Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:20 PM GMT

PDB ID	:	1JXB
Title	:	I53A, a point mutant of the cysteine-free variant of E. coli Rnase HI
Authors	:	Spudich, G.; Lorenz, S.; Marqusee, S.
Deposited on	:	2001-09-06
Resolution	:	1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

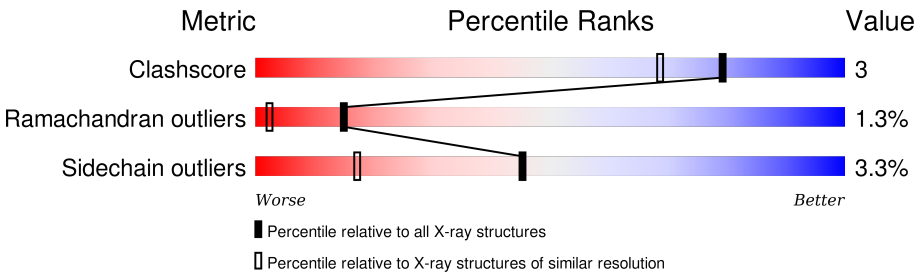
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	155	77% 13% 5% • •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1369 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 Ribonuclease HI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	152	1208	757	224	224	3	34	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ALA	ILE	ENGINEERED	UNP P0A7Y4
A	13	ALA	CYS	VARIANT	UNP P0A7Y4
A	63	ALA	CYS	VARIANT	UNP P0A7Y4
A	133	ALA	CYS	VARIANT	UNP P0A7Y4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	161	161	161	0	0

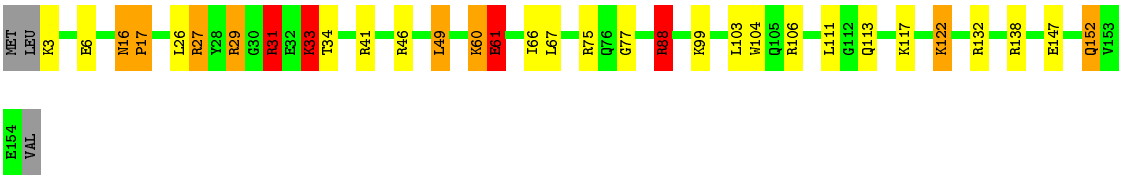
3 Residue-property plots (i)

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

Note EDS was not executed.

- Molecule 1: Ribonuclease HI

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	36.87Å 40.83Å 85.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.50 – 1.60	Depositor
% Data completeness (in resolution range)	(Not available) (12.50-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.207 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1369	wwPDB-VP
Average B, all atoms ($Å^2$)	26.0	wwPDB-VP

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	3.87	21/1236 (1.7%)	3.63	37/1672 (2.2%)

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	A	0	8

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	29	ARG	NE-CZ	74.51	2.29	1.33
1	A	29	ARG	CZ-NH1	-63.28	0.50	1.33
1	A	152	GLN	CD-NE2	58.44	2.79	1.32
1	A	3	LYS	CE-NZ	31.48	2.27	1.49
1	A	33	LYS	CE-NZ	27.41	2.17	1.49
1	A	60	LYS	CA-CB	25.54	2.10	1.53
1	A	31	ARG	CG-CD	-24.36	0.91	1.51
1	A	61	GLU	CG-CD	20.40	1.82	1.51
1	A	31	ARG	CZ-NH2	15.53	1.53	1.33
1	A	29	ARG	CD-NE	-12.74	1.24	1.46
1	A	122	LYS	C-O	12.65	1.47	1.23
1	A	61	GLU	CD-OE1	-12.35	1.12	1.25
1	A	60	LYS	CB-CG	-11.87	1.20	1.52
1	A	31	ARG	CZ-NH1	-11.30	1.18	1.33
1	A	99	LYS	CE-NZ	-10.56	1.22	1.49
1	A	31	ARG	CD-NE	10.17	1.63	1.46
1	A	117	LYS	CE-NZ	9.54	1.73	1.49
1	A	29	ARG	CG-CD	-8.88	1.29	1.51
1	A	138	ARG	CZ-NH1	8.09	1.43	1.33
1	A	152	GLN	CD-OE1	7.74	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	88	ARG	CZ-NH1	6.65	1.41	1.33

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	29	ARG	NE-CZ-NH2	-116.69	61.96	120.30
1	A	29	ARG	NE-CZ-NH1	-40.50	100.05	120.30
1	A	122	LYS	O-C-N	-23.78	82.77	123.20
1	A	31	ARG	CB-CG-CD	22.29	169.56	111.60
1	A	31	ARG	CG-CD-NE	20.53	154.92	111.80
1	A	3	LYS	CA-CB-CG	19.42	156.11	113.40
1	A	31	ARG	NE-CZ-NH1	14.71	127.65	120.30
1	A	88	ARG	NE-CZ-NH1	-13.92	113.34	120.30
1	A	3	LYS	CB-CG-CD	12.87	145.05	111.60
1	A	60	LYS	N-CA-CB	-12.43	88.23	110.60
1	A	31	ARG	NE-CZ-NH2	-11.35	114.63	120.30
1	A	60	LYS	CB-CG-CD	10.85	139.81	111.60
1	A	88	ARG	NE-CZ-NH2	-10.54	115.03	120.30
1	A	117	LYS	CD-CE-NZ	-10.22	88.20	111.70
1	A	111	LEU	CB-CG-CD2	10.04	128.08	111.00
1	A	31	ARG	CD-NE-CZ	-9.31	110.56	123.60
1	A	61	GLU	CB-CG-CD	9.12	138.84	114.20
1	A	46	ARG	NE-CZ-NH1	8.46	124.53	120.30
1	A	122	LYS	C-N-CA	7.63	138.32	122.30
1	A	152	GLN	CG-CD-NE2	-7.60	98.47	116.70
1	A	132	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	66	ILE	CB-CG1-CD1	6.79	132.91	113.90
1	A	147	GLU	OE1-CD-OE2	6.71	131.35	123.30
1	A	61	GLU	CG-CD-OE1	-6.68	104.94	118.30
1	A	61	GLU	CG-CD-OE2	6.63	131.56	118.30
1	A	27	ARG	NE-CZ-NH1	6.39	123.50	120.30
1	A	60	LYS	CB-CA-C	-6.39	97.62	110.40
1	A	111	LEU	CD1-CG-CD2	-6.35	91.45	110.50
1	A	132	ARG	NE-CZ-NH2	-6.31	117.15	120.30
1	A	29	ARG	CG-CD-NE	-6.14	98.91	111.80
1	A	46	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	A	75	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	26	LEU	CA-CB-CG	5.64	128.26	115.30
1	A	16	ASN	CA-C-O	-5.61	108.33	120.10
1	A	17	PRO	CA-N-CD	-5.46	103.86	111.50
1	A	41	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	106	ARG	CD-NE-CZ	5.01	130.62	123.60

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	GLN	Sidechain
1	A	122	LYS	Mainchain
1	A	152	GLN	Sidechain
1	A	16	ASN	Mainchain,Peptide
1	A	29	ARG	Sidechain
1	A	31	ARG	Sidechain
1	A	88	ARG	Sidechain

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	1208	0	1178	8	0
2	A	161	0	0	1	0
All	All	1369	0	1178	8	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 3.

All (8) 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:33:LYS:HE3	1:A:34:THR:H	1.42	0.82
1:A:61:GLU:CG	1:A:61:GLU:OE1	2.37	0.73
1:A:33:LYS:HE3	1:A:34:THR:N	2.10	0.66
1:A:88:ARG:HD2	2:A:191:HOH:O	2.11	0.50
1:A:49:LEU:HD13	1:A:103:LEU:HB3	1.98	0.44
1:A:6:GLU:OE1	1:A:27:ARG:HD2	2.17	0.44
1:A:77:GLY:HA3	1:A:104:TRP:CH2	2.53	0.43
1:A:67:LEU:C	1:A:67:LEU:HD23	2.39	0.42

There are no symmetry-related clashes.

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	150/155 (97%)	145 (97%)	3 (2%)	2 (1%)	15 2

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	GLU
1	A	17	PRO

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	120/123 (98%)	116 (97%)	4 (3%)	45 17

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ARG
1	A	33	LYS
1	A	49	LEU
1	A	60	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	45	ASN
1	A	105	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 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)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.