



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:53 PM GMT

PDB ID : 3V53  
Title : Crystal structure of human RBM25  
Authors : Gong, D.S.  
Deposited on : 2011-12-16  
Resolution : 2.90 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  
<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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

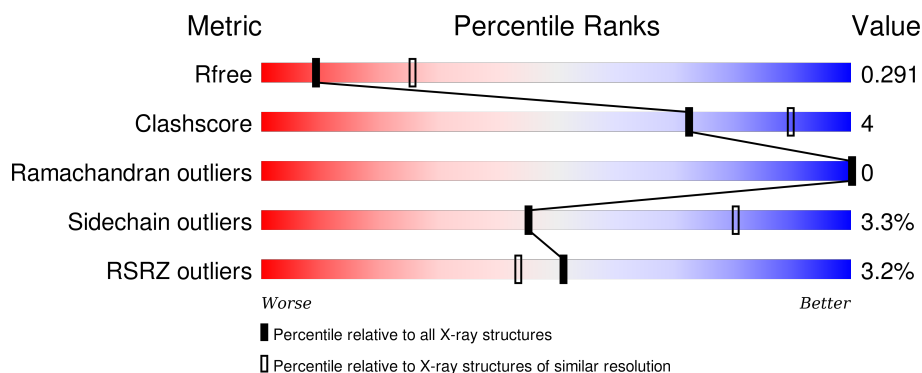
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	119	<div> <div>3%</div> <div>78% 14% 8%</div> </div>
1	B	119	<div> <div>3%</div> <div>84% 9% • 6%</div> </div>
1	C	119	<div> <div>79% 8% 13%</div> </div>
1	D	119	<div> <div>76% 13% • 8%</div> </div>
1	E	119	<div> <div>8%</div> <div>76% 9% 14%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4150 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 RNA-binding protein 25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	1	0	0
			833	541	137	149	6			
1	B	112	Total	C	N	O	S	1	0	0
			861	559	138	159	5			
1	C	104	Total	C	N	O	S	0	0	0
			840	546	134	155	5			
1	D	109	Total	C	N	O	S	0	0	0
			876	572	144	154	6			
1	E	102	Total	C	N	O	S	0	0	0
			740	480	119	137	4			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	725	MET	-	EXPRESSION TAG	UNP P49756
A	726	GLY	-	EXPRESSION TAG	UNP P49756
A	727	HIS	-	EXPRESSION TAG	UNP P49756
A	728	HIS	-	EXPRESSION TAG	UNP P49756
A	729	HIS	-	EXPRESSION TAG	UNP P49756
A	730	HIS	-	EXPRESSION TAG	UNP P49756
A	731	HIS	-	EXPRESSION TAG	UNP P49756
A	732	HIS	-	EXPRESSION TAG	UNP P49756
A	733	MET	-	EXPRESSION TAG	UNP P49756
B	725	MET	-	EXPRESSION TAG	UNP P49756
B	726	GLY	-	EXPRESSION TAG	UNP P49756
B	727	HIS	-	EXPRESSION TAG	UNP P49756
B	728	HIS	-	EXPRESSION TAG	UNP P49756
B	729	HIS	-	EXPRESSION TAG	UNP P49756
B	730	HIS	-	EXPRESSION TAG	UNP P49756
B	731	HIS	-	EXPRESSION TAG	UNP P49756
B	732	HIS	-	EXPRESSION TAG	UNP P49756
B	733	MET	-	EXPRESSION TAG	UNP P49756
C	725	MET	-	EXPRESSION TAG	UNP P49756

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Chain	Residue	Modelled	Actual	Comment	Reference
C	726	GLY	-	EXPRESSION TAG	UNP P49756
C	727	HIS	-	EXPRESSION TAG	UNP P49756
C	728	HIS	-	EXPRESSION TAG	UNP P49756
C	729	HIS	-	EXPRESSION TAG	UNP P49756
C	730	HIS	-	EXPRESSION TAG	UNP P49756
C	731	HIS	-	EXPRESSION TAG	UNP P49756
C	732	HIS	-	EXPRESSION TAG	UNP P49756
C	733	MET	-	EXPRESSION TAG	UNP P49756
D	725	MET	-	EXPRESSION TAG	UNP P49756
D	726	GLY	-	EXPRESSION TAG	UNP P49756
D	727	HIS	-	EXPRESSION TAG	UNP P49756
D	728	HIS	-	EXPRESSION TAG	UNP P49756
D	729	HIS	-	EXPRESSION TAG	UNP P49756
D	730	HIS	-	EXPRESSION TAG	UNP P49756
D	731	HIS	-	EXPRESSION TAG	UNP P49756
D	732	HIS	-	EXPRESSION TAG	UNP P49756
D	733	MET	-	EXPRESSION TAG	UNP P49756
E	725	MET	-	EXPRESSION TAG	UNP P49756
E	726	GLY	-	EXPRESSION TAG	UNP P49756
E	727	HIS	-	EXPRESSION TAG	UNP P49756
E	728	HIS	-	EXPRESSION TAG	UNP P49756
E	729	HIS	-	EXPRESSION TAG	UNP P49756
E	730	HIS	-	EXPRESSION TAG	UNP P49756
E	731	HIS	-	EXPRESSION TAG	UNP P49756
E	732	HIS	-	EXPRESSION TAG	UNP P49756
E	733	MET	-	EXPRESSION TAG	UNP P49756



- Molecule 1: RNA-binding protein 25



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.58Å 86.17Å 197.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.29 – 2.90 49.29 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.0 (49.29-2.90) 98.0 (49.29-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.264 , 0.298 0.256 , 0.291	Depositor DCC
$R_{free}$ test set	765 reflections (5.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	73.7	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 40.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 15498 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4150	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.54	1/851 (0.1%)	0.56	1/1156 (0.1%)
1	B	0.55	2/879 (0.2%)	0.54	1/1195 (0.1%)
1	C	0.35	0/858	0.50	0/1162
1	D	0.37	0/895	0.51	0/1212
1	E	0.31	0/754	0.46	0/1030
All	All	0.44	3/4237 (0.1%)	0.52	2/5755 (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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	737	HIS	CG-CD2	12.58	1.57	1.35
1	A	822	PHE	CG-CD1	11.75	1.56	1.38
1	B	737	HIS	CD2-NE2	-5.37	1.26	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	822	PHE	CB-CG-CD1	8.24	126.57	120.80
1	B	737	HIS	ND1-CG-CD2	-5.45	98.38	106.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	737	HIS	Sidechain

## 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	833	0	788	6	0
1	B	861	0	833	8	0
1	C	840	0	846	4	0
1	D	876	0	894	11	0
1	E	740	0	670	6	0
All	All	4150	0	4031	34	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 4.

The worst 5 of 34 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:737:HIS:O	1:A:741:LEU:HD12	1.97	0.65
1:D:830:LEU:O	1:D:834:THR:HB	2.01	0.61
1:B:783:ILE:HG22	1:B:784:GLY:N	2.20	0.57
1:A:776:ASN:O	1:A:779:ILE:HG22	2.07	0.55
1:C:775:ILE:O	1:C:779:ILE:HG12	2.07	0.55

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	106/119 (89%)	100 (94%)	6 (6%)	0	100	100
1	B	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
1	C	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
1	D	107/119 (90%)	102 (95%)	5 (5%)	0	100	100
1	E	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
All	All	523/595 (88%)	501 (96%)	22 (4%)	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	81/109 (74%)	77 (95%)	4 (5%)	31	67
1	B	88/109 (81%)	87 (99%)	1 (1%)	80	95
1	C	92/109 (84%)	89 (97%)	3 (3%)	45	80
1	D	95/109 (87%)	89 (94%)	6 (6%)	22	54
1	E	68/109 (62%)	68 (100%)	0	100	100
All	All	424/545 (78%)	410 (97%)	14 (3%)	45	80

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	742	ILE
1	C	826	MET
1	D	772	ARG
1	C	741	LEU
1	D	764	SER

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

Mol	Chain	Res	Type
1	B	801	HIS
1	C	801	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 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	110/119 (92%)	0.39	4 (3%) 46 38	71, 108, 126, 142	7 (6%)
1	B	112/119 (94%)	0.21	4 (3%) 46 38	56, 78, 121, 128	4 (3%)
1	C	104/119 (87%)	-0.10	0 100 100	47, 64, 82, 87	7 (6%)
1	D	109/119 (91%)	-0.06	0 100 100	37, 54, 81, 88	1 (0%)
1	E	102/119 (85%)	0.48	9 (8%) 12 8	76, 106, 134, 144	2 (1%)
All	All	537/595 (90%)	0.19	17 (3%) 51 43	37, 80, 126, 144	21 (3%)

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	740	SER	3.4
1	E	741	LEU	3.0
1	E	770	ARG	2.9
1	E	836	ALA	2.6
1	E	827	TRP	2.6

### 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.