



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 10:56 AM EDT

PDB ID : 6THL  
Title : Crystal structure of the complex between RTT106 and BCD1  
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Deposited on : 2019-11-20  
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

<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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

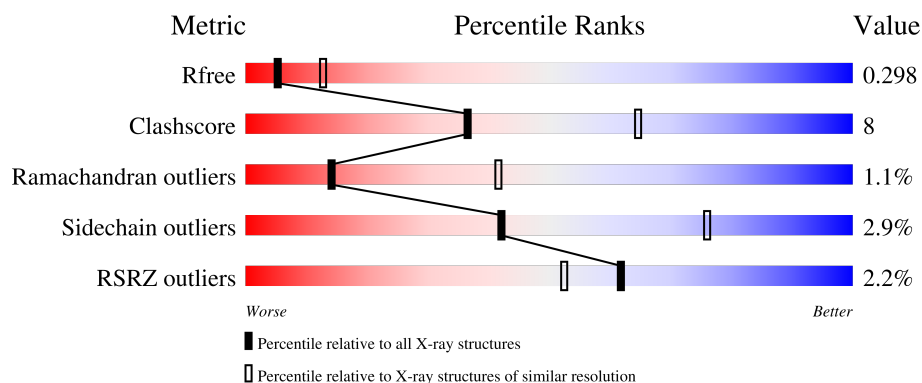
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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	240	
2	B	185	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3007 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 Rtt106p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1770	1148	278	337	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	GLY	-	expression tag	UNP C7GTH4
A	63	HIS	-	expression tag	UNP C7GTH4
A	64	MET	-	expression tag	UNP C7GTH4

- Molecule 2 is a protein called Box C/D snoRNA protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	150	Total	C	N	O	S	0	0	0
			1237	796	208	221	12			

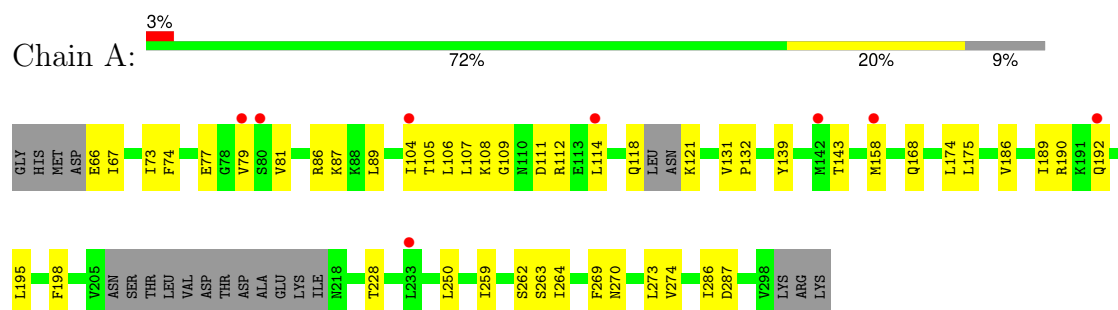
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	119	MET	-	initiating methionine	UNP P38772

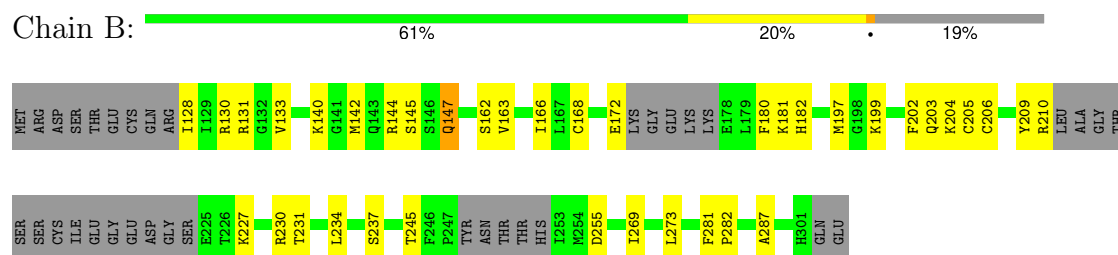
### 3 Residue-property plots

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: Rtt106p



#### • Molecule 2: Box C/D snoRNA protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.71Å 66.68Å 65.12Å 90.00° 104.72° 90.00°	Depositor
Resolution (Å)	19.86 – 2.80 19.86 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.86-2.80) 97.3 (19.86-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.210 , 0.300 0.218 , 0.298	Depositor DCC
$R_{free}$ test set	1135 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.9	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 46.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3007	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.35% 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	0.71	0/1805	0.87	0/2436
2	B	0.64	0/1260	0.85	1/1687 (0.1%)
All	All	0.68	0/3065	0.86	1/4123 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	255	ASP	CB-CG-OD1	5.49	123.24	118.30

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	1770	0	1784	28	0
2	B	1237	0	1256	21	0
All	All	3007	0	3040	48	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 8.

All (48) 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:81:VAL:HG21	1:A:89:LEU:HD12	1.58	0.85
1:A:77:GLU:H	1:A:168:GLN:HE22	1.27	0.81
2:B:234:LEU:O	2:B:237:SER:HB3	1.87	0.73
2:B:202:PHE:O	2:B:203:GLN:C	2.27	0.72
1:A:118:GLN:O	1:A:121:LYS:NZ	2.26	0.69
1:A:106:LEU:HD12	1:A:114:LEU:HD23	1.74	0.69
1:A:104:ILE:HD11	1:A:198:PHE:CE1	2.30	0.67
1:A:259:ILE:HG12	1:A:273:LEU:HD23	1.80	0.64
1:A:143:THR:HG21	1:A:250:LEU:HD22	1.80	0.63
2:B:144:ARG:HA	2:B:147:GLN:HG3	1.82	0.61
2:B:227:LYS:HE2	2:B:231:THR:OG1	2.03	0.58
2:B:163:VAL:HG12	2:B:282:PRO:HG2	1.85	0.57
1:A:186:VAL:O	1:A:190:ARG:HG3	2.05	0.56
1:A:264:ILE:HD11	1:A:270:ASN:CG	2.27	0.54
1:A:79:VAL:HG11	1:A:158:MET:SD	2.48	0.53
2:B:144:ARG:HA	2:B:147:GLN:CG	2.38	0.53
1:A:192:GLN:O	1:A:195:LEU:HB2	2.09	0.53
1:A:131:VAL:O	1:A:132:PRO:C	2.46	0.52
1:A:77:GLU:N	1:A:168:GLN:HE22	2.03	0.51
1:A:264:ILE:HD11	1:A:270:ASN:OD1	2.10	0.50
1:A:286:ILE:HG22	1:A:287:ASP:O	2.11	0.50
1:A:86:ARG:O	1:A:87:LYS:HG3	2.12	0.49
1:A:81:VAL:CG2	1:A:89:LEU:HD12	2.38	0.48
2:B:180:PHE:CE2	2:B:182:HIS:HB2	2.47	0.48
1:A:262:SER:O	1:A:269:PHE:HB2	2.14	0.46
2:B:269:ILE:HG22	2:B:273:LEU:HD12	1.96	0.46
1:A:77:GLU:H	1:A:168:GLN:NE2	2.06	0.46
2:B:209:TYR:O	2:B:210:ARG:HD3	2.16	0.45
1:A:139:TYR:HA	1:A:158:MET:O	2.17	0.45
2:B:133:VAL:HG22	2:B:273:LEU:O	2.17	0.45
2:B:140:LYS:HA	2:B:145:SER:OG	2.16	0.45
1:A:174:LEU:O	1:A:175:LEU:HD23	2.17	0.44
2:B:202:PHE:O	2:B:204:LYS:N	2.50	0.44
2:B:166:ILE:HG12	2:B:181:LYS:HG2	1.99	0.44
2:B:202:PHE:O	2:B:205:CYS:N	2.51	0.44
2:B:168:CYS:HB2	2:B:287:ALA:HB2	2.00	0.44
1:A:73:ILE:HD13	2:B:142:MET:SD	2.58	0.43
1:A:105:THR:HG21	1:A:107:LEU:HD21	2.00	0.43
2:B:144:ARG:NH2	2:B:281:PHE:O	2.51	0.43
2:B:202:PHE:CG	2:B:230:ARG:HD2	2.54	0.43
2:B:209:TYR:O	2:B:210:ARG:HG2	2.19	0.43
2:B:202:PHE:CB	2:B:230:ARG:HD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:PHE:CZ	1:A:189:ILE:HG12	2.55	0.41
1:A:108:LYS:HB3	1:A:111:ASP:HB2	2.02	0.41
2:B:130:ARG:O	2:B:133:VAL:N	2.54	0.41
1:A:79:VAL:CG1	1:A:158:MET:HB2	2.50	0.40
1:A:269:PHE:CD1	1:A:269:PHE:C	2.95	0.40
1:A:66:GLU:HB3	1:A:112:ARG:HH22	1.87	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	213/240 (89%)	201 (94%)	11 (5%)	1 (0%)	29	61
2	B	142/185 (77%)	124 (87%)	15 (11%)	3 (2%)	7	23
All	All	355/425 (84%)	325 (92%)	26 (7%)	4 (1%)	14	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	199	LYS
2	B	197	MET
2	B	131	ARG
1	A	109	GLY

### 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	205/224 (92%)	201 (98%)	4 (2%)	55	84
2	B	140/170 (82%)	134 (96%)	6 (4%)	29	62
All	All	345/394 (88%)	335 (97%)	10 (3%)	42	76

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	ILE
1	A	228	THR
1	A	263	SER
1	A	274	VAL
2	B	128	ILE
2	B	147	GLN
2	B	162	SER
2	B	172	GLU
2	B	206	CYS
2	B	245	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	223	GLN
2	B	147	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 monosaccharides 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	219/240 (91%)	-0.11	8 (3%) 41 31	21, 51, 74, 78	15 (6%)
2	B	150/185 (81%)	-0.20	0 100 100	37, 64, 91, 98	0
All	All	369/425 (86%)	-0.15	8 (2%) 62 52	21, 55, 84, 98	15 (4%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	MET	6.3
1	A	192	GLN	3.4
1	A	158	MET	3.3
1	A	79	VAL	2.6
1	A	233	LEU	2.4
1	A	104	ILE	2.1
1	A	114	LEU	2.0
1	A	80	SER	2.0

### 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.