

# wwPDB X-ray Structure Validation Summary Report (i)

Oct 12, 2021 – 02:47 PM EDT

PDB ID : 1U6B

Title : CRYSTAL STRUCTURE OF A SELF-SPLICING GROUP I INTRON WITH

BOTH EXONS

Authors: Adams, P.L.; Stahley, M.R.; Kosek, A.B.; Wang, J.; Strobel, S.A.

Deposited on : 2004-07-29

Resolution : 3.10 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.23.2

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)

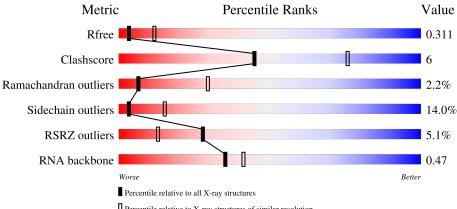
Validation Pipeline (wwPDB-VP) : 2.23.2

#### Overall quality at a glance (i) 1

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

The reported resolution of this entry is 3.10 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.



Percentile relative to X-ray structures of similar resolution

Metric	Whole archive $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
$R_{free}$	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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  $\geq =3, 2, 1$  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 <=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	В	197	53%	33%	10% •			
2	С	22	55%	36%	5% 5%			
3	D	3	67%	33%				
4	A	98	72%	22%				



## 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5615 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 197-MER.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	В	197	Total 4241	C 1885	N 786	O 1370	P 200	0	0	0

• Molecule 2 is a RNA chain called 5'-R(\*AP\*AP\*GP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*AP\*AP\*CP\*CP\*AP\*CP\*GP \*GP\*CP\*C)-3'.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	С	22	Total 467	C 211	N	0	P	3	0	0
			407	Z11	92	143	Z1			

• Molecule 3 is a RNA chain called 5'-R(\*CP\*AP\*(5MU))-3'.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	D	3	Total 60	C 29	N 10	O 19	P 2	1	0	0

• Molecule 4 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	A	95	Total 775	C 496	N 137	O 138	S 4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	HIS	TYR	engineered mutation	UNP P09012
A	36	ARG	GLN	engineered mutation	UNP P09012

• Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	5	Total K 5 5	0	0

 $\bullet$  Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	13	Total Mg 13 13	0	0

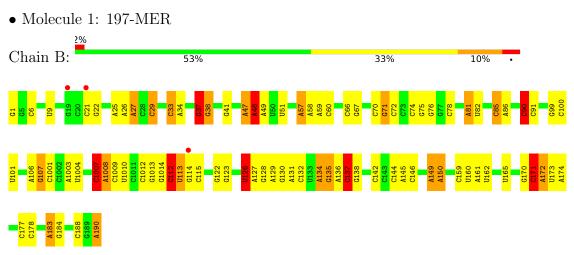
• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	В	47	Total O 47 47	0	0
7	С	4	Total O 4 4	0	0
7	D	3	Total O 3 3	0	0

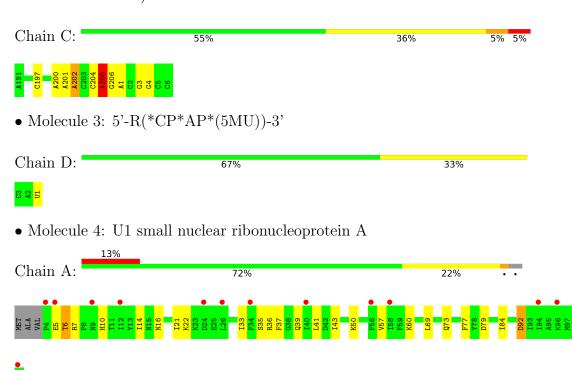


## 3 Residue-property plots (i)

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 2: 5'-R(\*AP\*AP\*GP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*AP\*AP\*CP\*CP\*AP\*GP\*AP\*CP\*CP\*AP\*CP\*CP\*AP\*CP\*CP\*C)-3'





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants	108.54Å 108.54Å 249.16Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.22 - 3.10	Depositor
Resolution (A)	48.37 - 3.10	EDS
% Data completeness	89.6 (48.22-3.10)	Depositor
(in resolution range)	88.3 (48.37-3.10)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.58 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
D.D.	0.246 , 0.279	Depositor
$R, R_{free}$	0.269 , 0.311	DCC
$R_{free}$ test set	1210 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.1	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.15, 40.9	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	5615	wwPDB-VP
Average B, all atoms $(Å^2)$	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.96% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: A23, GTP, MG, 5MU, K

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	Mol Chain		nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	В	0.64	$2/4683 \ (0.0\%)$	1.20	$23/7304 \ (0.3\%)$	
2	С	1.75	2/523~(0.4%)	1.25	$2/813 \ (0.2\%)$	
3	D	0.58	0/43	1.07	0/65	
4	A	0.30	0/789	0.63	2/1053~(0.2%)	
All	All	0.77	4/6038 (0.1%)	1.15	$27/9235 \ (0.3\%)$	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	С	206	G	C2'-O2'	36.65	1.89	1.41
2	С	205	A	C2'-O2'	-6.74	1.32	1.41
1	В	47	A	O3'-P	-5.08	1.55	1.61
1	В	106	A	O3'-P	5.00	1.67	1.61

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	В	37	G	P-O3'-C3'	9.55	131.17	119.70
1	В	106	A	P-O3'-C3'	-8.52	109.47	119.70
2	С	206	G	C1'-C2'-O2'	-8.35	85.56	110.60
1	В	135	G	O4'-C1'-N9	7.55	114.24	108.20
1	В	1007	С	P-O3'-C3'	7.39	128.57	119.70

There are no chirality outliers.

There are no planarity outliers.



### 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	В	4241	0	2136	47	0
2	С	467	0	244	3	0
3	D	60	0	36	0	0
4	A	775	0	807	5	0
5	В	5	0	0	0	0
6	В	13	0	0	0	0
7	В	47	0	0	0	0
7	С	4	0	0	0	0
7	D	3	0	0	0	0
All	All	5615	0	3223	54	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 6.

The worst 5 of 54 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	$egin{array}{c}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{array}$
1:B:72:C:O2	1:B:72:C:H2'	1.96	0.64
1:B:26:A:H2'	1:B:27:A:C8	2.36	0.60
1:B:33:C:H2'	1:B:34:A:C8	2.37	0.59
1:B:25:A:H2'	1:B:26:A:C8	2.38	0.59
1:B:170:G:H4'	1:B:172:A:H5"	1.84	0.58

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
4	A	93/98 (95%)	84 (90%)	7 (8%)	2 (2%)	6 29

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	36	ARG
4	A	41	LEU

#### 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
4	A	86/88 (98%)	74 (86%)	12 (14%)	3 15

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

Mol	Chain	Res	Type
4	A	39	GLN
4	A	50	LYS
4	A	92	ASP
4	A	60	LYS
4	A	16	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	16	ASN

#### 5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	В	195/197 (98%)	46 (23%)	8 (4%)
2	С	21/22 (95%)	6 (28%)	0
3	D	2/3 (66%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	$218/222 \ (98\%)$	52 (23%)	8 (3%)

5 of 52 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	В	6	С
1	В	21	С
1	В	22	G
1	В	27	A
1	В	29	С

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	В	183	A
1	В	149	A
1	В	126	U
1	В	112	С
1	В	137	С

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Mol Type	Chain	Chain	Res	Link	Bond lengths			Bond angles		
Moi Type Cr	Chain	rtes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	$\mid \# Z  > 2$		
1	A23	В	190	1	19,28,29	1.05	1 (5%)	19,43,46	1.26	3 (15%)	
3	5MU	D	1	3,1,6,5	15,22,23	2.81	5 (33%)	16,32,35	3.85	4 (25%)	
1	GTP	В	1	1,2	26,34,34	1.26	3 (11%)	33,54,54	2.22	5 (15%)	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A23	В	190	1	-	0/3/35/36	0/4/4/4
3	5MU	D	1	3,1,6,5	-	0/5/25/26	0/2/2/2
1	GTP	В	1	1,2	-	2/18/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
3	D	1	5MU	O2'-C2'	8.43	1.62	1.43
3	D	1	5MU	C2'-C1'	-3.99	1.47	1.53
1	В	1	GTP	C6-N1	3.52	1.39	1.33
3	D	1	5MU	O4'-C1'	3.48	1.45	1.41
3	D	1	5MU	C4-N3	2.91	1.38	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
3	D	1	5MU	C4-N3-C2	14.26	127.19	115.14
1	В	1	GTP	C5-C6-N1	-8.34	112.03	123.43
1	В	1	GTP	C6-N1-C2	5.60	124.83	115.93
1	В	1	GTP	PA-O3A-PB	-4.19	118.45	132.83
1	В	1	GTP	C2-N3-C4	-3.43	111.44	115.36

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	Atoms
1	В	1	GTP	PB-O3A-PA-O2A
1	В	1	GTP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	$\operatorname{Res}$	Type	Clashes	Symm-Clashes
1	В	190	A23	1	0

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 18 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,  $95^{th}$  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>	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	В	195/197 (98%)	0.02	3 (1%) 73 54	14, 60, 161, 195	0
2	С	22/22 (100%)	0.12	0 100 100	16, 56, 129, 143	0
3	D	2/3~(66%)	0.01	0 100 100	20, 20, 20, 25	0
4	A	95/98 (96%)	0.66	13 (13%) 3 1	112, 144, 181, 191	3 (3%)
All	All	314/320 (98%)	0.22	16 (5%) 28 13	14, 80, 174, 195	3 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	9	ASN	3.4
1	В	21	С	3.3
4	A	56	PHE	3.3
4	A	94	ILE	3.0
4	A	34	PHE	2.9

## 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
1	GTP	В	1	32/32	0.88	0.15	46,89,142,144	0
1	A23	В	190	25/26	0.91	0.20	59,71,78,80	0
3	5MU	D	1	21/22	0.97	0.17	2,19,23,26	1



### 6.3 Carbohydrates (i)

There are no monosaccharides 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,  $95^{th}$  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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
5	K	В	1017	1/1	0.58	0.23	92,92,92,92	0
5	K	В	4	1/1	0.76	0.09	53,53,53,53	0
5	K	В	1015	1/1	0.83	0.38	92,92,92,92	0
6	MG	В	1025	1/1	0.83	0.17	74,74,74,74	0
6	MG	В	1029	1/1	0.84	0.16	27,27,27,27	0
6	MG	В	1028	1/1	0.87	0.10	31,31,31,31	0
6	MG	В	1021	1/1	0.87	0.14	27,27,27,27	0
5	K	В	1016	1/1	0.91	0.15	55,55,55,55	0
5	K	В	2	1/1	0.92	0.32	57,57,57,57	0
6	MG	В	1022	1/1	0.94	0.41	64,64,64,64	0
6	MG	В	1018	1/1	0.95	0.25	16,16,16,16	0
6	MG	В	1027	1/1	0.95	0.18	57,57,57,57	0
6	MG	В	1020	1/1	0.96	0.14	38,38,38,38	0
6	MG	В	1026	1/1	0.96	0.09	56,56,56,56	0
6	MG	В	3	1/1	0.96	0.27	12,12,12,12	0
6	MG	В	1019	1/1	0.96	0.28	27,27,27,27	0
6	MG	В	1024	1/1	0.96	0.27	30,30,30,30	0
6	MG	В	1023	1/1	0.97	0.20	53,53,53,53	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

