



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4Q96  
Title : CID of human RPRD1B in complex with an unmodified CTD peptide  
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Deposited on : 2014-04-29  
Resolution : 1.85 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	<b>FAILED</b>
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

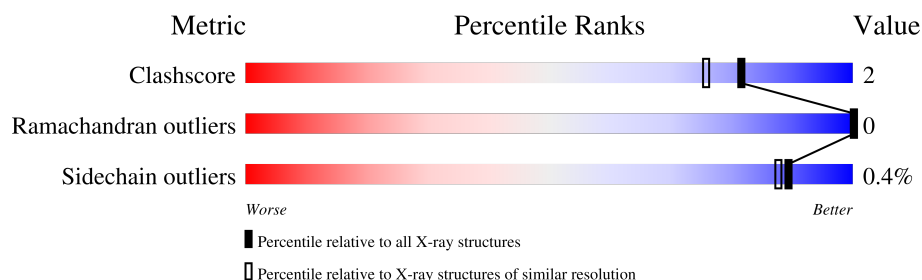
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)

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  $\leq 5\%$ .

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	135	90% 5% .
1	B	135	87% 7% . 5%
1	D	135	87% 7% 5%
1	E	135	90% . 5%
2	C	21	86% 14%
2	F	21	90% 10%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4795 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 Regulation of nuclear pre-mRNA domain-containing protein 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	3	1
			1052	670	189	191	2			
1	B	128	Total	C	N	O	S	0	7	0
			1068	682	192	192	2			
1	D	128	Total	C	N	O	S	0	6	1
			1056	674	190	190	2			
1	E	128	Total	C	N	O	S	0	3	0
			1038	666	186	184	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q9NQG5
A	21	HIS	GLN	SEE REMARK 999	UNP Q9NQG5
B	1	GLY	-	expression tag	UNP Q9NQG5
B	21	HIS	GLN	SEE REMARK 999	UNP Q9NQG5
D	1	GLY	-	expression tag	UNP Q9NQG5
D	21	HIS	GLN	SEE REMARK 999	UNP Q9NQG5
E	1	GLY	-	expression tag	UNP Q9NQG5
E	21	HIS	GLN	SEE REMARK 999	UNP Q9NQG5

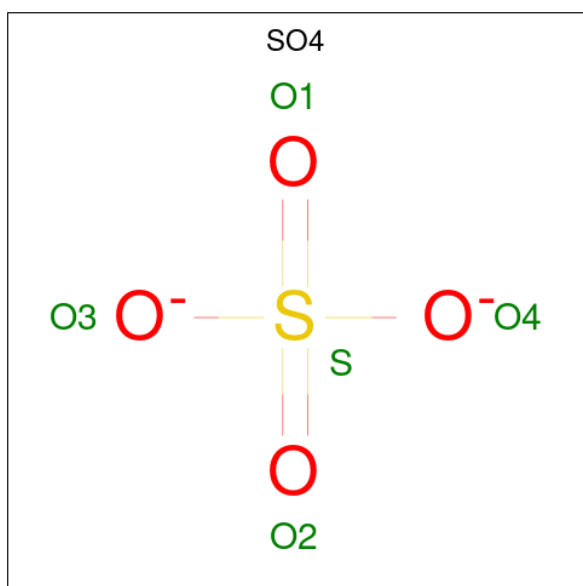
- Molecule 2 is a protein called RPB1-CTD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	21	Total	C	N	O	S	0	0	1
			155	97	22	35	1			
2	F	21	Total	C	N	O	S	0	0	1
			155	97	22	35	1			

- Molecule 3 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	8	Total X 8 8	0	0
3	B	1	Total X 1 1	0	0
3	D	7	Total X 7 7	0	0
3	E	6	Total X 6 6	0	0
3	F	1	Total X 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	42	Total O 42 42	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	62	Total 63	O 63	0	1
5	C	13	Total 13	O 13	0	0
5	D	44	Total 44	O 44	0	0
5	E	51	Total 51	O 51	0	0
5	F	15	Total 15	O 15	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. 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.


Note EDS failed to run properly.

- Molecule 1: Regulation of nuclear pre-mRNA domain-containing protein 1B

Chain A: 



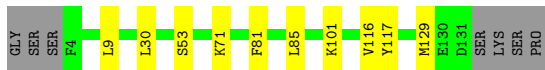
- Molecule 1: Regulation of nuclear pre-mRNA domain-containing protein 1B

Chain B: 



- Molecule 1: Regulation of nuclear pre-mRNA domain-containing protein 1B

Chain D: 



- Molecule 1: Regulation of nuclear pre-mRNA domain-containing protein 1B

Chain E: 



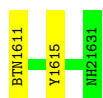
- Molecule 2: RPB1-CTD

Chain C: 



- Molecule 2: RPB1-CTD

Chain F:



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.65Å 134.71Å 55.71Å 90.00° 106.64° 90.00°	Depositor
Resolution (Å)	44.65 – 1.85	Depositor
% Data completeness (in resolution range)	99.9 (44.65-1.85)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.67 (at 1.86Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, $R_{free}$	0.238 , 0.271	Depositor
Wilson B-factor (Å <sup>2</sup> )	20.9	Xtriage
Anisotropy	0.206	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.448 for l,-k,h	Xtriage
Total number of atoms	4795	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.77% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BTN, UNX, SO4, NH2

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	0.36	0/1083	0.49	0/1458
1	B	0.37	0/1121	0.48	0/1506
1	D	0.39	0/1099	0.47	0/1479
1	E	0.38	0/1075	0.47	0/1446
2	C	0.45	0/146	0.52	0/203
2	F	0.39	0/146	0.56	0/203
All	All	0.38	0/4670	0.48	0/6295

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 [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	1052	0	1037	4	0
1	B	1068	0	1061	8	0
1	D	1056	0	1044	6	0
1	E	1038	0	1032	4	0
2	C	155	0	135	2	0
2	F	155	0	135	3	0
3	A	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	D	7	0	0	0	0
3	E	6	0	0	0	0
3	F	1	0	0	0	0
4	B	5	0	0	0	0
4	D	10	0	0	0	0
4	E	5	0	0	0	0
5	A	42	0	0	0	0
5	B	63	0	0	0	0
5	C	13	0	0	0	0
5	D	44	0	0	1	0
5	E	51	0	0	0	0
5	F	15	0	0	0	0
All	All	4795	0	4444	22	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 2.

The worst 5 of 22 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:110:ILE:HD11	2:F:1611:BTN:H62	1.71	0.72
1:E:49:ARG:HH22	1:E:94:ARG:HH12	1.45	0.62
1:E:12:LYS:HE3	1:E:29:TRP:CE2	2.38	0.58
2:C:1611:BTN:H62	1:E:110:ILE:HD11	1.86	0.58
1:B:80:GLU:O	1:B:83:SER:OG	2.22	0.57

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
1	B	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
1	D	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
1	E	129/135 (96%)	128 (99%)	1 (1%)	0	100	100
2	C	18/21 (86%)	18 (100%)	0	0	100	100
2	F	18/21 (86%)	18 (100%)	0	0	100	100
All	All	560/582 (96%)	551 (98%)	9 (2%)	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	113/122 (93%)	113 (100%)	0	100	100
1	B	118/122 (97%)	116 (98%)	2 (2%)	56	44
1	D	113/122 (93%)	113 (100%)	0	100	100
1	E	110/122 (90%)	110 (100%)	0	100	100
2	C	19/19 (100%)	19 (100%)	0	100	100
2	F	19/19 (100%)	19 (100%)	0	100	100
All	All	492/526 (94%)	490 (100%)	2 (0%)	89	88

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	98	GLU
1	B	102	LYS

Sometimes 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 27 ligands modelled in this entry, 23 are unknown - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SO4	D	208	-	4,4,4	0.22	0	6,6,6	0.12	0
4	SO4	E	207	-	4,4,4	0.24	0	6,6,6	0.14	0
4	SO4	B	202	-	4,4,4	0.23	0	6,6,6	0.12	0
4	SO4	D	209	-	4,4,4	0.25	0	6,6,6	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.