



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2017 – 10:28 PM EDT

PDB ID : 5UBC  
Title : The structure of the Arabidopsis thaliana Toc75 POTRA domains  
Authors : O'Neil, P.K.; Noinaj, N.  
Deposited on : unknown  
Resolution : 2.86 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  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

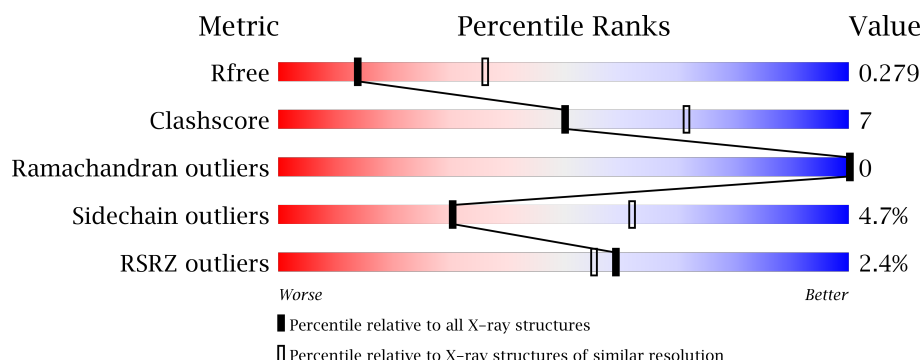
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


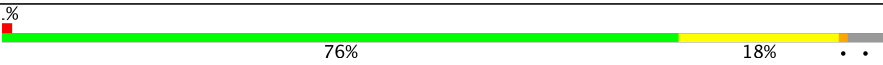
The reported resolution of this entry is 2.86 Å.

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))
$R_{free}$	100719	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (2.90-2.82)

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.

Mol	Chain	Length	Quality of chain
1	A	314	
1	B	314	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4501 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 Protein TOC75-3, chloroplastic.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	Se	0	0	0
			2249	1416	397	425	5	6			
1	B	300	Total	C	N	O	S	Se	0	0	0
			2252	1418	398	425	5	6			

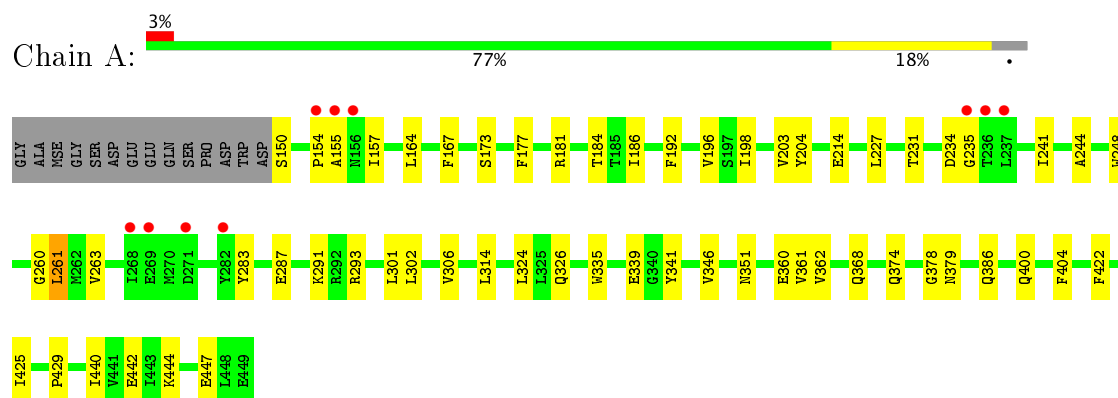
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	GLY	-	expression tag	UNP Q9STE8
A	137	ALA	-	expression tag	UNP Q9STE8
A	138	MSE	-	expression tag	UNP Q9STE8
A	139	GLY	-	expression tag	UNP Q9STE8
A	140	SER	-	expression tag	UNP Q9STE8
B	136	GLY	-	expression tag	UNP Q9STE8
B	137	ALA	-	expression tag	UNP Q9STE8
B	138	MSE	-	expression tag	UNP Q9STE8
B	139	GLY	-	expression tag	UNP Q9STE8
B	140	SER	-	expression tag	UNP Q9STE8

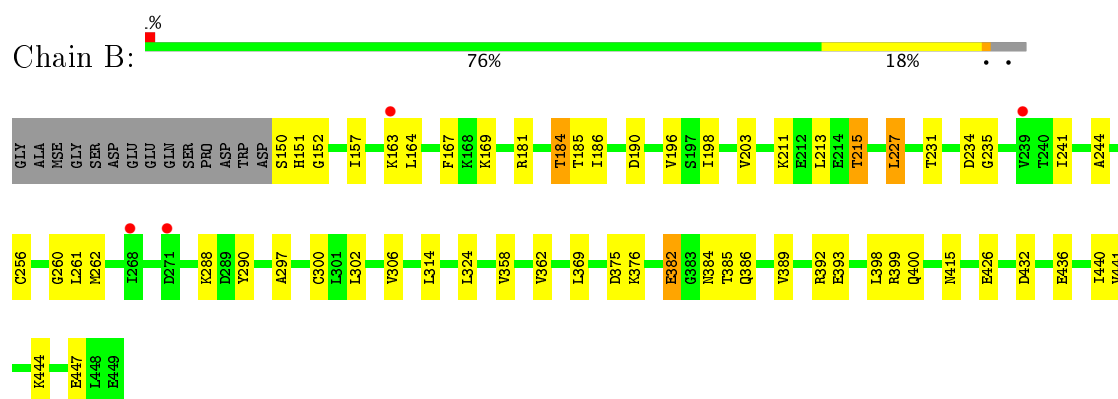
### 3 Residue-property plots [i](#)

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 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: Protein TOC75-3, chloroplastic



- Molecule 1: Protein TOC75-3, chloroplastic



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.37Å 50.45Å 94.80Å 90.00° 115.56° 90.00°	Depositor
Resolution (Å)	47.21 – 2.86 47.21 – 2.86	Depositor EDS
% Data completeness (in resolution range)	89.7 (47.21-2.86) 81.2 (47.21-2.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.224 , 0.280 0.224 , 0.279	Depositor DCC
$R_{free}$ test set	1501 reflections (9.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.1	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , 33.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	4501	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.19% 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	0.35	0/2278	0.59	1/3080 (0.0%)
1	B	0.37	0/2281	0.58	0/3083
All	All	0.36	0/4559	0.59	1/6163 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	378	GLY	N-CA-C	5.72	127.39	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	152	GLY	Peptide

### 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	2249	0	2124	29	0
1	B	2252	0	2129	29	0
All	All	4501	0	4253	58	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 7.

All (58) 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:B:386:GLN:NE2	1:B:447:GLU:OE2	2.18	0.75
1:A:386:GLN:NE2	1:A:447:GLU:OE2	2.25	0.70
1:B:262:MSE:HE1	1:B:297:ALA:HA	1.77	0.66
1:B:150:SER:HB3	1:B:203:VAL:HG11	1.77	0.64
1:B:227:LEU:HD23	1:B:241:ILE:HG12	1.82	0.62
1:B:426:GLU:HB2	1:B:444:LYS:HB2	1.82	0.61
1:A:368:GLN:HB3	1:A:440:ILE:HG12	1.81	0.61
1:A:263:VAL:O	1:A:293:ARG:NH1	2.34	0.60
1:A:155:ALA:H	1:A:231:THR:HG21	1.68	0.59
1:B:432:ASP:HB3	1:B:440:ILE:HG13	1.84	0.59
1:B:384:ASN:O	1:B:385:THR:HG22	2.02	0.59
1:A:150:SER:HB3	1:A:203:VAL:HG11	1.84	0.58
1:A:157:ILE:O	1:A:231:THR:OG1	2.12	0.57
1:B:302:LEU:HD11	1:B:306:VAL:HG11	1.89	0.55
1:A:314:LEU:HD23	1:A:324:LEU:HD21	1.91	0.52
1:B:382:GLU:HG3	1:B:384:ASN:H	1.72	0.52
1:B:181:ARG:HD2	1:B:244:ALA:HB1	1.91	0.52
1:B:256:CYS:HG	1:B:300:CYS:HG	1.58	0.51
1:B:196:VAL:HG12	1:B:198:ILE:H	1.76	0.50
1:A:293:ARG:NH2	1:A:360:GLU:OE1	2.41	0.50
1:B:213:LEU:HD13	1:B:227:LEU:HB2	1.93	0.50
1:A:181:ARG:HD2	1:A:244:ALA:HB1	1.93	0.49
1:B:261:LEU:HA	1:B:436:GLU:HB3	1.94	0.49
1:A:346:VAL:HG22	1:A:361:VAL:HG12	1.94	0.48
1:B:151:HIS:HB3	1:B:169:LYS:O	2.13	0.48
1:B:290:TYR:HE2	1:B:358:VAL:HG21	1.78	0.48
1:A:301:LEU:HD13	1:A:341:TYR:CZ	2.49	0.47
1:A:177:PHE:HB3	1:A:186:ILE:HB	1.95	0.47
1:A:293:ARG:HH21	1:A:360:GLU:CD	2.18	0.47
1:B:393:GLU:HB3	1:B:415:ASN:HB3	1.97	0.47
1:A:302:LEU:HD11	1:A:306:VAL:HG11	1.97	0.46
1:B:234:ASP:HA	1:B:235:GLY:HA2	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ILE:HG23	1:A:204:TYR:CE2	2.50	0.46
1:A:196:VAL:HG12	1:A:198:ILE:H	1.81	0.46
1:A:154:PRO:HB3	1:A:231:THR:HB	1.97	0.46
1:A:260:GLY:O	1:A:261:LEU:HB2	2.16	0.46
1:B:211:LYS:O	1:B:215:THR:OG1	2.34	0.46
1:B:389:VAL:HG12	1:B:392:ARG:NH2	2.31	0.46
1:A:234:ASP:HA	1:A:235:GLY:HA2	1.55	0.44
1:A:374:GLN:HE22	1:A:444:LYS:HE3	1.82	0.44
1:B:314:LEU:HD23	1:B:324:LEU:HD21	2.00	0.44
1:A:404:PHE:CE2	1:A:429:PRO:HG3	2.52	0.44
1:A:227:LEU:HG	1:A:241:ILE:HG12	1.99	0.43
1:A:192:PHE:HA	1:A:326:GLN:HE22	1.83	0.43
1:A:422:PHE:HB2	1:A:425:ILE:HD11	2.00	0.43
1:B:398:LEU:HD22	1:B:441:VAL:HG11	2.01	0.42
1:A:248:TRP:CH2	1:A:351:ASN:HB3	2.55	0.41
1:A:287:GLU:O	1:A:291:LYS:HG2	2.20	0.41
1:A:335:TRP:CZ2	1:A:339:GLU:HG3	2.55	0.41
1:A:260:GLY:HA2	1:A:362:VAL:HG12	2.01	0.41
1:A:154:PRO:CB	1:A:231:THR:HB	2.50	0.41
1:B:157:ILE:O	1:B:231:THR:OG1	2.25	0.41
1:B:389:VAL:HG12	1:B:392:ARG:HH22	1.86	0.41
1:B:184:THR:HG22	1:B:185:THR:H	1.86	0.41
1:B:186:ILE:HG23	1:B:190:ASP:OD2	2.21	0.41
1:B:260:GLY:HA2	1:B:362:VAL:HG12	2.03	0.40
1:B:393:GLU:OE2	1:B:415:ASN:HB3	2.22	0.40
1:B:375:ASP:HA	1:B:376:LYS:HA	1.85	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	298/314 (95%)	281 (94%)	17 (6%)	0	100	100
1	B	298/314 (95%)	282 (95%)	16 (5%)	0	100	100
All	All	596/628 (95%)	563 (94%)	33 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	225/268 (84%)	215 (96%)	10 (4%)	33	64
1	B	225/268 (84%)	214 (95%)	11 (5%)	29	60
All	All	450/536 (84%)	429 (95%)	21 (5%)	30	62

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	164	LEU
1	A	167	PHE
1	A	173	SER
1	A	184	THR
1	A	214	GLU
1	A	261	LEU
1	A	283	TYR
1	A	379	ASN
1	A	400	GLN
1	A	442	GLU
1	B	163	LYS
1	B	164	LEU
1	B	167	PHE
1	B	184	THR
1	B	215	THR
1	B	227	LEU
1	B	288	LYS
1	B	369	LEU

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Mol	Chain	Res	Type
1	B	382	GLU
1	B	399	ARG
1	B	400	GLN

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 [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	292/314 (92%)	-0.02	10 (3%) 46 39	30, 61, 104, 142	0
1	B	292/314 (92%)	-0.18	4 (1%) 75 74	31, 59, 106, 142	0
All	All	584/628 (92%)	-0.10	14 (2%) 59 55	30, 61, 105, 142	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	ILE	5.2
1	B	271	ASP	4.9
1	A	155	ALA	4.6
1	A	271	ASP	3.8
1	A	269	GLU	3.3
1	A	154	PRO	3.1
1	A	156	ASN	3.0
1	B	239	VAL	2.9
1	A	237	LEU	2.7
1	B	268	ILE	2.5
1	B	163	LYS	2.4
1	A	282	TYR	2.3
1	A	236	THR	2.3
1	A	235	GLY	2.2

### 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 carbohydrates 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.