wwPDB X-ray Structure Validation Summary Report (i)

Jun 13, 2024 – 12:29 AM EDT

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 X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

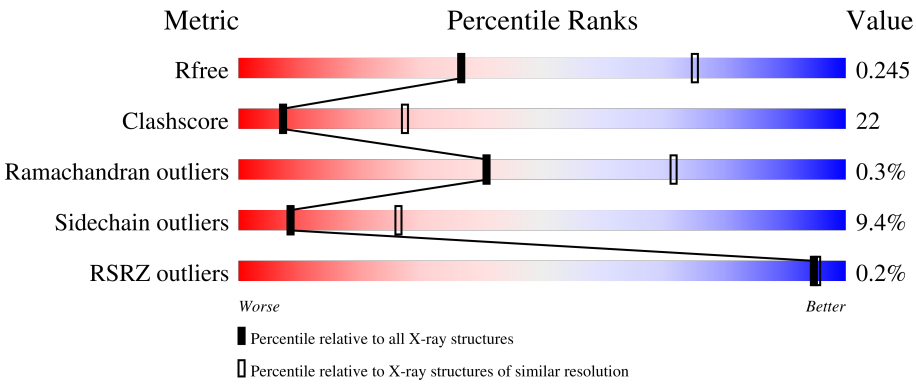
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	161	75% 20%
1	B	161	63% 30%
1	C	161	67% 29%
2	D	170	% 45% 42% 12%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4993 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 REGULATOR OF RIBONUCLEASE ACTIVITY A.

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

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

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

- Molecule 3 is water.

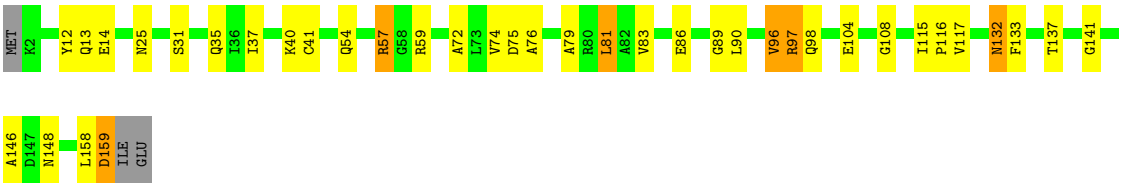
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	10	10	10	0	0
3	B	10	10	10	0	0
3	C	6	6	6	0	0
3	D	3	3	3	0	0

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 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.

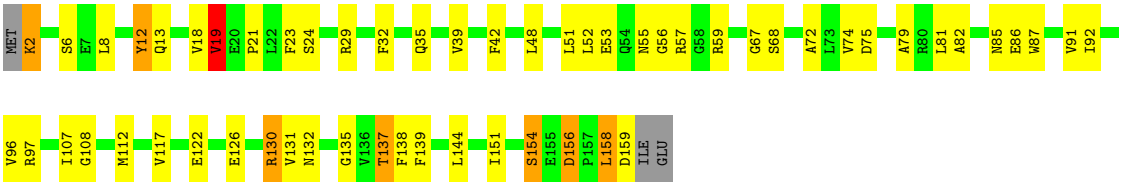
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain A:



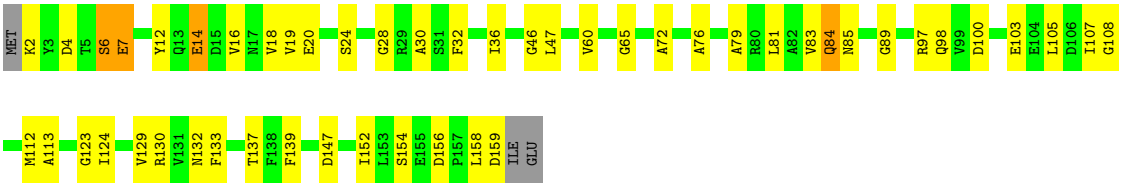
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain B:



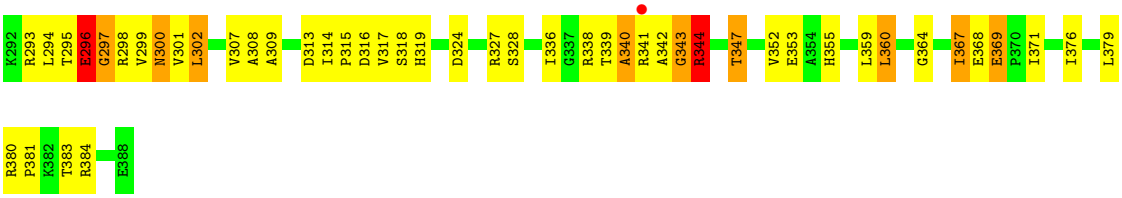
• Molecule 1: REGULATOR OF RIBONUCLEASE ACTIVITY A

Chain C:



• Molecule 2: ATP-DEPENDENT RNA HELICASE SRMB

Chain D:


K292
R293
L294
T295
E296
G297
R298
V299
N300
V301
L302
V307
A308
A309
D313
I314
P315
D316
V317
S318
H319
D324
R327
S328
I336
G337
R338
T339
A340
R341
A342
G343
R344
T347
V352
E353
A354
H355
L359
L360
G364
I367
E368
E369
P370
I371
I376
L379
R380
P381
K382
T383
R384
E388

4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [1]	2.68 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.192 , 0.257 0.198 , 0.245	Depositor DCC
R_{free} test set	806 reflections (5.02%)	wwPDB-VP
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 , 27.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	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.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	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(^{o})	Ideal(^{o})
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 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	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

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 22.

The worst 5 of 220 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: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	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:ASP:OD2	2:D:226:TYR:OH[3_555]	2.00	0.20
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 (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	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%)	13	40
All	All	636/653 (97%)	592 (93%)	42 (7%)	2 (0%)	41	71

All (2) Ramachandran outliers are listed below:

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

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	125/128 (98%)	117 (94%)	8 (6%)	17	45
1	B	125/128 (98%)	115 (92%)	10 (8%)	12	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	125/128 (98%)	119 (95%)	6 (5%)	25 58
2	D	144/144 (100%)	119 (83%)	25 (17%)	2 6
All	All	519/528 (98%)	470 (91%)	49 (9%)	8 26

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

Mol	Chain	Res	Type
2	D	251	SER
2	D	278	LEU
2	D	257	LYS
2	D	263	GLU
2	D	286	LYS

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

Mol	Chain	Res	Type
2	D	241	HIS
2	D	284	GLN
2	D	319	HIS
1	A	132	ASN
1	C	35	GLN

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 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, 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%)	-0.48	0	100	100	20, 30, 46, 52	0
1	B	158/161 (98%)	-0.42	0	100	100	20, 31, 45, 52	0
1	C	158/161 (98%)	-0.41	0	100	100	21, 30, 44, 49	0
2	D	170/170 (100%)	0.10	1 (0%)	89	89	25, 56, 81, 85	0
All	All	644/653 (98%)	-0.29	1 (0%)	95	95	20, 34, 74, 85	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	341	ARG	4.0

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.