



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5W1H  
Title : Crystal structure of LbaCas13a (C2c2) bound to mature crRNA (24-nt spacer)  
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Deposited on : 2017-06-03  
Resolution : 1.99 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.37.1  
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) : 2.37.1

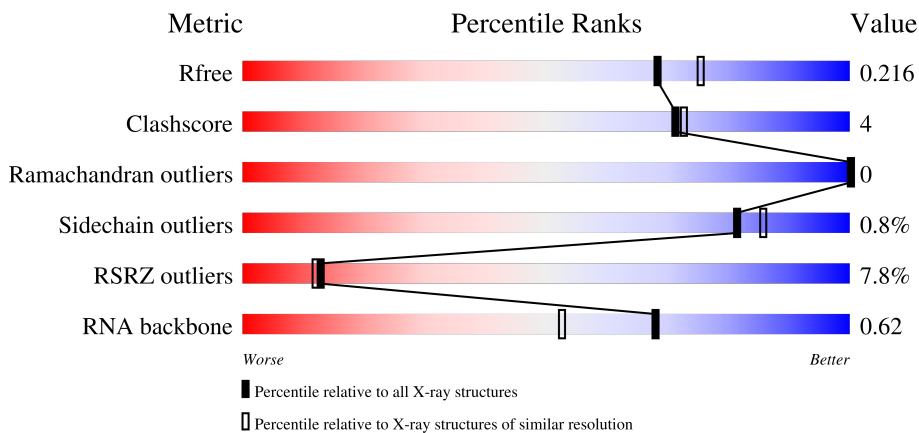
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.99 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)
RNA backbone	3102	1079 (2.50-1.50)

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  $\leq 5\%$ . 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	1440	
2	B	52	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	IOD	A	1515	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12499 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 LbaCas13a (C2c2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1301	10760	6847	1820	2052	41	0	0	0

- Molecule 2 is a RNA chain called mature crRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	42	886	397	174	274	41	0	0	0

- Molecule 3 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	I	0	0
			23	23		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	692	Total O 692 692	0	0
5	B	120	Total O 120 120	0	0





## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.84Å 92.21Å 115.86Å 90.00° 92.42° 90.00°	Depositor
Resolution (Å)	47.12 – 1.99 47.12 – 1.99	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.12-1.99) 94.1 (47.12-1.99)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.16 (at 1.98Å)	Xtrriage
Refinement program	PHENIX 1.11.1-2575-000	Depositor
R, $R_{free}$	0.185 , 0.216 0.185 , 0.216	Depositor DCC
$R_{free}$ test set	5242 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtrriage
Anisotropy	0.115	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.008 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12499	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, IOD

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	0.25	0/10962	0.40	0/14729
2	B	0.24	0/995	0.71	0/1550
All	All	0.25	0/11957	0.44	0/16279

There are no bond length outliers.

There are no bond angle outliers.

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	10760	0	10599	78	0
2	B	886	0	447	5	0
3	A	23	0	0	4	0
4	A	18	0	24	2	0
5	A	692	0	0	12	0
5	B	120	0	0	0	0
All	All	12499	0	11070	80	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 4.

The worst 5 of 80 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:1048:ARG:NH2	1:A:1253:SER:O	2.26	0.69
1:A:1278:ARG:NH1	5:A:1608:HOH:O	2.28	0.66
1:A:235:GLN:NE2	5:A:1606:HOH:O	2.26	0.66
1:A:789:ARG:NH1	5:A:1612:HOH:O	2.30	0.64
1:A:1278:ARG:NH2	5:A:1611:HOH:O	2.29	0.64

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	1283/1440 (89%)	1246 (97%)	37 (3%)	0	<b>100</b> <b>100</b>

There are no Ramachandran outliers to report.

### 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	1174/1296 (91%)	1165 (99%)	9 (1%)	<b>81</b> <b>86</b>

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1295	ASN
1	A	1343	LYS
1	A	908	ARG
1	A	1027	TYR
1	A	1100	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	40/52 (76%)	5 (12%)	2 (5%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	-15	A
2	B	-4	U
2	B	5	U
2	B	7	U
2	B	10	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	7	U
2	B	13	G

## 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

Of 26 ligands modelled in this entry, 23 are monoatomic - leaving 3 for Mogul analysis.

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	A	1525	-	5,5,5	0.38	0	5,5,5	0.24	0
4	GOL	A	1526	-	5,5,5	0.37	0	5,5,5	0.34	0
4	GOL	A	1524	-	5,5,5	0.36	0	5,5,5	0.21	0

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	1525	-	-	4/4/4/4	-
4	GOL	A	1526	-	-	2/4/4/4	-
4	GOL	A	1524	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1524	GOL	O1-C1-C2-C3
4	A	1525	GOL	O1-C1-C2-C3
4	A	1526	GOL	O1-C1-C2-C3
4	A	1525	GOL	C1-C2-C3-O3
4	A	1525	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1526	GOL	2	0

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1301/1440 (90%)	0.54	105 (8%) 12 11	20, 35, 57, 77	0
2	B	42/52 (80%)	-0.10	0 100 100	23, 30, 48, 88	0
All	All	1343/1492 (90%)	0.52	105 (7%) 13 12	20, 35, 57, 88	0

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	780	TYR	7.3
1	A	167	ASP	7.1
1	A	1316	ILE	6.5
1	A	18	ASN	5.8
1	A	746	VAL	5.1

### 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](#)

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<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	A	1524	6/6	0.73	0.31	31,40,45,46	0
3	IOD	A	1511	1/1	0.74	0.12	82,82,82,82	1
4	GOL	A	1525	6/6	0.84	0.23	48,52,54,54	0
4	GOL	A	1526	6/6	0.94	0.14	34,36,40,43	0
3	IOD	A	1518	1/1	0.95	0.07	74,74,74,74	1
3	IOD	A	1514	1/1	0.95	0.06	98,98,98,98	1
3	IOD	A	1512	1/1	0.96	0.05	105,105,105,105	1
3	IOD	A	1519	1/1	0.96	0.07	69,69,69,69	1
3	IOD	A	1523	1/1	0.96	0.05	63,63,63,63	1
3	IOD	A	1520	1/1	0.97	0.04	74,74,74,74	1
3	IOD	A	1508	1/1	0.98	0.17	87,87,87,87	1
3	IOD	A	1521	1/1	0.98	0.04	71,71,71,71	1
3	IOD	A	1507	1/1	0.98	0.04	70,70,70,70	1
3	IOD	A	1510	1/1	0.99	0.09	84,84,84,84	1
3	IOD	A	1506	1/1	0.99	0.07	45,45,45,45	1
3	IOD	A	1503	1/1	0.99	0.11	47,47,47,47	1
3	IOD	A	1505	1/1	0.99	0.06	56,56,56,56	1
3	IOD	A	1516	1/1	0.99	0.16	70,70,70,70	1
3	IOD	A	1517	1/1	0.99	0.04	70,70,70,70	1
3	IOD	A	1509	1/1	0.99	0.08	75,75,75,75	1
3	IOD	A	1502	1/1	1.00	0.13	42,42,42,42	1
3	IOD	A	1522	1/1	1.00	0.05	43,43,43,43	1
3	IOD	A	1501	1/1	1.00	0.09	48,48,48,48	1
3	IOD	A	1513	1/1	1.00	0.04	75,75,75,75	1
3	IOD	A	1504	1/1	1.00	0.10	37,37,37,37	1
3	IOD	A	1515	1/1	1.00	0.07	48,48,48,48	1

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.