



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2018 – 08:42 pm GMT

PDB ID : 1GOC  
Title : COOPERATIVE STABILIZATION OF ESCHERICHIA COLI RIBONUCLEASE HI BY INSERTION OF GLY-80B AND GLY-77-> ALA SUBSTITUTION  
Authors : Ishikawa, K.; Kimura, S.; Nakamura, H.; Morikawa, K.; Kanaya, S.  
Deposited on : 1993-05-10  
Resolution : 2.00 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](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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

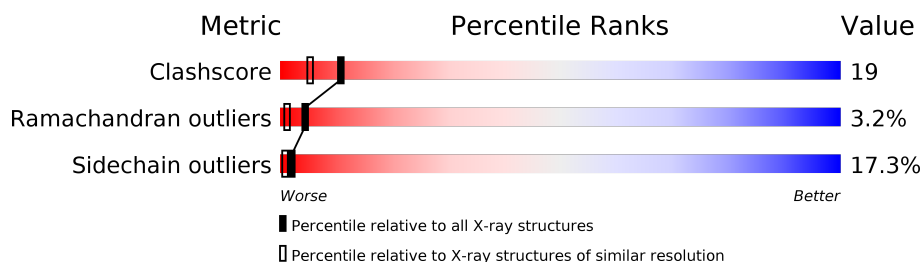
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	122078	8264 (2.00-2.00)
Ramachandran outliers	120005	8163 (2.00-2.00)
Sidechain outliers	119972	8162 (2.00-2.00)

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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	156	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1330 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 H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1243	779	228	229	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ALA	GLY	CONFLICT	UNP P0A7Y4
A	80B	GLY	-	INSERTION	UNP P0A7Y4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	87	Total	O	0	0
			87	87		

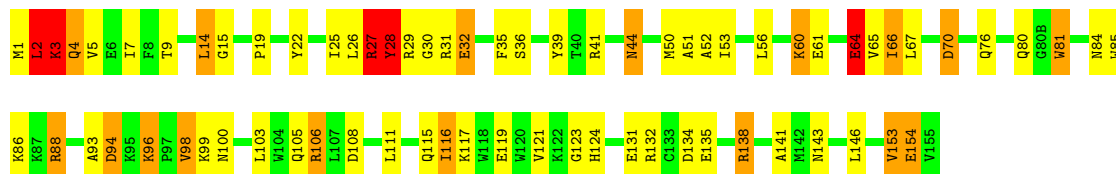
### 3 Residue-property plots [i](#)

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. 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. 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 H

Chain A: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.98Å 86.45Å 35.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.183 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1330	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	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	0.99	0/1271	1.80	26/1717 (1.5%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	ARG	CD-NE-CZ	11.75	140.06	123.60
1	A	41	ARG	NE-CZ-NH2	9.76	125.18	120.30
1	A	27	ARG	NE-CZ-NH1	-9.40	115.60	120.30
1	A	27	ARG	NE-CZ-NH2	8.56	124.58	120.30
1	A	138	ARG	CD-NE-CZ	8.43	135.41	123.60
1	A	27	ARG	CD-NE-CZ	8.34	135.28	123.60
1	A	28	TYR	CA-CB-CG	8.17	128.93	113.40
1	A	28	TYR	CB-CG-CD1	7.54	125.52	121.00
1	A	70	ASP	CB-CG-OD1	7.37	124.94	118.30
1	A	106	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	A	41	ARG	NE-CZ-NH1	-7.26	116.67	120.30
1	A	138	ARG	NE-CZ-NH2	7.25	123.92	120.30
1	A	2	LEU	C-N-CA	6.39	137.68	121.70
1	A	15	GLY	N-CA-C	-6.13	97.76	113.10
1	A	31	ARG	NE-CZ-NH2	5.68	123.14	120.30
1	A	108	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	A	138	ARG	NE-CZ-NH1	-5.56	117.52	120.30
1	A	2	LEU	CB-CA-C	5.40	120.45	110.20
1	A	93	ALA	C-N-CA	5.36	135.10	121.70
1	A	64	GLU	CG-CD-OE1	5.31	128.93	118.30
1	A	64	GLU	CB-CG-CD	5.25	128.37	114.20
1	A	88	ARG	CB-CA-C	5.16	120.72	110.40
1	A	15	GLY	O-C-N	5.09	130.84	122.70
1	A	44	ASN	CB-CG-OD1	-5.08	111.44	121.60
1	A	81	TRP	CB-CG-CD1	5.05	133.56	127.00
1	A	3	LYS	CA-C-N	-5.04	106.11	117.20

There are no chirality outliers.

There are no planarity outliers.

## 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	1243	0	1222	48	2
2	A	87	0	0	6	2
All	All	1330	0	1222	48	2

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 19.

All (48) 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:1:MET:HB3	1:A:2:LEU:HD22	1.43	1.00
1:A:3:LYS:HE3	1:A:4:GLN:H	1.40	0.86
1:A:52:ALA:O	1:A:56:LEU:HG	1.88	0.73
1:A:1:MET:C	1:A:3:LYS:H	1.91	0.72
1:A:29:ARG:HD2	2:A:244:HOH:O	1.88	0.72
1:A:99:LYS:HE3	1:A:100:ASN:ND2	2.06	0.71
1:A:26:LEU:HD13	1:A:35:PHE:CE2	2.27	0.70
1:A:26:LEU:HD13	1:A:35:PHE:HE2	1.56	0.69
1:A:66:ILE:HD11	1:A:119:GLU:HB2	1.75	0.69
1:A:32:GLU:OE2	1:A:132:ARG:NH1	2.26	0.68
1:A:53:ILE:HD11	1:A:103:LEU:O	1.97	0.64
1:A:1:MET:CB	1:A:2:LEU:HD22	2.24	0.64
1:A:3:LYS:HA	1:A:3:LYS:HE3	1.79	0.64
1:A:14:LEU:HD11	1:A:141:ALA:HB1	1.79	0.62
1:A:2:LEU:H	1:A:2:LEU:HD22	1.67	0.60
1:A:84:ASN:HB3	1:A:88:ARG:NH1	2.17	0.60
1:A:5:VAL:HG22	1:A:28:TYR:HD2	1.69	0.57
1:A:53:ILE:HD13	1:A:106:ARG:HB2	1.86	0.56
1:A:56:LEU:HD21	1:A:67:LEU:HD12	1.87	0.56
1:A:2:LEU:N	1:A:2:LEU:HD22	2.21	0.56
1:A:105:GLN:NE2	2:A:209:HOH:O	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ARG:NH1	2:A:247:HOH:O	2.40	0.53
1:A:14:LEU:CD1	1:A:141:ALA:HB1	2.38	0.52
1:A:32:GLU:CD	1:A:132:ARG:HH12	2.13	0.52
1:A:131:GLU:O	1:A:134:ASP:HB3	2.09	0.51
1:A:115:GLN:NE2	2:A:279:HOH:O	2.44	0.50
1:A:1:MET:N	2:A:232:HOH:O	2.36	0.50
1:A:94:ASP:HB3	1:A:96:LYS:HB2	1.94	0.50
1:A:9:THR:HB	1:A:51:ALA:HB1	1.95	0.49
1:A:66:ILE:HD13	1:A:117:LYS:HD3	1.95	0.48
1:A:5:VAL:HG22	1:A:28:TYR:CD2	2.47	0.47
1:A:22:TYR:O	1:A:36:SER:HB2	2.16	0.46
1:A:94:ASP:OD2	1:A:96:LYS:HD3	2.16	0.45
1:A:27:ARG:HH21	1:A:27:ARG:HG2	1.82	0.45
1:A:85:TRP:CD1	1:A:98:VAL:HG21	2.52	0.45
1:A:19:PRO:HA	1:A:39:TYR:O	2.17	0.45
1:A:80:GLN:OE1	1:A:81:TRP:NE1	2.50	0.44
1:A:44:ASN:N	2:A:270:HOH:O	2.49	0.44
1:A:66:ILE:HD12	1:A:117:LYS:O	2.18	0.43
1:A:1:MET:HB3	1:A:2:LEU:H	1.66	0.43
1:A:3:LYS:HE3	1:A:4:GLN:N	2.22	0.43
1:A:53:ILE:HD13	1:A:106:ARG:CB	2.49	0.43
1:A:14:LEU:HD11	1:A:141:ALA:CB	2.48	0.43
1:A:70:ASP:HB3	1:A:121:VAL:HG22	2.01	0.42
1:A:124:HIS:HB3	1:A:131:GLU:OE2	2.20	0.42
1:A:7:ILE:HA	1:A:25:ILE:O	2.20	0.41
1:A:60:LYS:HA	1:A:60:LYS:HD3	1.66	0.41
1:A:65:VAL:O	1:A:116:ILE:HA	2.21	0.40

All (2) 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:A:64:GLU:OE2	2:A:285:HOH:O[4_456]	1.97	0.23
1:A:153:VAL:CG1	2:A:280:HOH:O[4_555]	2.08	0.12



## 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	154/156 (99%)	141 (92%)	8 (5%)	5 (3%)	<b>4</b> <b>1</b>

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	VAL
1	A	154	GLU
1	A	123	GLY
1	A	2	LEU
1	A	30	GLY

### 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	127/127 (100%)	105 (83%)	22 (17%)	<b>2</b> <b>1</b>

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	4	GLN
1	A	14	LEU
1	A	27	ARG
1	A	28	TYR
1	A	32	GLU

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Mol	Chain	Res	Type
1	A	50	MET
1	A	60	LYS
1	A	61	GLU
1	A	64	GLU
1	A	66	ILE
1	A	76	GLN
1	A	86	LYS
1	A	94	ASP
1	A	96	LYS
1	A	98	VAL
1	A	111	LEU
1	A	116	ILE
1	A	135	GLU
1	A	143	ASN
1	A	146	LEU
1	A	154	GLU

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

Mol	Chain	Res	Type
1	A	4	GLN
1	A	45	ASN
1	A	127	HIS
1	A	152	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.