

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

#### Nov 22, 2023 – 08:32 PM JST

PDB ID	:	6LJM
Title	:	Crystal structure of human Sirt5 in complex with the fluorogenic tetrapeptide
		substrate P13
Authors	:	Chen, Q.; Yu, Y.
Deposited on	:	2019-12-17
Resolution	:	1.78 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:

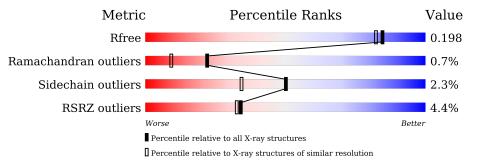
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

The reported resolution of this entry is 1.78 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	9185 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 ch	ain	
1	А	272	3% 97%		
			60%		
2	В	5	60%	20%	20%



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4540 atoms, of which 2102 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 NAD-dependent protein deacylase sirtuin-5, mitochondrial.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	А	267	Total 4059	C 1291	Н 2012	N 371	O 372	S 13	0	1	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	31	GLN	-	expression tag	UNP Q9NXA8
А	32	ALA	-	expression tag	UNP Q9NXA8
А	33	SER	-	expression tag	UNP Q9NXA8

• Molecule 2 is a protein called ACE-SER-LEU-GLY-SLL.

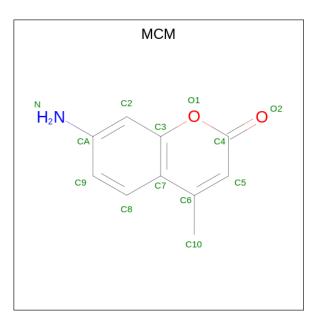
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	5	Total	C	H	N 10	0	0	5	0
			148	46	74	10	18			

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Μ	[o]	Chain	Residues	Ator	ns	ZeroOcc	AltConf
	3	А	1	Total 1	Zn 1	0	0

• Molecule 4 is 7-AMINO-4-METHYL-CHROMEN-2-ONE (three-letter code: MCM) (formula:  $C_{10}H_9NO_2$ ).





Mol	Chain	Residues		Ate	$\mathbf{oms}$			ZeroOcc	AltConf
4	В	1	Total	С	Η	Ν	Ο	0	1
4	D		42	20	16	2	4	0	

• Molecule 5 is water.

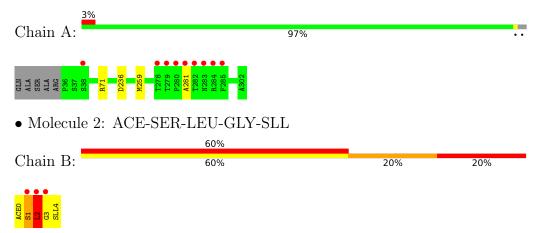
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	285	Total O 285 285	0	0
5	В	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	0	0



## 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: NAD-dependent protein deacylase sirtuin-5, mitochondrial





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants	42.20Å 55.27Å 124.52Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	41.34 - 1.78	Depositor
Resolution (A)	41.34 - 1.78	EDS
% Data completeness	98.7(41.34-1.78)	Depositor
(in resolution range)	97.6(41.34-1.78)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$5.25 (at 1.78 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
D D.	0.165 , $0.197$	Depositor
$R, R_{free}$	0.166 , $0.198$	DCC
$R_{free}$ test set	1454 reflections $(5.12\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.4	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.40 , 51.3	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4540	wwPDB-VP
Average B, all atoms $(Å^2)$	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.80% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<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: ACE, SLL, ZN, MCM

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).

Mal	Mol Chain		nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.51	0/2100	0.62	0/2850	
2	В	2.90	6/36~(16.7%)	2.77	2/46~(4.3%)	
All	All	0.63	6/2136~(0.3%)	0.71	2/2896~(0.1%)	

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	В	2[A]	LEU	C-N	7.92	1.47	1.33
2	В	2[B]	LEU	C-N	7.92	1.47	1.33
2	В	0[A]	ACE	C-N	5.99	1.47	1.34
2	В	0[B]	ACE	C-N	5.99	1.47	1.34
2	В	1[A]	SER	C-N	5.58	1.46	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	3[A]	GLY	N-CA-C	-7.19	95.12	113.10
2	В	3[B]	GLY	N-CA-C	-7.19	95.12	113.10

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	А	2047	2012	2011	0	0
2	В	74	74	72	0	0
3	А	1	0	0	0	0
4	В	26	16	16	0	0
5	А	285	0	0	0	1
5	В	5	0	0	0	0
All	All	2438	2102	2099	0	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

All (1) 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)
5:A:728:HOH:O	5:A:741:HOH:O[1_655]	2.07	0.13

#### 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	avoured Allowed		Percentiles
1	А	266/272~(98%)	259~(97%)	6(2%)	1 (0%)	34 19
2	В	6/5~(120%)	2(33%)	2(33%)	2(33%)	0 0
All	All	272/277~(98%)	261 (96%)	8(3%)	3~(1%)	22 4

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	2[A]	LEU
2	В	2[B]	LEU
1	А	281	ALA



#### 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	Rotameric Outliers	
1	А	214/216~(99%)	211~(99%)	3~(1%)	67 56
2	В	4/2~(200%)	0	4 (100%)	0 0
All	All	218/218~(100%)	211~(97%)	7 (3%)	50 22

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	1[A]	SER
2	В	1[B]	SER
2	В	2[B]	LEU
2	В	2[A]	LEU
1	А	259	MET

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

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	Trune	Chain	Res	Link	Bo	Bond lengths			Bond angles		
INIOI	Type	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
2	SLL	В	4[B]	4,2	14,15,16	1.65	2 (14%)	12,17,19	0.90	0	
2	SLL	В	4[A]	4,2	14,15,16	1.54	2 (14%)	12,17,19	1.70	2(16%)	

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
2	SLL	В	4[B]	4,2	-	7/14/15/17	-
2	SLL	В	4[A]	4,2	-	6/14/15/17	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	В	4[B]	SLL	CX-NZ	4.91	1.44	1.33
2	В	4[A]	SLL	CX-NZ	4.62	1.43	1.33
2	В	4[B]	SLL	OX-CX	-2.18	1.18	1.23
2	В	4[A]	SLL	OX-CX	-2.08	1.19	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	4[A]	SLL	CD-CE-NZ	-4.76	98.59	112.21
2	В	4[A]	SLL	CE-NZ-CX	-2.26	118.63	122.84

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	4[A]	SLL	C-CA-CB-CG
2	В	4[A]	SLL	N-CA-CB-CG
2	В	4[B]	SLL	C-CA-CB-CG
2	В	4[A]	SLL	CX-CK-CL-CP
2	В	4[B]	SLL	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.



#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	Chain	Chain	Chain	Res	Link	Bo	ond leng	$_{\rm ths}$	B	ond ang	les
1VIOI	Moi Type Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2			
4	MCM	В	103[B]	2	12,14,14	1.40	2 (16%)	16,20,20	1.17	1 (6%)		
4	MCM	В	103[A]	2	12,14,14	1.43	2 (16%)	16,20,20	1.66	4 (25%)		

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
4	MCM	В	103[B]	2	-	-	0/2/2/2
4	MCM	В	103[A]	2	-	-	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
4	В	103[A]	MCM	CA-N	2.81	1.48	1.38
4	В	103[B]	MCM	C7-C3	-2.79	1.37	1.41
4	В	103[A]	MCM	C2-C3	2.44	1.42	1.37
4	В	103[B]	MCM	C2-C3	2.00	1.41	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	В	103[A]	MCM	C10-C6-C5	-3.67	115.38	120.74
4	В	103[B]	MCM	C2-C3-C7	-2.52	120.26	123.05
4	В	103[A]	MCM	C10-C6-C7	2.45	124.87	121.08

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	В	103[A]	MCM	C9-CA-N	-2.37	116.51	120.91
4	В	103[A]	MCM	O1-C4-C5	-2.32	116.32	119.27

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 > 2	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	267/272 (98%)	0.11	9 (3%) 45 44	8, 16, 35, 89	0
2	В	3/5~(60%)	5.77	3 (100%) 0 0	26, 26, 38, 41	0
All	All	270/277~(97%)	0.18	12 (4%) 34 32	8, 16, 36, 89	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	1[A]	SER	8.8
1	А	278	THR	6.0
1	А	279	THR	5.9
2	В	2[A]	LEU	5.1
1	А	282	THR	4.7

### 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	SLL	В	4[A]	16/17	0.84	0.18	10,23,32,39	31
2	SLL	В	4[B]	16/17	0.84	0.18	17,23,30,37	31

### 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	B-factors(Å <sup>2</sup> )	Q < 0.9
4	MCM	В	103[A]	13/13	0.85	0.24	11,18,27,33	21
4	MCM	В	103[B]	13/13	0.85	0.24	13,17,22,24	21
3	ZN	А	401	1/1	0.99	0.07	16,16,16,16	0

#### 6.5 Other polymers (i)

There are no such residues in this entry.

