125.27	121.15
1	B	64	GLU	CB-CG-CD	8.40	126.89	112.60
1	A	49	GLN	OE1-CD-NE2	-7.22	115.38	122.60
1	B	10	GLY	N-CA-C	7.22	130.29	113.18
1	B	64	GLU	CA-C-N	7.15	133.26	121.39
1	B	64	GLU	C-N-CA	7.15	133.26	121.39
1	A	29	LYS	N-CA-C	-7.12	102.94	111.69
1	B	72	ARG	CA-CB-CG	7.10	128.31	114.10
1	A	52	ASP	N-CA-C	6.79	119.54	111.33
1	A	64	GLU	CA-CB-CG	6.71	127.51	114.10
1	A	18	GLU	CA-CB-CG	6.69	127.49	114.10
1	A	24	GLU	CA-CB-CG	6.67	127.44	114.10
1	B	21	ASP	CA-CB-CG	6.65	119.25	112.60
1	A	21	ASP	CA-CB-CG	6.63	119.23	112.60
1	B	36	ILE	CA-C-N	6.51	124.34	119.66
1	B	36	ILE	C-N-CA	6.51	124.34	119.66
1	B	51	GLU	CA-C-N	6.45	129.79	120.38
1	B	51	GLU	C-N-CA	6.45	129.79	120.38
1	B	48	LYS	N-CA-C	6.34	120.03	109.95
1	B	7	THR	CA-C-O	-6.30	113.38	120.43
1	A	43	LEU	O-C-N	6.29	130.37	123.27

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	23	ILE	CA-C-N	6.12	128.77	120.38
1	B	23	ILE	C-N-CA	6.12	128.77	120.38
1	A	64	GLU	CB-CG-CD	5.96	122.73	112.60
1	B	16	GLU	N-CA-C	-5.93	98.07	108.20
1	A	26	VAL	N-CA-CB	5.88	117.03	110.62
1	A	5	VAL	N-CA-CB	5.86	119.79	111.82
1	B	51	GLU	CB-CG-CD	5.81	122.48	112.60
1	A	32	ASP	CA-CB-CG	5.74	118.34	112.60
1	A	45	PHE	CA-CB-CG	5.68	119.48	113.80
1	A	61	ILE	O-C-N	5.64	128.82	122.68
1	B	10	GLY	CA-C-N	5.57	128.78	120.87
1	B	10	GLY	C-N-CA	5.57	128.78	120.87
1	B	7	THR	N-CA-C	-5.55	100.13	108.96
1	B	11	LYS	CA-C-O	5.49	127.31	121.16
1	B	7	THR	CA-CB-OG1	-5.48	101.38	109.60
1	B	11	LYS	N-CA-C	5.46	118.37	110.28
1	B	31	GLN	CB-CG-CD	5.42	121.81	112.60
1	B	60	ASN	OD1-CG-ND2	5.39	127.99	122.60
1	B	63	LYS	CA-CB-CG	5.30	124.70	114.10
1	A	26	VAL	CA-C-N	5.23	127.54	120.38
1	A	26	VAL	C-N-CA	5.23	127.54	120.38
1	A	49	GLN	CA-C-O	5.09	125.83	120.54
1	B	24	GLU	CA-C-O	5.03	126.06	120.63
1	A	61	ILE	N-CA-C	-5.01	100.41	107.98
1	A	71	LEU	CA-C-N	5.01	128.45	121.24
1	A	71	LEU	C-N-CA	5.01	128.45	121.24

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	601	0	629	32	0
1	B	574	0	597	31	0
All	All	1175	0	1226	63	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 26.

All (63) 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:17:VAL:HG12	1:A:29:LYS:HZ3	1.43	0.84
1:A:17:VAL:HG12	1:A:29:LYS:NZ	1.97	0.79
1:A:59:TYR:HB2	1:A:61:ILE:HD12	1.68	0.75
1:A:31:GLN:NE2	1:A:38:PRO:HD3	2.04	0.72
1:A:73:LEU:HD22	1:A:73:LEU:N	2.04	0.72
1:A:56:LEU:HD22	1:A:61:ILE:HG21	1.71	0.72
1:A:1:MET:N	1:A:17:VAL:O	2.23	0.71
1:B:48:LYS:HD3	1:B:48:LYS:H	1.55	0.70
1:A:45:PHE:HB2	1:A:67:LEU:HD22	1.73	0.70
1:A:73:LEU:HD22	1:A:73:LEU:H	1.61	0.66
1:A:7:THR:HG22	1:A:69:LEU:HD12	1.77	0.65
1:A:36:ILE:O	1:A:41:GLN:NE2	2.33	0.61
1:B:41:GLN:HB2	1:B:69:LEU:HD11	1.83	0.60
1:B:7:THR:O	1:B:9:THR:N	2.34	0.60
1:A:22:THR:HG23	1:A:24:GLU:HB3	1.84	0.59
1:A:22:THR:CG2	1:A:24:GLU:HB3	2.33	0.59
1:A:5:VAL:HG12	1:A:13:ILE:CG1	2.32	0.58
1:B:7:THR:C	1:B:9:THR:N	2.60	0.58
1:B:41:GLN:HB2	1:B:69:LEU:CD1	2.35	0.57
1:B:4:PHE:HB3	1:B:12:THR:CG2	2.35	0.56
1:A:22:THR:HA	1:A:55:THR:HA	1.88	0.55
1:B:8:LEU:HD13	1:B:70:VAL:HG22	1.89	0.54
1:A:60:ASN:ND2	1:A:62:GLN:OE1	2.41	0.54
1:B:2:GLN:O	1:B:64:GLU:N	2.30	0.53
1:B:24:GLU:HB2	1:B:52:ASP:HB3	1.89	0.53
1:B:22:THR:HA	1:B:55:THR:HA	1.92	0.52
1:A:63:LYS:O	1:A:64:GLU:HG2	2.11	0.51
1:B:26:VAL:HG21	1:B:56:LEU:HD11	1.94	0.50
1:B:5:VAL:HG11	1:B:30:ILE:CD1	2.42	0.49
1:B:7:THR:O	1:B:8:LEU:C	2.56	0.48
1:B:8:LEU:HD13	1:B:70:VAL:CG2	2.44	0.48
1:B:45:PHE:O	1:B:48:LYS:HE2	2.13	0.48
1:B:3:ILE:HG12	1:B:17:VAL:HG21	1.96	0.48
1:A:44:ILE:CD1	1:A:70:VAL:HG21	2.44	0.48
1:A:6:LYS:HZ3	1:A:10:GLY:CA	2.27	0.47
1:B:54:ARG:NH1	1:B:58:ASP:OD2	2.48	0.47
1:A:5:VAL:HG12	1:A:13:ILE:HD11	1.97	0.46

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:THR:O	1:B:7:THR:OG1	2.33	0.46
1:B:33:LYS:HA	1:B:33:LYS:HE2	1.97	0.46
1:A:73:LEU:N	1:A:73:LEU:CD2	2.76	0.46
1:A:11:LYS:HG3	1:A:12:THR:N	2.30	0.46
1:B:3:ILE:HG12	1:B:17:VAL:CG2	2.46	0.46
1:A:17:VAL:HA	1:A:29:LYS:HZ1	1.82	0.45
1:B:45:PHE:O	1:B:46:ALA:C	2.60	0.44
1:A:2:GLN:HA	1:A:15:LEU:O	2.17	0.44
1:A:6:LYS:HG3	1:A:12:THR:OG1	2.17	0.44
1:A:22:THR:HG23	1:A:24:GLU:H	1.82	0.44
1:B:7:THR:C	1:B:9:THR:H	2.26	0.44
1:B:56:LEU:HD23	1:B:56:LEU:HA	1.86	0.44
1:A:73:LEU:H	1:A:73:LEU:CD2	2.29	0.43
1:B:48:LYS:HD3	1:B:48:LYS:N	2.25	0.43
1:B:50:LEU:HB3	1:B:59:TYR:CE2	2.53	0.42
1:B:62:GLN:NE2	1:B:62:GLN:HA	2.34	0.42
1:A:43:LEU:HA	1:A:68:HIS:O	2.20	0.42
1:B:44:ILE:HD12	1:B:44:ILE:N	2.35	0.42
1:A:2:GLN:OE1	1:A:14:THR:HG21	2.20	0.42
1:A:44:ILE:HD12	1:A:70:VAL:HG21	2.01	0.41
1:B:42:ARG:HG2	1:B:44:ILE:HD11	2.02	0.41
1:A:31:GLN:O	1:A:35:GLY:N	2.50	0.41
1:B:5:VAL:HG11	1:B:30:ILE:HD13	2.02	0.41
1:B:45:PHE:O	1:B:48:LYS:HD3	2.21	0.41
1:B:54:ARG:HH11	1:B:54:ARG:HD3	1.64	0.41
1:A:42:ARG:HE	1:A:49:GLN:NE2	2.20	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 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 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	74/76 (97%)	71 (96%)	2 (3%)	1 (1%)	9	13
1	B	70/76 (92%)	63 (90%)	6 (9%)	1 (1%)	9	13
All	All	144/152 (95%)	134 (93%)	8 (6%)	2 (1%)	9	13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	8	LEU
1	A	74	ARG

### 5.3.2 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 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	68/68 (100%)	57 (84%)	11 (16%)	2	2
1	B	66/68 (97%)	53 (80%)	13 (20%)	1	1
All	All	134/136 (98%)	110 (82%)	24 (18%)	1	2

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	5	VAL
1	A	11	LYS
1	A	22	THR
1	A	23	ILE
1	A	54	ARG
1	A	61	ILE
1	A	63	LYS
1	A	69	LEU
1	A	73	LEU
1	A	74	ARG
1	B	1	MET
1	B	7	THR
1	B	8	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	11	LYS
1	B	23	ILE
1	B	29	LYS
1	B	40	GLN
1	B	44	ILE
1	B	48	LYS
1	B	61	ILE
1	B	62	GLN
1	B	64	GLU
1	B	67	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	31	GLN
1	A	49	GLN
1	A	60	ASN
1	A	62	GLN
1	B	31	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	76/76 (100%)	-0.81	0 100 100	9, 14, 18, 24	0
1	B	72/76 (94%)	-0.87	0 100 100	8, 14, 19, 20	0
All	All	148/152 (97%)	-0.84	0 100 100	8, 14, 19, 24	0

There are no RSRZ outliers to report.

### 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.