



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 02:32 am BST

PDB ID : 4OM2  
Title : Crystal structure of TLE1 N-terminal Q-domain residues 1-156  
Authors : Chodaparambil, J.V.; Weis, W.I.  
Deposited on : 2014-01-25  
Resolution : 4.00 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.

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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 : 2.11  
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) : 2.11

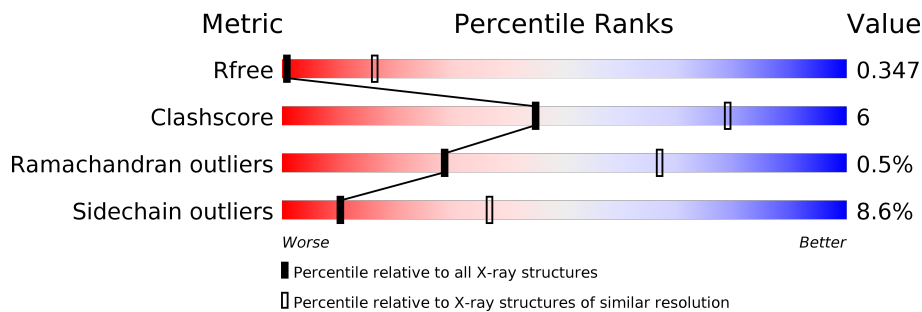
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)

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 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	163	49% (green), 19% (yellow), 31% (grey)
1	B	163	50% (green), 15% (yellow), 34% (grey)
1	C	163	54% (green), 13% (yellow), 33% (grey)
1	D	163	52% (green), 12% (yellow), 34% (grey)

## 2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 3512 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 Transducin-like enhancer protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	112	907	570	158	172	7	0	0	0
1	B	107	862	542	150	164	6	0	0	0
1	C	110	878	547	155	170	6	0	0	0
1	D	108	865	543	149	167	6	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	EXPRESSION TAG	UNP Q04724
A	-4	ALA	-	EXPRESSION TAG	UNP Q04724
A	-3	MET	-	EXPRESSION TAG	UNP Q04724
A	-2	GLY	-	EXPRESSION TAG	UNP Q04724
A	-1	SER	-	EXPRESSION TAG	UNP Q04724
A	0	GLY	-	EXPRESSION TAG	UNP Q04724
A	1	GLN	-	EXPRESSION TAG	UNP Q04724
B	-5	GLY	-	EXPRESSION TAG	UNP Q04724
B	-4	ALA	-	EXPRESSION TAG	UNP Q04724
B	-3	MET	-	EXPRESSION TAG	UNP Q04724
B	-2	GLY	-	EXPRESSION TAG	UNP Q04724
B	-1	SER	-	EXPRESSION TAG	UNP Q04724
B	0	GLY	-	EXPRESSION TAG	UNP Q04724
B	1	GLN	-	EXPRESSION TAG	UNP Q04724
C	-5	GLY	-	EXPRESSION TAG	UNP Q04724
C	-4	ALA	-	EXPRESSION TAG	UNP Q04724
C	-3	MET	-	EXPRESSION TAG	UNP Q04724
C	-2	GLY	-	EXPRESSION TAG	UNP Q04724
C	-1	SER	-	EXPRESSION TAG	UNP Q04724
C	0	GLY	-	EXPRESSION TAG	UNP Q04724
C	1	GLN	-	EXPRESSION TAG	UNP Q04724

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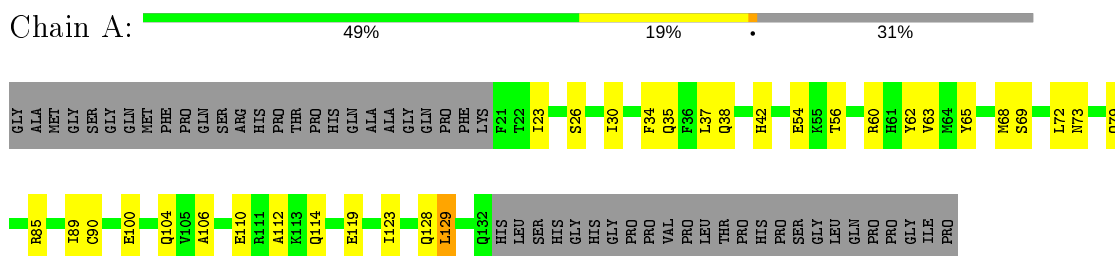
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<b>Chain</b>	<b>Residue</b>	<b>Modelled</b>	<b>Actual</b>	<b>Comment</b>	<b>Reference</b>
D	-5	GLY	-	EXPRESSION TAG	UNP Q04724
D	-4	ALA	-	EXPRESSION TAG	UNP Q04724
D	-3	MET	-	EXPRESSION TAG	UNP Q04724
D	-2	GLY	-	EXPRESSION TAG	UNP Q04724
D	-1	SER	-	EXPRESSION TAG	UNP Q04724
D	0	GLY	-	EXPRESSION TAG	UNP Q04724
D	1	GLN	-	EXPRESSION TAG	UNP Q04724

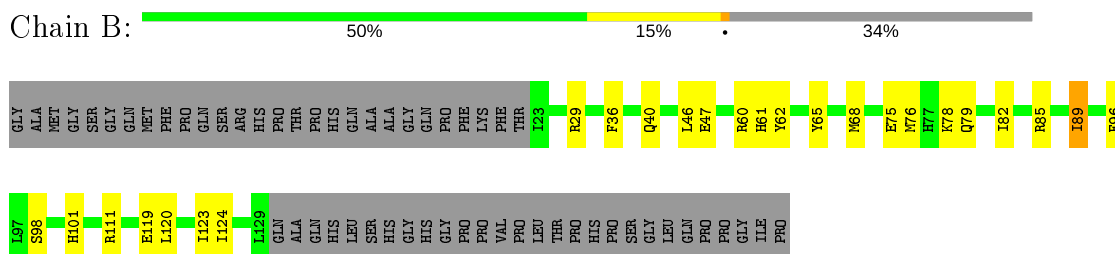
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

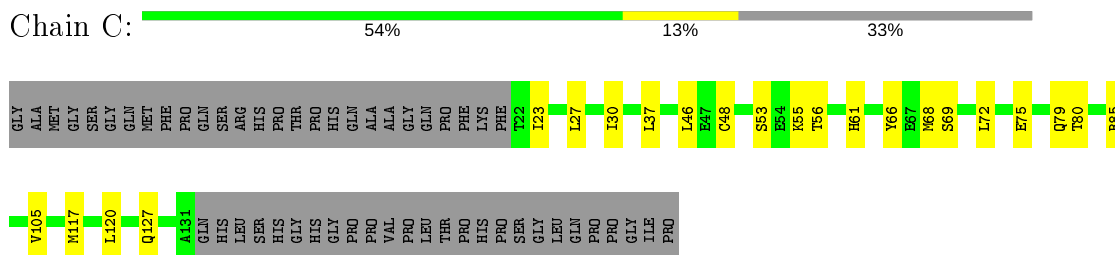
- Molecule 1: Transducin-like enhancer protein 1



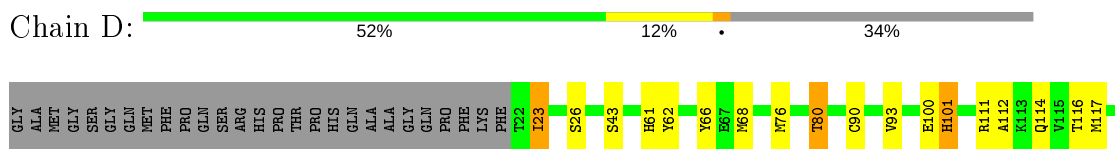
- Molecule 1: Transducin-like enhancer protein 1



- Molecule 1: Transducin-like enhancer protein 1



- Molecule 1: Transducin-like enhancer protein 1



I120	I124	Q128	GLN	GLN	ALA	HIS	GLN	HIS	LEU	SER	HIS	HIS	HIS	GLY	GLY	PRO	PRO	VAL	PRO	PRO	LEU	THR	PRO	HIS	PRO	SER	SER	GLY	LEU	GLN	PRO	PRO	GLY	ILE	PRO
M121	G125	L129	ALA	GLN	GLN	HIS	LEU	SER	HIS	HIS	HIS	GLY	GLY	PRO	PRO	VAL	PRO	PRO	LEU	THR	PRO	HIS	PRO	SER	SER	GLY	LEU	GLN	PRO	PRO	GLY	ILE	PRO		

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.59Å 94.91Å 130.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.69 – 4.00 76.70 – 3.50	Depositor EDS
% Data completeness (in resolution range)	98.0 (53.69-4.00) 98.9 (76.70-3.50)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 3.49Å)	Xtrriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, $R_{free}$	0.287 , 0.347 0.287 , 0.347	Depositor DCC
$R_{free}$ test set	815 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	136.0	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 97.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3512	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	132.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.08% 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

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	0.26	0/921	0.41	0/1238
1	B	0.26	0/875	0.44	0/1178
1	C	0.26	0/890	0.42	0/1199
1	D	0.26	0/878	0.43	0/1184
All	All	0.26	0/3564	0.42	0/4799

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	907	0	887	17	0
1	B	862	0	840	17	0
1	C	878	0	851	13	0
1	D	865	0	834	15	0
All	All	3512	0	3412	45	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 6.

All (45) 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:D:117:MET:O	1:D:121:ASN:ND2	2.24	0.69
1:B:96:PHE:HD2	1:D:101:HIS:HE2	1.41	0.69
1:A:54:GLU:OE1	1:C:55:LYS:NZ	2.28	0.65
1:C:117:MET:HA	1:C:120:LEU:HD12	1.80	0.61
1:A:128:GLN:HG3	1:A:129:LEU:HD13	1.83	0.61
1:D:76:MET:O	1:D:80:THR:OG1	2.21	0.58
1:A:65:TYR:HA	1:A:68:MET:HG2	1.85	0.58
1:B:96:PHE:HD2	1:D:101:HIS:NE2	2.00	0.58
1:A:119:GLU:OE2	1:C:85:ARG:NH1	2.37	0.57
1:A:112:ALA:O	1:C:85:ARG:NH2	2.33	0.56
1:A:35:GLN:HA	1:A:38:GLN:HG2	1.88	0.55
1:B:120:LEU:O	1:B:124:ILE:HG12	2.08	0.54
1:D:125:GLY:HA2	1:D:128:GLN:HG2	1.91	0.53
1:A:73:ASN:HB2	1:C:72:LEU:HD13	1.94	0.50
1:C:75:GLU:O	1:C:79:GLN:HG2	2.12	0.49
1:B:85:ARG:HD3	1:D:112:ALA:HA	1.95	0.48
1:B:85:ARG:O	1:B:89:ILE:HG12	2.13	0.48
1:B:65:TYR:HA	1:B:68:MET:HB2	1.95	0.48
1:A:26:SER:HB2	1:B:29:ARG:NH2	2.29	0.48
1:D:120:LEU:O	1:D:124:ILE:HG12	2.15	0.47
1:A:62:TYR:CD1	1:C:61:HIS:HB3	2.51	0.46
1:A:106:ALA:O	1:A:110:GLU:HG2	2.15	0.46
1:A:112:ALA:HA	1:C:85:ARG:HD3	1.96	0.46
1:B:119:GLU:O	1:B:123:ILE:HG12	2.15	0.46
1:B:75:GLU:O	1:B:79:GLN:HG2	2.15	0.46
1:B:98:SER:HB3	1:B:101:HIS:HB2	1.98	0.46
1:D:90:CYS:HA	1:D:93:VAL:HG12	1.98	0.45
1:A:85:ARG:O	1:A:89:ILE:HG12	2.15	0.45
1:A:37:LEU:HD13	1:C:37:LEU:HD22	1.98	0.45
1:A:119:GLU:O	1:A:123:ILE:HG12	2.16	0.44
1:C:27:LEU:HA	1:C:30:ILE:HD12	1.98	0.44
1:A:65:TYR:HD2	1:C:66:TYR:HA	1.83	0.44
1:B:36:PHE:O	1:B:40:GLN:HG2	2.18	0.43
1:C:53:SER:O	1:C:56:THR:OG1	2.34	0.42
1:D:117:MET:HA	1:D:120:LEU:HB2	2.00	0.42
1:B:65:TYR:CD2	1:D:66:TYR:HB2	2.55	0.42
1:B:78:LYS:O	1:B:82:ILE:HG13	2.20	0.42
1:D:120:LEU:HA	1:D:120:LEU:HD12	1.81	0.42
1:A:34:PHE:CE1	1:D:23:ILE:HG21	2.55	0.41
1:A:69:SER:HB2	1:C:68:MET:HG2	2.03	0.41
1:B:89:ILE:H	1:B:89:ILE:HG12	1.44	0.41
1:B:61:HIS:HB3	1:D:62:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:ARG:HA	1:D:114:GLN:HG2	2.02	0.40
1:B:62:TYR:CE2	1:D:61:HIS:HB3	2.55	0.40
1:B:111:ARG:HD2	1:B:111:ARG:HA	1.88	0.40

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	110/163 (68%)	108 (98%)	2 (2%)	0	100	100
1	B	105/163 (64%)	102 (97%)	3 (3%)	0	100	100
1	C	108/163 (66%)	103 (95%)	4 (4%)	1 (1%)	17	55
1	D	106/163 (65%)	102 (96%)	3 (3%)	1 (1%)	17	55
All	All	429/652 (66%)	415 (97%)	12 (3%)	2 (0%)	29	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	23	ILE
1	D	23	ILE

### 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	96/140 (69%)	83 (86%)	13 (14%)	4	21
1	B	91/140 (65%)	86 (94%)	5 (6%)	21	50
1	C	92/140 (66%)	86 (94%)	6 (6%)	17	45
1	D	91/140 (65%)	83 (91%)	8 (9%)	10	35
All	All	370/560 (66%)	338 (91%)	32 (9%)	10	37

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ILE
1	A	30	ILE
1	A	42	HIS
1	A	56	THR
1	A	60	ARG
1	A	63	VAL
1	A	72	LEU
1	A	79	GLN
1	A	90	CYS
1	A	100	GLU
1	A	104	GLN
1	A	114	GLN
1	A	129	LEU
1	B	46	LEU
1	B	47	GLU
1	B	60	ARG
1	B	76	MET
1	B	89	ILE
1	C	46	LEU
1	C	48	CYS
1	C	69	SER
1	C	80	THR
1	C	105	VAL
1	C	127	GLN
1	D	26	SER
1	D	43	SER
1	D	68	MET
1	D	80	THR
1	D	100	GLU
1	D	101	HIS
1	D	116	THR
1	D	120	LEU

Some 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 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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.