



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:25 PM GMT

PDB ID : 1TLK  
Title : X-RAY STRUCTURE DETERMINATION OF TELOKIN, THE C-  
TERMINAL DOMAIN OF MYOSIN LIGHT CHAIN KINASE, AT 2.8  
ANGSTROMS RESOLUTION  
Authors : Holden, H.M.; Rayment, I.  
Deposited on : 1992-07-20  
Resolution : 2.80 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  
<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)  
Xtriage (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

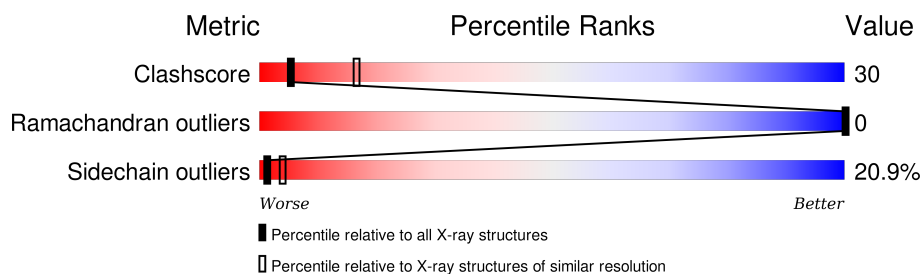
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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	154	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 837 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 TELOKIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	0	0	0
			806	503	126	169	8			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	31	Total	O	0	0
			31	31		



Note EDS was not executed.

- Chain A:
- 
- Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.25). The x-axis shows positions 1 to 150. The logo highlights conserved residues, with a peak of conservation around position 100 (approx. 0.25 bits). A color key identifies amino acids: E (blue), K (green), R (red), G (yellow), L (cyan), I (grey), M (orange), A (light green), S (light blue), P (pink), T (light yellow), N (light green), Q (light blue), D (red), V (orange), C (yellow), F (dark blue), Y (dark red), W (dark orange), H (dark blue), and X (grey).
- | Position | Amino Acid | Information Content (bits) |
|----------|------------|----------------------------|
| 1        | T127       | 0.05                       |
| 2        | A128       | 0.05                       |
| 3        | E129       | 0.05                       |
| 4        | L130       | 0.05                       |
| 5        | L131       | 0.05                       |
| 6        | V132       | 0.05                       |
| 7        | E133       | 0.05                       |
| 8        | T134       | 0.05                       |
| 9        | M135       | 0.05                       |
| 10       | G136       | 0.05                       |
| 11       | L137       | 0.05                       |
| 12       | L138       | 0.05                       |
| 13       | G139       | 0.05                       |
| 14       | G140       | 0.05                       |
| 15       | G141       | 0.05                       |
| 16       | G142       | 0.05                       |
| 17       | G143       | 0.05                       |
| 18       | G144       | 0.05                       |
| 19       | G145       | 0.05                       |
| 20       | G146       | 0.05                       |
| 21       | G147       | 0.05                       |
| 22       | G148       | 0.05                       |
| 23       | G149       | 0.05                       |
| 24       | G150       | 0.05                       |
| 25       | G151       | 0.05                       |
| 26       | G152       | 0.05                       |
| 27       | G153       | 0.05                       |
| 28       | G154       | 0.05                       |
| 29       | G155       | 0.05                       |
| 30       | G156       | 0.05                       |
| 31       | G157       | 0.05                       |
| 32       | G158       | 0.05                       |
| 33       | G159       | 0.05                       |
| 34       | G160       | 0.05                       |
| 35       | G161       | 0.05                       |
| 36       | G162       | 0.05                       |
| 37       | G163       | 0.05                       |
| 38       | G164       | 0.05                       |
| 39       | G165       | 0.05                       |
| 40       | G166       | 0.05                       |
| 41       | G167       | 0.05                       |
| 42       | G168       | 0.05                       |
| 43       | G169       | 0.05                       |
| 44       | G170       | 0.05                       |
| 45       | G171       | 0.05                       |
| 46       | G172       | 0.05                       |
| 47       | G173       | 0.05                       |
| 48       | G174       | 0.05                       |
| 49       | G175       | 0.05                       |
| 50       | G176       | 0.05                       |
| 51       | G177       | 0.05                       |
| 52       | G178       | 0.05                       |
| 53       | G179       | 0.05                       |
| 54       | G180       | 0.05                       |
| 55       | G181       | 0.05                       |
| 56       | G182       | 0.05                       |
| 57       | G183       | 0.05                       |
| 58       | G184       | 0.05                       |
| 59       | G185       | 0.05                       |
| 60       | G186       | 0.05                       |
| 61       | G187       | 0.05                       |
| 62       | G188       | 0.05                       |
| 63       | G189       | 0.05                       |
| 64       | G190       | 0.05                       |
| 65       | G191       | 0.05                       |
| 66       | G192       | 0.05                       |
| 67       | G193       | 0.05                       |
| 68       | G194       | 0.05                       |
| 69       | G195       | 0.05                       |
| 70       | G196       | 0.05                       |
| 71       | G197       | 0.05                       |
| 72       | G198       | 0.05                       |
| 73       | G199       | 0.05                       |
| 74       | G200       | 0.05                       |
| 75       | G201       | 0.05                       |
| 76       | G202       | 0.05                       |
| 77       | G203       | 0.05                       |
| 78       | G204       | 0.05                       |
| 79       | G205       | 0.05                       |
| 80       | G206       | 0.05                       |
| 81       | G207       | 0.05                       |
| 82       | G208       | 0.05                       |
| 83       | G209       | 0.05                       |
| 84       | G210       | 0.05                       |
| 85       | G211       | 0.05                       |
| 86       | G212       | 0.05                       |
| 87       | G213       | 0.05                       |
| 88       | G214       | 0.05                       |
| 89       | G215       | 0.05                       |
| 90       | G216       | 0.05                       |
| 91       | G217       | 0.05                       |
| 92       | G218       | 0.05                       |
| 93       | G219       | 0.05                       |
| 94       | G220       | 0.05                       |
| 95       | G221       | 0.05                       |
| 96       | G222       | 0.05                       |
| 97       | G223       | 0.05                       |
| 98       | G224       | 0.05                       |
| 99       | G225       | 0.05                       |
| 100      | G226       | 0.05                       |
| 101      | G227       | 0.05                       |
| 102      | G228       | 0.05                       |
| 103      | G229       | 0.05                       |
| 104      | G230       | 0.05                       |
| 105      | G231       | 0.05                       |
| 106      | G232       | 0.05                       |
| 107      | G233       | 0.05                       |
| 108      | G234       | 0.05                       |
| 109      | G235       | 0.05                       |
| 110      | G236       | 0.05                       |
| 111      | G237       | 0.05                       |
| 112      | G238       | 0.05                       |
| 113      | G239       | 0.05                       |
| 114      | G240       | 0.05                       |
| 115      | G241       | 0.05                       |
| 116      | G242       | 0.05                       |
| 117      | G243       | 0.05                       |
| 118      | G244       | 0.05                       |
| 119      | G245       | 0.05                       |
| 120      | G246       | 0.05                       |
| 121      | G247       | 0.05                       |
| 122      | G248       | 0.05                       |
| 123      | G249       | 0.05                       |
| 124      | G250       | 0.05                       |
| 125      | G251       | 0.05                       |
| 126      | G252       | 0.05                       |
| 127      | G253       | 0.05                       |
| 128      | G254       | 0.05                       |
| 129      | G255       | 0.05                       |
| 130      | G256       | 0.05                       |
| 131      | G257       | 0.05                       |
| 132      | G258       | 0.05                       |
| 13       |            |                            |

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.40 Å 64.40 Å 59.60 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	TNT	Depositor
R, $R_{free}$	0.184 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	837	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	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	1.12	12/822 (1.5%)	1.76	24/1114 (2.2%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	35	GLU	CD-OE2	5.75	1.31	1.25
1	A	36	GLU	CD-OE1	5.61	1.31	1.25
1	A	94	GLU	CD-OE2	5.48	1.31	1.25
1	A	72	GLU	CD-OE1	5.46	1.31	1.25
1	A	129	GLU	CD-OE1	5.45	1.31	1.25
1	A	123	GLU	CD-OE1	5.42	1.31	1.25
1	A	66	GLU	CD-OE1	5.40	1.31	1.25
1	A	95	GLU	CD-OE1	5.27	1.31	1.25
1	A	55	GLU	CD-OE1	5.22	1.31	1.25
1	A	104	GLU	CD-OE2	5.17	1.31	1.25
1	A	84	GLU	CD-OE2	5.14	1.31	1.25
1	A	133	GLU	CD-OE1	5.07	1.31	1.25

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	ASP	CB-CA-C	-9.28	91.85	110.40
1	A	123	GLU	N-CA-CB	-7.77	96.61	110.60
1	A	62	ASP	CB-CG-OD2	-7.30	111.73	118.30
1	A	79	ASP	CB-CG-OD2	-7.05	111.95	118.30
1	A	93	ASP	CB-CG-OD1	-7.03	111.98	118.30
1	A	68	TYR	CB-CG-CD1	-7.01	116.80	121.00
1	A	79	ASP	CB-CG-OD1	6.86	124.47	118.30
1	A	62	ASP	CB-CA-C	-6.09	98.22	110.40
1	A	108	ASP	CB-CG-OD1	-6.09	112.82	118.30
1	A	123	GLU	CB-CA-C	-6.01	98.39	110.40
1	A	110	ASP	CB-CG-OD1	-5.95	112.94	118.30
1	A	103	SER	N-CA-C	5.75	126.52	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	70	ASP	CB-CG-OD1	-5.62	113.25	118.30
1	A	108	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	62	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	110	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	109	ASP	CB-CG-OD1	-5.40	113.44	118.30
1	A	78	ASP	CB-CG-OD1	-5.36	113.47	118.30
1	A	113	TYR	CB-CG-CD2	5.29	124.18	121.00
1	A	93	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	70	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	78	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	68	TYR	CB-CA-C	-5.16	100.08	110.40

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	806	0	756	47	1
2	A	31	0	0	3	0
All	All	837	0	756	47	1

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 30.

All (47) 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:93:ASP:HB3	1:A:95:GLU:H	1.30	0.93
1:A:87:HIS:HE2	1:A:109:ASP:CG	1.84	0.80
1:A:42:PRO:HD3	1:A:119:ASN:OD1	1.81	0.79
1:A:45:THR:HG23	2:A:176:HOH:O	1.84	0.78
1:A:93:ASP:HB3	1:A:95:GLU:N	2.03	0.73
1:A:45:THR:CG2	2:A:176:HOH:O	2.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:ILE:HG13	1:A:128:ALA:HB2	1.79	0.65
1:A:112:LYS:CB	1:A:129:GLU:OE2	2.45	0.65
1:A:51:MET:CE	1:A:59:ALA:HB1	2.26	0.64
1:A:78:ASP:O	1:A:79:ASP:HB2	1.97	0.64
1:A:64:LYS:HD2	1:A:97:ASN:ND2	2.16	0.61
1:A:68:TYR:HA	1:A:69:PRO:C	2.21	0.60
1:A:112:LYS:HB3	1:A:129:GLU:OE2	2.04	0.57
1:A:112:LYS:HB2	1:A:129:GLU:OE2	2.04	0.57
1:A:51:MET:HE1	1:A:59:ALA:HB1	1.87	0.57
1:A:110:ASP:O	1:A:111:ALA:HB2	2.05	0.56
1:A:53:VAL:HG21	1:A:59:ALA:HB2	1.88	0.56
1:A:120:SER:HB2	1:A:121:LEU:HD12	1.88	0.56
1:A:73:VAL:HG11	1:A:98:CYS:SG	2.47	0.54
1:A:51:MET:HE3	1:A:59:ALA:HB1	1.89	0.54
1:A:87:HIS:NE2	1:A:109:ASP:OD2	2.39	0.54
1:A:106:CYS:O	1:A:132:VAL:HG21	2.09	0.53
1:A:57:SER:OG	1:A:58:ALA:N	2.42	0.52
1:A:115:CYS:O	1:A:125:THR:HA	2.11	0.51
1:A:48:ILE:O	1:A:48:ILE:HG13	2.10	0.50
1:A:90:ILE:HA	1:A:99:SER:O	2.14	0.47
1:A:73:VAL:CG1	1:A:115:CYS:SG	3.04	0.46
1:A:54:VAL:HG12	1:A:55:GLU:O	2.16	0.45
1:A:121:LEU:N	1:A:121:LEU:HD12	2.32	0.44
1:A:51:MET:HA	2:A:183:HOH:O	2.18	0.44
1:A:52:ASP:O	1:A:53:VAL:HG23	2.17	0.44
1:A:87:HIS:NE2	1:A:109:ASP:OD1	2.46	0.44
1:A:68:TYR:CD1	1:A:69:PRO:HA	2.53	0.43
1:A:86:ARG:H	1:A:86:ARG:CD	2.29	0.43
1:A:75:TRP:HA	1:A:114:THR:O	2.18	0.43
1:A:89:GLN:HB3	1:A:101:THR:HB	2.01	0.43
1:A:127:THR:HG22	1:A:128:ALA:N	2.34	0.42
1:A:63:CYS:SG	1:A:98:CYS:HB3	2.59	0.42
1:A:105:VAL:CG1	1:A:132:VAL:HG22	2.50	0.42
1:A:72:GLU:O	1:A:117:ALA:HA	2.20	0.41
1:A:93:ASP:CG	1:A:97:ASN:HB2	2.41	0.41
1:A:77:LYS:NZ	1:A:108:ASP:O	2.50	0.41
1:A:93:ASP:HB2	1:A:97:ASN:H	1.86	0.41
1:A:48:ILE:HD12	1:A:128:ALA:HB3	2.03	0.40
1:A:94:GLU:H	1:A:94:GLU:HG3	1.49	0.40
1:A:40:VAL:HG12	1:A:41:LYS:O	2.21	0.40
1:A:42:PRO:CD	1:A:119:ASN:OD1	2.63	0.40



All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:GLU:OE1	1:A:94:GLU:OE2[2_654]	1.96	0.24

## 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	101/154 (66%)	94 (93%)	7 (7%)	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	91/131 (70%)	72 (79%)	19 (21%)	1	4

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	GLU
1	A	45	THR
1	A	49	LEU
1	A	62	ASP
1	A	74	MET
1	A	79	ASP

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Mol	Chain	Res	Type
1	A	80	ASN
1	A	83	LYS
1	A	84	GLU
1	A	86	ARG
1	A	94	GLU
1	A	99	SER
1	A	103	SER
1	A	104	GLU
1	A	106	CYS
1	A	112	LYS
1	A	125	THR
1	A	130	LEU
1	A	134	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	97	ASN

### 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

### 6.5 Other polymers [i](#)

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