



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 12:15 AM GMT

PDB ID : 2YJT
Title : Crystal structure of E. coli DEAD-box protein SrmB bound to regulator of ribonuclease activity A (RraA)
Authors : Pietras, Z.; Hardwick, S.W.; Luisi, B.F.
Deposited on : 2011-05-23
Resolution : 2.90 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

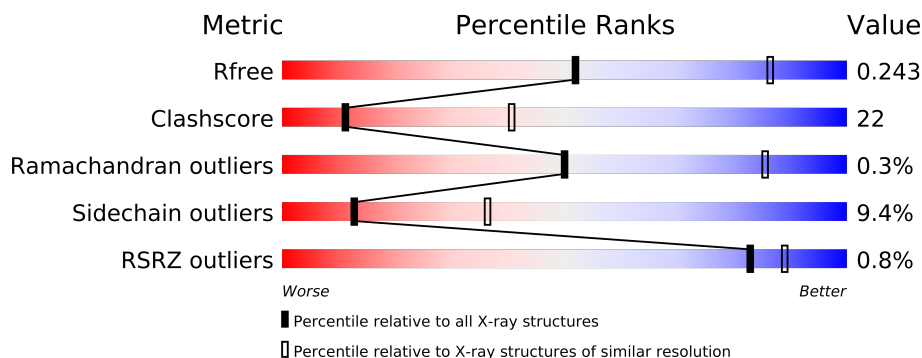
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

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}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	161	
1	B	161	
1	C	161	
2	D	170	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4993 atoms, of which 0 are hydrogen and 0 are deuterium.

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 REGULATOR OF RIBONUCLEASE ACTIVITY A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	158	Total	C	N	O	S	0	0	0
			1196	750	200	243	3			
1	B	158	Total	C	N	O	S	0	0	0
			1196	750	200	243	3			
1	C	158	Total	C	N	O	S	0	0	0
			1196	750	200	243	3			

- Molecule 2 is a protein called ATP-DEPENDENT RNA HELICASE SRMB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	170	Total	C	N	O	S	0	0	0
			1376	862	268	243	3			

- Molecule 3 is water.

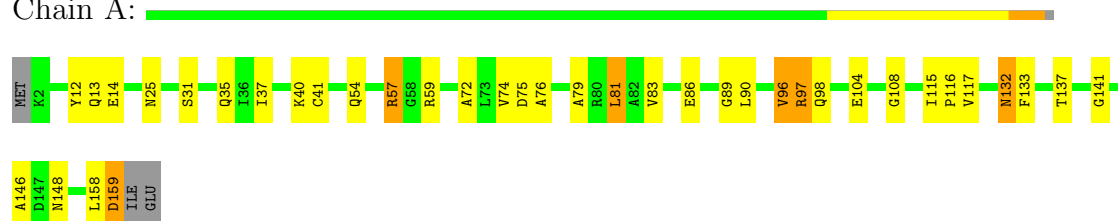
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	10	Total	O	0	0
			10	10		
3	B	10	Total	O	0	0
			10	10		
3	C	6	Total	O	0	0
			6	6		
3	D	3	Total	O	0	0
			3	3		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

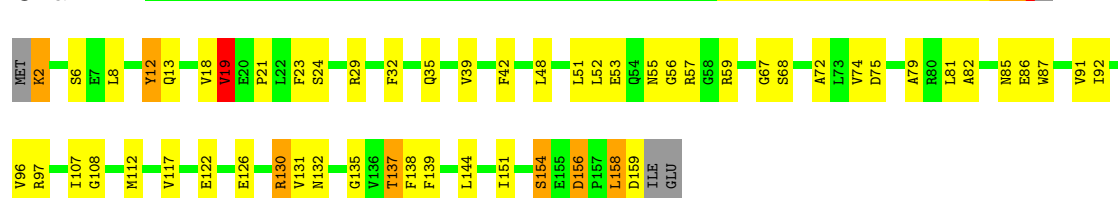
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain A:



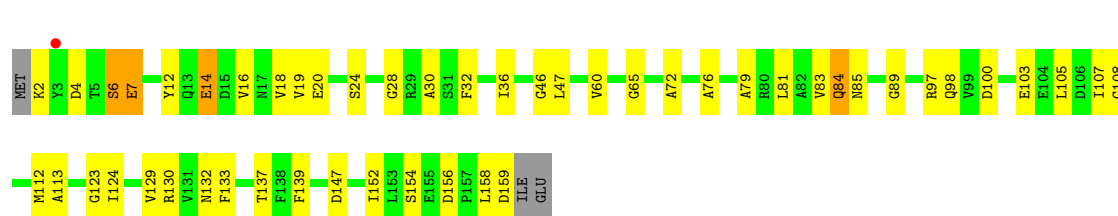
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain B:



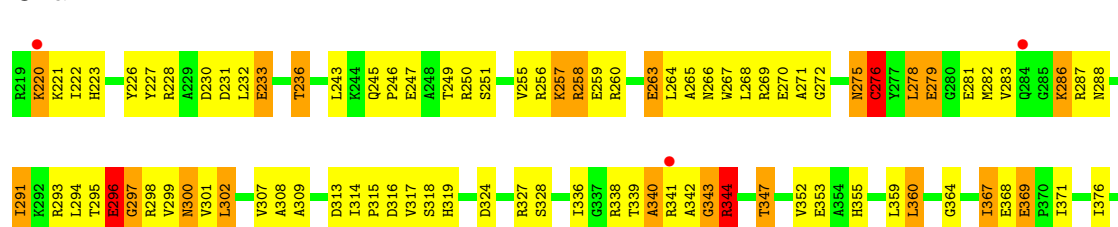
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain C:



• Molecule 2: ATP-DEPENDENT RNA HELICASE SRMB

Chain D:



L379	R380	P381	K382	T383	R384	S387	E388



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	73.39Å 73.39Å 222.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	74.30 – 2.90 63.56 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.1 (74.30-2.90) 99.1 (63.56-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.192 , 0.257 0.198 , 0.243	Depositor DCC
R_{free} test set	804 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 10.1	EDS
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 16051 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4993	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	1.10	1/1213 (0.1%)	0.87	1/1644 (0.1%)
1	B	1.01	3/1213 (0.2%)	0.82	0/1644
1	C	1.05	2/1213 (0.2%)	0.84	0/1644
2	D	1.20	2/1401 (0.1%)	0.96	2/1888 (0.1%)
All	All	1.10	8/5040 (0.2%)	0.88	3/6820 (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
2	D	0	6

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	12	TYR	CD1-CE1	-5.91	1.30	1.39
2	D	369	GLU	CG-CD	-5.70	1.43	1.51
1	C	12	TYR	CD2-CE2	-5.62	1.30	1.39
1	B	12	TYR	CD2-CE2	-5.43	1.31	1.39
2	D	276	CYS	CB-SG	-5.40	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	LEU	CA-CB-CG	7.05	131.51	115.30
2	D	360	LEU	CA-CB-CG	7.03	131.47	115.30
2	D	297	GLY	N-CA-C	-5.65	98.97	113.10

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	296	GLU	Peptide
2	D	340	ALA	Peptide
2	D	342	ALA	Peptide
2	D	343	GLY	Peptide
2	D	344	ARG	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1196	0	1147	37	0
1	B	1196	0	1147	48	0
1	C	1196	0	1147	37	1
2	D	1376	0	1407	107	3
3	A	10	0	0	2	0
3	B	10	0	0	3	0
3	C	6	0	0	3	0
3	D	3	0	0	6	0
All	All	4993	0	4848	220	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 22.

The worst 5 of 220 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:340:ALA:O	2:D:341:ARG:CG	1.84	1.25
2:D:233:GLU:HB3	3:D:2001:HOH:O	1.39	1.22
1:B:29:ARG:HD3	3:B:2003:HOH:O	1.42	1.16
1:C:124:ILE:O	3:C:2003:HOH:O	1.59	1.15
1:C:65:GLY:O	3:C:2004:HOH:O	1.59	1.14

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:156:ASP:OD2	2:D:226:TYR:OH[3_555]	2.00	0.20

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:344:ARG:NH1	2:D:355:HIS:N[4_455]	2.15	0.05
2:D:344:ARG:NH1	2:D:355:HIS:CB[4_455]	2.16	0.04

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	156/161 (97%)	149 (96%)	7 (4%)	0	100	100
1	B	156/161 (97%)	142 (91%)	14 (9%)	0	100	100
1	C	156/161 (97%)	147 (94%)	9 (6%)	0	100	100
2	D	168/170 (99%)	154 (92%)	12 (7%)	2 (1%)	19	57
All	All	636/653 (97%)	592 (93%)	42 (7%)	2 (0%)	50	85

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	308	ALA
2	D	220	LYS

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	125/128 (98%)	117 (94%)	8 (6%)	25	59
1	B	125/128 (98%)	115 (92%)	10 (8%)	17	45
1	C	125/128 (98%)	119 (95%)	6 (5%)	35	74
2	D	144/144 (100%)	119 (83%)	25 (17%)	3	8
All	All	519/528 (98%)	470 (91%)	49 (9%)	13	36

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	47	LEU
2	D	246	PRO
2	D	353	GLU
2	D	221	LYS
2	D	251	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	35	GLN
1	C	98	GLN
2	D	241	HIS
1	A	132	ASN
1	C	110	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
1	A	158/161 (98%)	-0.45	0 100 100	20, 30, 46, 52	0
1	B	158/161 (98%)	-0.37	0 100 100	20, 31, 45, 52	0
1	C	158/161 (98%)	-0.37	1 (0%) 86 91	21, 30, 44, 49	0
2	D	170/170 (100%)	0.19	4 (2%) 56 65	25, 56, 81, 85	0
All	All	644/653 (98%)	-0.24	5 (0%) 83 89	20, 34, 74, 85	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	341	ARG	4.4
2	D	220	LYS	2.1
2	D	284	GLN	2.1
1	C	3	TYR	2.1
2	D	387	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.