



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 28, 2016 – 04:02 PM EST

PDB ID : 5BWO
Title : Crystal Structure of Human SIRT3 in Complex with a Palmitoyl H3K9 Peptide
Authors : Gai, W.; Jiang, H.; Liu, D.
Deposited on : 2015-06-08
Resolution : 2.38 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028320
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

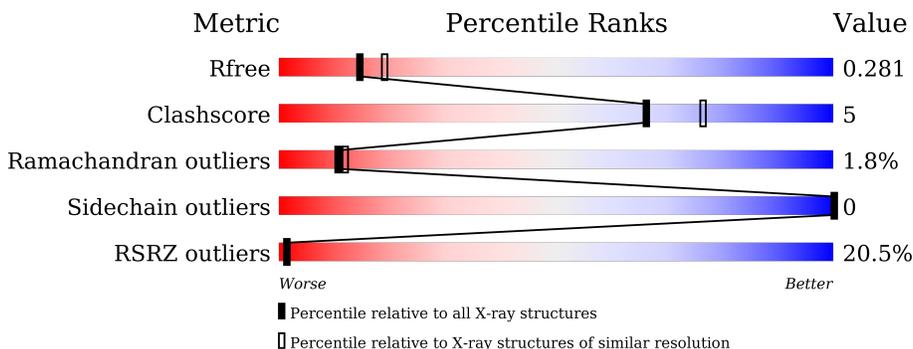
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	91344	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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 $\leq 5\%$. 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	B	10	
2	A	309	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PLM	B	101	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4595 atoms, of which 2258 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 Palmitoyl H3K9 Peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
1	B	9	131	41	64	14	12	0	0	0

- Molecule 2 is a protein called NAD-dependent protein deacetylase sirtuin-3, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	A	274	4311	1384	2163	370	385	9	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

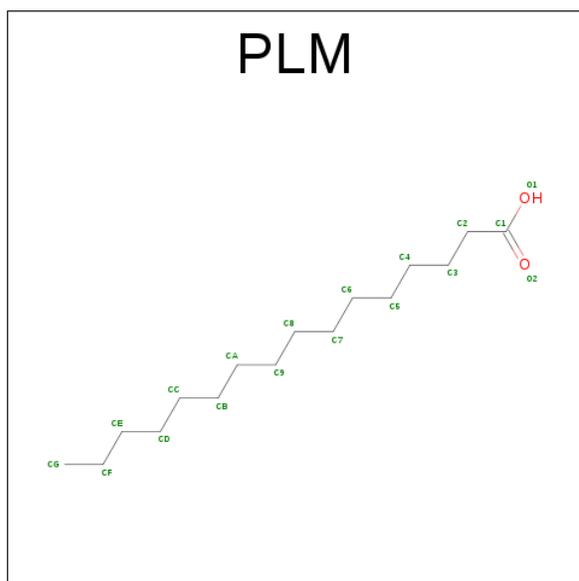
Chain	Residue	Modelled	Actual	Comment	Reference
A	91	MET	-	expression tag	UNP Q9NTG7
A	92	ALA	-	expression tag	UNP Q9NTG7
A	93	SER	-	expression tag	UNP Q9NTG7
A	94	MET	-	expression tag	UNP Q9NTG7
A	95	THR	-	expression tag	UNP Q9NTG7
A	96	GLY	-	expression tag	UNP Q9NTG7
A	97	GLY	-	expression tag	UNP Q9NTG7
A	98	GLN	-	expression tag	UNP Q9NTG7
A	99	GLN	-	expression tag	UNP Q9NTG7
A	100	MET	-	expression tag	UNP Q9NTG7
A	101	GLY	-	expression tag	UNP Q9NTG7
A	102	ARG	-	expression tag	UNP Q9NTG7
A	103	GLY	-	expression tag	UNP Q9NTG7
A	104	SER	-	expression tag	UNP Q9NTG7
A	105	HIS	-	expression tag	UNP Q9NTG7
A	106	HIS	-	expression tag	UNP Q9NTG7
A	107	HIS	-	expression tag	UNP Q9NTG7
A	108	HIS	-	expression tag	UNP Q9NTG7
A	109	HIS	-	expression tag	UNP Q9NTG7
A	110	HIS	-	expression tag	UNP Q9NTG7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	111	GLU	-	expression tag	UNP Q9NTG7
A	112	ASN	-	expression tag	UNP Q9NTG7
A	113	LEU	-	expression tag	UNP Q9NTG7
A	114	TYR	-	expression tag	UNP Q9NTG7
A	115	PHE	-	expression tag	UNP Q9NTG7
A	116	GLN	-	expression tag	UNP Q9NTG7
A	117	GLY	-	expression tag	UNP Q9NTG7

- Molecule 3 is PALMITIC ACID (three-letter code: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	H			O
3	B	1	48	16	31	1	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	B	7	7	7	0	0

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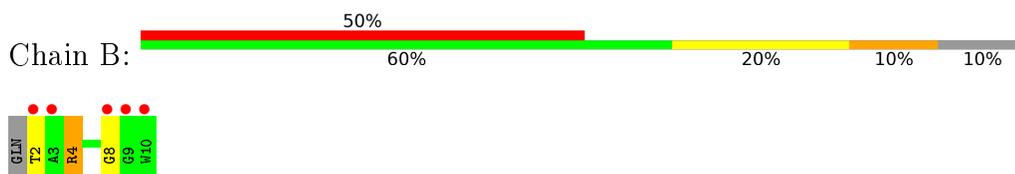
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	97	Total O 97 97	0	0

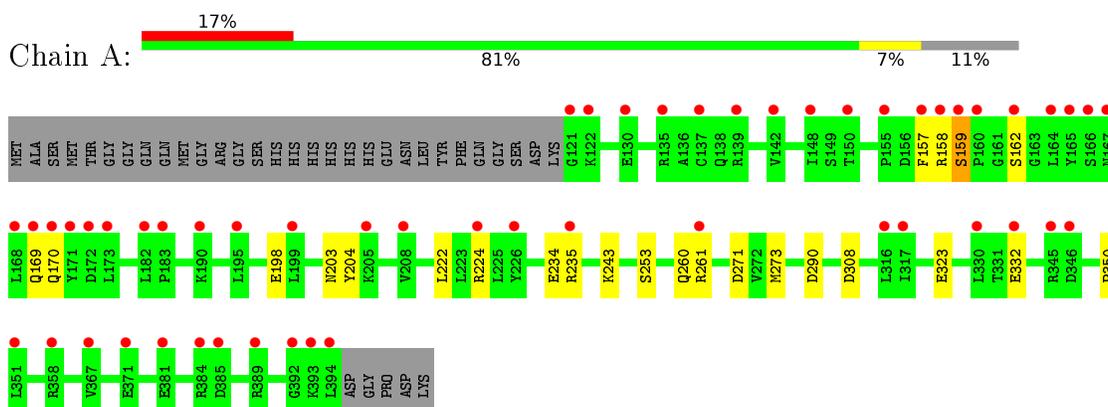
3 Residue-property plots [i](#)

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.

- Molecule 1: Palmitoyl H3K9 Peptide



- Molecule 2: NAD-dependent protein deacetylase sirtuin-3, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	43.45Å 54.64Å 113.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.15 – 2.38 29.15 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.15-2.38) 95.6 (29.15-2.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.09 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.239 , 0.287 0.236 , 0.281	Depositor DCC
R_{free} test set	1087 reflections (9.98%)	DCC
Wilson B-factor (Å ²)	28.0	Xtrriage
Anisotropy	0.299	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4595	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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

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	B	0.35	0/68	0.69	0/90
2	A	0.25	0/2203	0.43	0/3001
All	All	0.25	0/2271	0.44	0/3091

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 [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	B	67	64	63	3	0
2	A	2148	2163	2163	19	0
3	B	17	31	31	0	0
4	A	1	0	0	0	0
5	A	97	0	0	10	0
5	B	7	0	0	3	0
All	All	2337	2258	2257	22	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 5.

All (22) 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)
2:A:308:ASP:OD1	5:A:501:HOH:O	1.81	0.97
2:A:224:ARG:NH2	5:A:503:HOH:O	2.02	0.91
2:A:271:ASP:OD2	5:A:502:HOH:O	1.92	0.88
2:A:260:GLN:OE1	5:A:504:HOH:O	2.07	0.70
2:A:273:MET:O	5:A:505:HOH:O	2.09	0.69
2:A:157:PHE:O	2:A:159:SER:N	2.26	0.68
1:B:2:THR:N	5:B:202:HOH:O	2.26	0.67
1:B:4:ARG:NH2	5:B:203:HOH:O	2.30	0.64
2:A:234:GLU:OE1	5:A:506:HOH:O	2.17	0.57
2:A:235:ARG:HD2	5:A:587:HOH:O	2.05	0.55
2:A:261:ARG:NH2	5:A:509:HOH:O	2.38	0.51
1:B:4:ARG:O	5:B:201:HOH:O	2.19	0.51
2:A:198:GLU:OE2	2:A:204:TYR:OH	2.28	0.50
2:A:169:GLN:O	2:A:170:GLN:HB3	2.16	0.46
2:A:253:SER:OG	2:A:290:ASP:OD2	2.24	0.46
2:A:224:ARG:HG3	2:A:308:ASP:OD2	2.17	0.45
2:A:235:ARG:NH2	5:A:513:HOH:O	2.46	0.45
2:A:323:GLU:N	2:A:323:GLU:OE1	2.47	0.44
2:A:222:LEU:O	2:A:243:LYS:NZ	2.49	0.43
2:A:332:GLU:OE2	2:A:350:PRO:HB3	2.19	0.42
2:A:203:ASN:HB2	5:A:550:HOH:O	2.19	0.41
2:A:169:GLN:O	2:A:170:GLN:CB	2.69	0.41

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	B	7/10 (70%)	3 (43%)	2 (29%)	2 (29%)	0 0
2	A	272/309 (88%)	256 (94%)	13 (5%)	3 (1%)	17 23
All	All	279/319 (88%)	259 (93%)	15 (5%)	5 (2%)	11 12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	158	ARG
2	A	159	SER
1	B	4	ARG
1	B	8	GLY
2	A	162	SER

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	B	6/7 (86%)	6 (100%)	0	100	100
2	A	237/265 (89%)	237 (100%)	0	100	100
All	All	243/272 (89%)	243 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some 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](#)

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
3	PLM	B	101	1	16,16,17	0.84	0	15,15,17	1.25	1 (6%)

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
3	PLM	B	101	1	-	0/13/14/15	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	101	PLM	C3-C2-C1	-2.44	106.57	113.35

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

6.1 Protein, DNA and RNA chains

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, 95th 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)	Q<0.9
1	B	9/10 (90%)	6.75	5 (55%) 0 0	30, 44, 53, 59	0
2	A	274/309 (88%)	1.26	53 (19%) 2 1	20, 28, 59, 75	0
All	All	283/319 (88%)	1.44	58 (20%) 1 1	20, 29, 59, 75	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ALA	15.9
1	B	10	TRP	14.6
1	B	9	GLY	12.1
1	B	2	THR	10.0
2	A	170	GLN	8.8
2	A	157	PHE	8.1
2	A	394	LEU	7.9
2	A	121	GLY	6.7
1	B	8	GLY	6.2
2	A	159	SER	5.3
2	A	165	TYR	5.1
2	A	160	PRO	5.1
2	A	164	LEU	4.9
2	A	166	SER	4.6
2	A	169	GLN	4.3
2	A	168	LEU	4.2
2	A	393	LYS	3.7
2	A	122	LYS	3.6
2	A	167	ASN	3.6
2	A	135	ARG	3.6
2	A	158	ARG	3.4
2	A	162	SER	3.2
2	A	316	LEU	3.2
2	A	142	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
2	A	199	LEU	3.0
2	A	171	TYR	2.9
2	A	384	ARG	2.6
2	A	346	ASP	2.6
2	A	358	ARG	2.5
2	A	351	LEU	2.5
2	A	208	VAL	2.4
2	A	148	ILE	2.4
2	A	332	GLU	2.4
2	A	139	ARG	2.4
2	A	172	ASP	2.4
2	A	371	GLU	2.4
2	A	317	ILE	2.3
2	A	345	ARG	2.3
2	A	155	PRO	2.3
2	A	150	THR	2.3
2	A	381	GLU	2.3
2	A	182	LEU	2.3
2	A	226	TYR	2.3
2	A	183	PRO	2.3
2	A	235	ARG	2.2
2	A	385	ASP	2.2
2	A	224	ARG	2.2
2	A	205	LYS	2.2
2	A	173	LEU	2.2
2	A	130	GLU	2.2
2	A	190	LYS	2.2
2	A	195	LEU	2.1
2	A	137	CYS	2.1
2	A	261	ARG	2.1
2	A	330	LEU	2.0
2	A	392	GLY	2.0
2	A	367	VAL	2.0
2	A	389	ARG	2.0

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(\AA^2)	Q<0.9
3	PLM	B	101	17/18	0.56	0.41	1.76	30,51,65,67	0
4	ZN	A	401	1/1	0.89	0.08	-1.37	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.