



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:41 AM UTC

PDB ID : 3HTM / pdb\_00003htm  
Title : Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases: SPOBTTB/3-box  
Authors : Zhuang, M.; Walden, H.; Schulman, B.A.  
Deposited on : 2009-06-11  
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	2022.3.0, CSD as543be (2022)
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

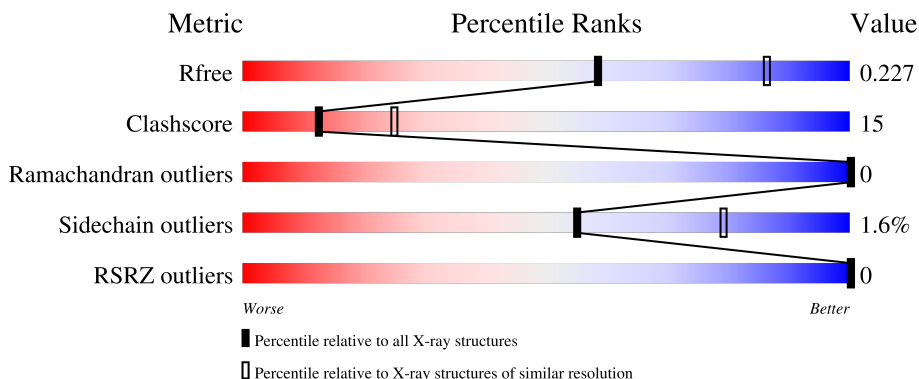
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*





The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	172	
1	B	172	
1	C	172	
1	D	172	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5092 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 Speckle-type POZ protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	Se	0	0	0
			1191	748	199	230	7	7			
1	B	153	Total	C	N	O	S	Se	0	0	0
			1191	747	198	232	7	7			
1	C	152	Total	C	N	O	S	Se	0	0	0
			1187	745	198	231	7	6			
1	D	152	Total	C	N	O	S	Se	0	0	0
			1187	745	198	231	7	6			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	GLY	-	expression tag	UNP O43791
A	167	SER	-	expression tag	UNP O43791
A	168	GLY	-	expression tag	UNP O43791
A	169	GLY	-	expression tag	UNP O43791
A	170	SER	-	expression tag	UNP O43791
A	171	GLY	-	expression tag	UNP O43791
A	330	THR	-	linker	UNP O43791
A	331	ASP	-	linker	UNP O43791
A	332	VAL	-	linker	UNP O43791
A	333	LEU	-	linker	UNP O43791
A	334	GLU	-	linker	UNP O43791
A	335	THR	-	linker	UNP O43791
A	336	SER	-	linker	UNP O43791
A	337	GLY	-	linker	UNP O43791
B	166	GLY	-	expression tag	UNP O43791
B	167	SER	-	expression tag	UNP O43791
B	168	GLY	-	expression tag	UNP O43791
B	169	GLY	-	expression tag	UNP O43791
B	170	SER	-	expression tag	UNP O43791
B	171	GLY	-	expression tag	UNP O43791
B	330	THR	-	linker	UNP O43791

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Chain	Residue	Modelled	Actual	Comment	Reference
B	331	ASP	-	linker	UNP O43791
B	332	VAL	-	linker	UNP O43791
B	333	LEU	-	linker	UNP O43791
B	334	GLU	-	linker	UNP O43791
B	335	THR	-	linker	UNP O43791
B	336	SER	-	linker	UNP O43791
B	337	GLY	-	linker	UNP O43791
C	166	GLY	-	expression tag	UNP O43791
C	167	SER	-	expression tag	UNP O43791
C	168	GLY	-	expression tag	UNP O43791
C	169	GLY	-	expression tag	UNP O43791
C	170	SER	-	expression tag	UNP O43791
C	171	GLY	-	expression tag	UNP O43791
C	330	THR	-	linker	UNP O43791
C	331	ASP	-	linker	UNP O43791
C	332	VAL	-	linker	UNP O43791
C	333	LEU	-	linker	UNP O43791
C	334	GLU	-	linker	UNP O43791
C	335	THR	-	linker	UNP O43791
C	336	SER	-	linker	UNP O43791
C	337	GLY	-	linker	UNP O43791
D	166	GLY	-	expression tag	UNP O43791
D	167	SER	-	expression tag	UNP O43791
D	168	GLY	-	expression tag	UNP O43791
D	169	GLY	-	expression tag	UNP O43791
D	170	SER	-	expression tag	UNP O43791
D	171	GLY	-	expression tag	UNP O43791
D	330	THR	-	linker	UNP O43791
D	331	ASP	-	linker	UNP O43791
D	332	VAL	-	linker	UNP O43791
D	333	LEU	-	linker	UNP O43791
D	334	GLU	-	linker	UNP O43791
D	335	THR	-	linker	UNP O43791
D	336	SER	-	linker	UNP O43791
D	337	GLY	-	linker	UNP O43791

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	82	Total O 82 82	0	0
2	B	93	Total O 93 93	0	0

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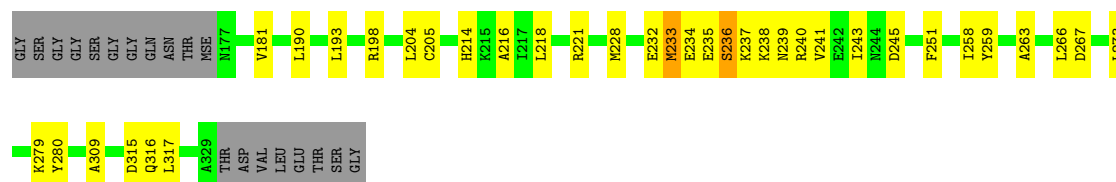
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	73	Total 73	O 73	0	0
2	D	88	Total 88	O 88	0	0

### 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.

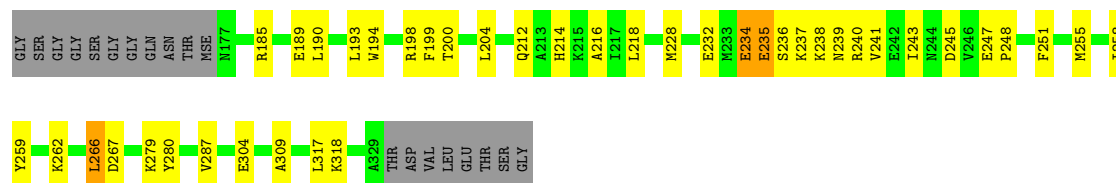
- Molecule 1: Speckle-type POZ protein

Chain A: 



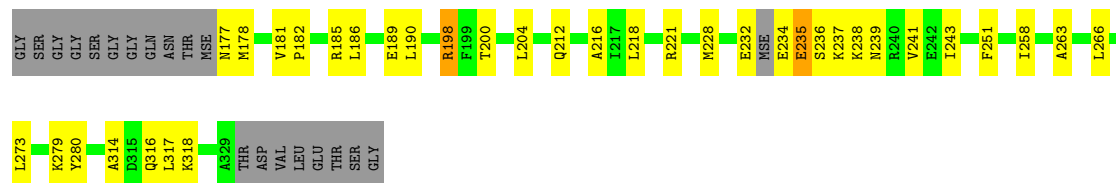
- Molecule 1: Speckle-type POZ protein

Chain B: 



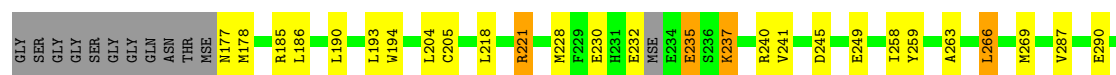
- Molecule 1: Speckle-type POZ protein

Chain C: 



- Molecule 1: Speckle-type POZ protein

Chain D: 



A314	D315	Q316	A329	THR	ASP	VAL	LEU	GLU	THR	SER	GLY
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	36.80Å 88.70Å 88.70Å 90.80° 89.30° 89.90°	Depositor
Resolution (Å)	44.34 – 2.50 44.34 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (44.34-2.50) 95.5 (44.34-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.90 (at 2.42Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.217 , 0.256 0.226 , 0.227	Depositor DCC
$R_{free}$ test set	2072 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 29.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for h,-l,k 0.013 for h,l,-k 0.470 for h,-k,-l 0.015 for -h,-k,l 0.014 for -h,k,-l 0.477 for -h,l,k 0.470 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5092	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.12% 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 [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	0.42	0/1203	0.93	4/1611 (0.2%)
1	B	0.45	0/1203	0.95	3/1612 (0.2%)
1	C	0.41	0/1199	0.93	3/1606 (0.2%)
1	D	0.42	0/1199	0.94	4/1606 (0.2%)
All	All	0.42	0/4804	0.94	14/6435 (0.2%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	235	GLU	N-CA-C	-9.90	100.57	111.36
1	D	235	GLU	N-CA-C	-8.86	101.73	112.54
1	C	235	GLU	N-CA-C	-7.84	102.98	112.54
1	D	237	LYS	N-CA-C	-5.89	104.81	112.23
1	A	315	ASP	N-CA-C	5.55	117.80	111.02

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	1191	0	1164	36	0
1	B	1191	0	1157	50	0
1	C	1187	0	1158	44	0
1	D	1187	0	1158	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	82	0	0	6	0
2	B	93	0	0	13	0
2	C	73	0	0	7	0
2	D	88	0	0	9	0
All	All	5092	0	4637	144	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 15.

The worst 5 of 144 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:C:200:THR:HG21	1:C:212:GLN:HB3	1.45	0.99
1:C:190:LEU:HD11	1:D:190:LEU:HD11	1.47	0.96
1:D:205:CYS:HB3	2:D:370:HOH:O	1.68	0.93
1:C:228:MSE:O	1:C:232:GLU:HG2	1.71	0.90
1:A:266:LEU:HD13	1:A:273:LEU:HD23	1.54	0.88

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	151/172 (88%)	143 (95%)	8 (5%)	0	100	100
1	B	151/172 (88%)	147 (97%)	4 (3%)	0	100	100
1	C	148/172 (86%)	140 (95%)	8 (5%)	0	100	100
1	D	148/172 (86%)	140 (95%)	8 (5%)	0	100	100
All	All	598/688 (87%)	570 (95%)	28 (5%)	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	128/134 (96%)	126 (98%)	2 (2%)	55	79
1	B	128/134 (96%)	126 (98%)	2 (2%)	55	79
1	C	128/134 (96%)	127 (99%)	1 (1%)	73	88
1	D	128/134 (96%)	125 (98%)	3 (2%)	44	72
All	All	512/536 (96%)	504 (98%)	8 (2%)	55	79

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	266	LEU
1	D	245	ASP
1	C	198	ARG
1	B	266	LEU
1	D	221	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	196	ASN
1	D	212	GLN
1	D	244	ASN
1	D	231	HIS
1	B	312	HIS

### 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](#)

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	146/172 (84%)	-1.19	0 100 100	24, 44, 71, 93	0
1	B	146/172 (84%)	-1.22	0 100 100	25, 43, 69, 93	0
1	C	146/172 (84%)	-1.22	0 100 100	24, 44, 72, 94	0
1	D	146/172 (84%)	-1.17	0 100 100	24, 44, 68, 92	0
All	All	584/688 (84%)	-1.20	0 100 100	24, 44, 71, 94	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 oligosaccharides 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.