



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 01:06 am BST

PDB ID : 2R8S  
Title : High resolution structure of a specific synthetic FAB bound to P4-P6 RNA ribozyme domain  
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Deposited on : 2007-09-11  
Resolution : 1.95 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.

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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)	:	1.13
EDS	:	2.11
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)	:	2.11

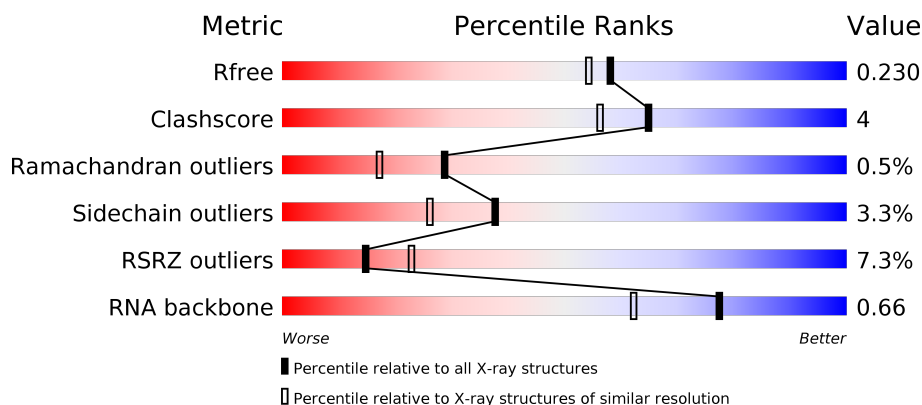
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)
RNA backbone	3102	1124 (2.50-1.42)

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 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	R	159	<div> <div>9%</div> <div> <div></div> <div>84%</div> <div>13%</div> <div>..</div> </div> </div>
2	L	214	<div> <div>8%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div>.</div> </div> </div>
3	H	224	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7217 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 RNA chain called P4-P6 RNA RIBOZYME DOMAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	159	Total	C	N	O	P	0	0	0
			3404	1522	623	1101	158			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	102	G	-	EXPRESSION TAG	GB 10840
R	103	G	-	EXPRESSION TAG	GB 10840
R	?	-	C	DELETION	GB 10840

- Molecule 2 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	4	0
			1644	1027	274	336	7			

- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	2	1
			1632	1031	271	321	9			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	R	4	Total	Mg	0	0
			4	4		


- Molecule 5 is water.

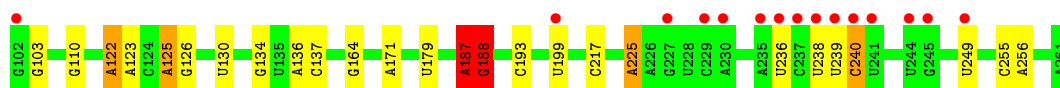
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	R	257	Total 260	O 260	0	3
5	L	131	Total 132	O 132	0	1
5	H	141	Total 141	O 141	0	0

### 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.

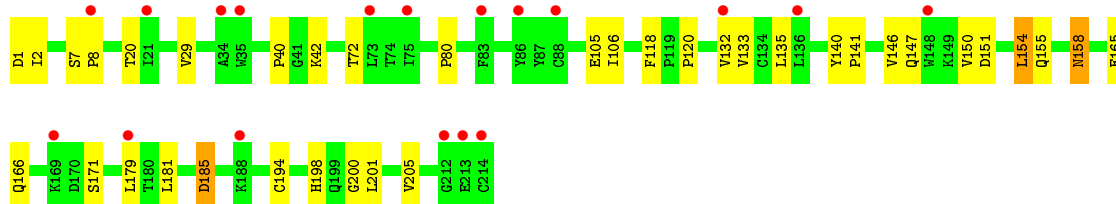
#### • Molecule 1: P4-P6 RNA RIBOZYME DOMAIN

Chain R: 




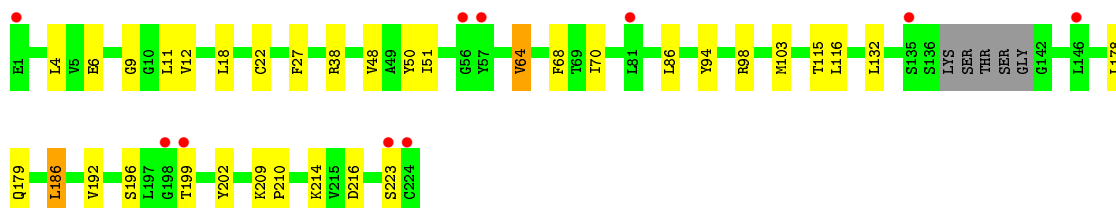
#### • Molecule 2: Fab light chain

Chain L: 



#### • Molecule 3: Fab heavy chain

Chain H: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.09Å 53.23Å 160.56Å 90.00° 108.42° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95 19.69 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-1.95) 98.6 (19.69-1.95)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.50 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.195 , 0.226 0.199 , 0.230	Depositor DCC
$R_{free}$ test set	3875 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.0	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 58.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7217	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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: MG

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	R	0.69	0/3812	1.21	12/5943 (0.2%)
2	L	0.45	0/1687	0.87	3/2288 (0.1%)
3	H	0.45	0/1682	0.84	0/2290
All	All	0.59	0/7181	1.07	15/10521 (0.1%)

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
2	L	0	1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	164	G	O4'-C1'-N9	9.15	115.52	108.20
1	R	193	C	O4'-C1'-N1	7.18	113.94	108.20
1	R	125	A	C1'-O4'-C4'	-6.33	104.83	109.90
2	L	151	ASP	CB-CG-OD2	6.17	123.86	118.30
1	R	134	G	N1-C6-O6	-6.08	116.25	119.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	7	SER	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	R	3404	0	1715	3	0
2	L	1644	0	1588	24	0
3	H	1632	0	1581	22	0
4	R	4	0	0	0	0
5	H	141	0	0	0	0
5	L	132	0	0	0	0
5	R	260	0	0	3	0
All	All	7217	0	4884	47	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 47 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)
2:L:118:PHE:HB2	2:L:133:VAL:HG22	1.64	0.79
3:H:12:VAL:HG11	3:H:18:LEU:HG	1.69	0.72
3:H:4:LEU:HG	3:H:22:CYS:SG	2.32	0.69
2:L:198:HIS:CD2	2:L:200:GLY:H	2.16	0.64
2:L:118:PHE:HD2	2:L:133:VAL:HG23	1.62	0.64

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	
2	L	214/214 (100%)	205 (96%)	8 (4%)	1 (0%)	29	17
3	H	217/224 (97%)	209 (96%)	7 (3%)	1 (0%)	29	17
All	All	431/438 (98%)	414 (96%)	15 (4%)	2 (0%)	29	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	8	PRO
3	H	223	SER

### 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	
2	L	191/189 (101%)	185 (97%)	6 (3%)	40	28
3	H	181/184 (98%)	175 (97%)	6 (3%)	38	26
All	All	372/373 (100%)	360 (97%)	12 (3%)	38	27

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	165[A]	GLU
3	H	11	LEU
3	H	98	ARG
2	L	158	ASN
3	H	64	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	100	GLN
2	L	158	ASN
2	L	198	HIS
3	H	3	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	158/159 (99%)	14 (8%)	5 (3%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	103	G
1	R	123	A
1	R	125	A
1	R	126	G
1	R	179	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	R	122	A
1	R	125	A
1	R	188	G
1	R	225	A
1	R	240	C

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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](#)

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	R	159/159 (100%)	0.37	15 (9%) <b>8</b> <b>13</b>	30, 45, 96, 148	0
2	L	214/214 (100%)	0.57	18 (8%) <b>11</b> <b>17</b>	27, 38, 52, 78	2 (0%)
3	H	219/224 (97%)	0.41	10 (4%) <b>32</b> <b>42</b>	22, 36, 50, 75	1 (0%)
All	All	592/597 (99%)	0.45	43 (7%) <b>15</b> <b>23</b>	22, 38, 64, 148	3 (0%)

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	224	CYS	11.2
2	L	214	CYS	10.2
2	L	213	GLU	9.2
1	R	238	U	8.1
3	H	223	SER	8.0

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MG	R	1004	1/1	0.89	0.09	35,35,35,35	0
4	MG	R	1002	1/1	0.94	0.16	36,36,36,36	0
4	MG	R	1001	1/1	0.94	0.18	32,32,32,32	0
4	MG	R	1003	1/1	0.95	0.06	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.