



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 04:01 PM UTC

PDB ID : 4R8M / pdb_00004r8m
Title : Human SIRT2 crystal structure in complex with BHJH-TM1
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Deposited on : 2014-09-02
Resolution : 2.10 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

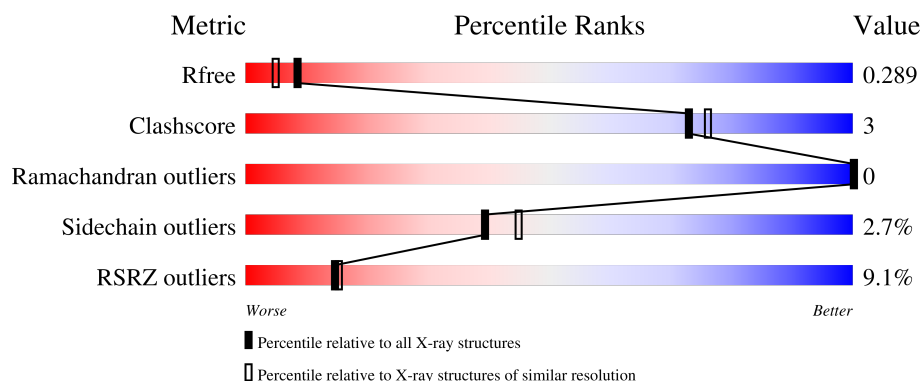
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 $\leq 5\%$. 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	319	8% 83% 6% 10%
1	B	319	8% 80% 9% 11%
2	C	5	40% 100%
2	D	5	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4647 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 NAD-dependent protein deacetylase sirtuin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	1	0
			2252	1447	375	413	17			
1	B	285	Total	C	N	O	S	0	2	0
			2266	1457	377	415	17			

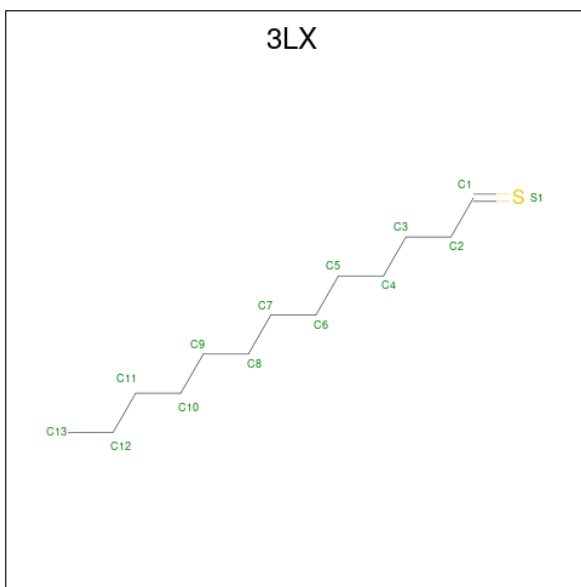
- Molecule 2 is a protein called BHJH-TM1 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			36	23	7	6			
2	D	5	Total	C	N	O	0	0	0
			36	23	7	6			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is tridecanethial (CCD ID: 3LX) (formula: C₁₃H₂₆S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	S	0	0
			14	13	1		
4	D	1	Total	C	S	0	0
			14	13	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	12	Total	O	0	0
			12	12		
5	B	15	Total	O	0	0
			15	15		

- Molecule 1: NAD-dependent protein deacetylase sirtuin-2



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	36.94Å 116.80Å 70.91Å 90.00° 91.77° 90.00°	Depositor
Resolution (Å)	45.11 – 2.10 45.11 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.7 (45.11-2.10) 97.7 (45.11-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.221 , 0.273 (Not available) , 0.289	Depositor DCC
R_{free} test set	1727 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 31.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.064 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4647	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.12% 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: 3LX, ZN

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	0.67	1/2302 (0.0%)	0.82	0/3110
1	B	0.64	0/2317	0.79	0/3129
2	C	0.53	0/36	0.60	0/45
2	D	0.45	0/36	0.56	0/45
All	All	0.65	1/4691 (0.0%)	0.80	0/6329

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	LEU	C-O	-5.48	1.17	1.24

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	A	2252	0	2215	11	0
1	B	2266	0	2224	18	0
2	C	36	0	42	0	0
2	D	36	0	43	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	14	0	25	0	0
4	D	14	0	25	0	0
5	A	12	0	0	0	0
5	B	15	0	0	0	0
All	All	4647	0	4574	29	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 3.

All (29) 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:B:248[A]:GLN:HE21	1:B:248[A]:GLN:HA	1.38	0.88
1:B:167:GLN:HE22	1:B:262:THR:HG21	1.38	0.87
1:B:167:GLN:HE22	1:B:262:THR:CG2	1.88	0.86
1:B:262:THR:HG22	1:B:264:LEU:H	1.40	0.85
1:B:170:ASP:O	1:B:171:THR:HG22	1.79	0.82
1:B:134:LEU:HD21	1:B:138:LEU:HD12	1.76	0.66
1:B:248[A]:GLN:HA	1:B:248[A]:GLN:NE2	2.10	0.64
1:A:163:ARG:HD2	1:A:250:ASP:OD2	2.03	0.59
1:A:115:PRO:O	1:A:118:ILE:HG22	2.03	0.58
1:A:169:ILE:C	1:A:169:ILE:HD12	2.29	0.58
1:A:171:THR:O	1:A:171:THR:HG22	2.08	0.54
1:A:267:GLN:HE21	1:A:268:PRO:HA	1.73	0.53
1:B:167:GLN:HE22	1:B:262:THR:HG23	1.71	0.51
1:B:194:HIS:HD2	1:B:231:ASP:OD1	1.95	0.50
1:B:255:ASP:O	1:B:281:PRO:HD2	2.13	0.48
1:B:244:PHE:O	1:B:248[A]:GLN:HG2	2.14	0.48
1:A:169:ILE:C	1:A:169:ILE:CD1	2.88	0.46
1:B:286:ASN:ND2	1:B:288:GLU:O	2.43	0.45
1:B:64:LEU:HD22	1:B:320:TRP:CD1	2.53	0.43
1:A:255:ASP:O	1:A:281:PRO:HD2	2.19	0.43
1:B:248[A]:GLN:HE21	1:B:248[A]:GLN:CA	2.11	0.42
1:B:262:THR:HG22	1:B:264:LEU:N	2.20	0.42
1:B:267:GLN:HE21	1:B:268:PRO:HA	1.84	0.42
1:A:171:THR:O	1:A:171:THR:CG2	2.68	0.41
1:A:209:MET:HE3	1:A:209:MET:HB2	1.93	0.41
1:A:335:LEU:HD13	1:A:337:TRP:CZ3	2.56	0.41
1:B:273:ILE:HG23	1:B:282:ARG:NH1	2.36	0.41
1:B:153:ARG:NH2	1:B:348:GLU:OE2	2.55	0.40
1:A:170:ASP:O	1:A:171:THR:HB	2.21	0.40

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	281/319 (88%)	274 (98%)	7 (2%)	0	100	100
1	B	281/319 (88%)	274 (98%)	7 (2%)	0	100	100
2	C	3/5 (60%)	3 (100%)	0	0	100	100
2	D	3/5 (60%)	3 (100%)	0	0	100	100
All	All	568/648 (88%)	554 (98%)	14 (2%)	0	100	100

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	242/279 (87%)	236 (98%)	6 (2%)	42	48
1	B	243/279 (87%)	236 (97%)	7 (3%)	37	42
2	C	4/4 (100%)	4 (100%)	0	100	100
2	D	4/4 (100%)	4 (100%)	0	100	100
All	All	493/566 (87%)	480 (97%)	13 (3%)	39	46

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ARG
1	A	190	PHE
1	A	209	MET
1	A	210	LYS
1	A	252	LEU
1	A	262	THR
1	B	77	ARG
1	B	103	LEU
1	B	109	LYS
1	B	116	GLU
1	B	239	LEU
1	B	262	THR
1	B	265	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	106	ASN
1	A	202	HIS
1	A	248	GLN
1	A	267	GLN
1	B	167	GLN
1	B	194	HIS
1	B	267	GLN
1	B	355	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	3LX	D	600	2	12,13,13	0.78	1 (8%)	11,12,12	0.68	1 (9%)
4	3LX	C	600	2	12,13,13	0.71	1 (8%)	11,12,12	0.75	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	3LX	D	600	2	-	5/10/11/11	-
4	3LX	C	600	2	-	3/10/11/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	600	3LX	C2-C1	2.46	1.51	1.49
4	C	600	3LX	C2-C1	2.27	1.51	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	600	3LX	C3-C2-C1	-2.02	108.34	114.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	600	3LX	C2-C3-C4-C5
4	C	600	3LX	C9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
4	D	600	3LX	C2-C3-C4-C5
4	C	600	3LX	C7-C8-C9-C10
4	D	600	3LX	C5-C6-C7-C8
4	D	600	3LX	C4-C5-C6-C7
4	D	600	3LX	C6-C7-C8-C9
4	D	600	3LX	C10-C11-C12-C13

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	A	286/319 (89%)	0.82	26 (9%) 15 15	22, 45, 70, 89	1 (0%)
1	B	285/319 (89%)	0.79	25 (8%) 15 16	23, 43, 66, 88	2 (0%)
2	C	5/5 (100%)	1.79	2 (40%) 1 1	41, 51, 68, 78	0
2	D	5/5 (100%)	0.97	0 100 100	44, 51, 64, 86	0
All	All	581/648 (89%)	0.81	53 (9%) 15 15	22, 44, 69, 89	3 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	98	SER	5.3
1	A	138	LEU	5.1
2	C	5	GLY	4.5
1	B	96	PHE	3.9
1	A	105	ASP	3.8
1	B	248[A]	GLN	3.5
1	A	306	GLY	3.4
1	A	214	PHE	3.4
1	A	100	SER	3.3
1	B	351	SER	3.3
1	B	103	LEU	3.2
1	A	351	SER	3.2
1	B	353	ASP	3.1
1	A	332	ALA	3.1
1	B	66	GLY	3.0
1	A	324	CYS	3.0
1	A	141	GLY	3.0
1	A	200	CYS	3.0
1	B	273	ILE	2.9
1	A	310	ASP	2.9
1	A	101	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	311	SER	2.8
1	B	223	ASP	2.8
1	A	134	LEU	2.8
1	A	325	ASP	2.7
1	A	92	GLY	2.7
1	B	306	GLY	2.7
2	C	1	PRO	2.7
1	A	208	TRP	2.7
1	A	106	ASN	2.6
1	B	249	SER	2.6
1	B	181	GLU	2.6
1	B	330	ALA	2.6
1	B	182	ASP	2.5
1	B	321	LEU	2.5
1	B	180	GLN	2.4
1	A	354	ALA	2.4
1	B	290	ALA	2.3
1	B	114	TYR	2.3
1	B	92	GLY	2.3
1	A	99	PRO	2.3
1	A	96	PHE	2.2
1	A	330	ALA	2.2
1	B	138	LEU	2.2
1	B	310	ASP	2.2
1	B	143	PHE	2.2
1	B	109	LYS	2.2
1	B	263	SER	2.1
1	A	292	GLN	2.1
1	A	190	PHE	2.1
1	A	328	CYS	2.1
1	A	89[A]	THR	2.1
1	B	94	PRO	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 oligosaccharides 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, 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	B-factors($\text{\AA}^2$)	Q<0.9
4	3LX	C	600	14/14	0.90	0.14	42,72,85,85	0
4	3LX	D	600	14/14	0.91	0.12	42,57,62,62	0
3	ZN	A	401	1/1	0.98	0.06	47,47,47,47	0
3	ZN	B	401	1/1	0.99	0.04	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.