



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2016 – 04:50 PM EDT

PDB ID : 5BW4
Title : Crystal structure of the 16S rRNA (adenine(1408)-N(1))-methyltransferase W203A mutant with cosubstrate SAM from Catenulisporales acidiphilia
Authors : Witek, M.A.; Conn, G.L.
Deposited on : 2015-06-05
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
<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027107
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-20027107

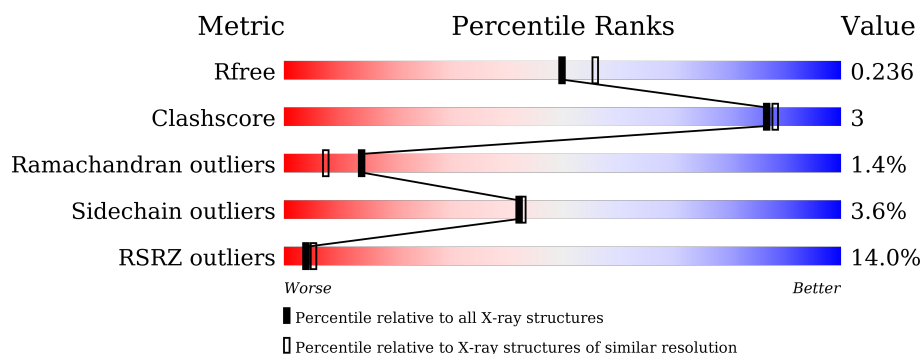
1 Overall quality at a glance

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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (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 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	A	267	<div> <div>8%</div> <div>69%</div> <div>8%</div> <div>23%</div> </div>
1	B	267	<div> <div>14%</div> <div>74%</div> <div>8%</div> <div>16%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3320 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 16S rRNA (adenine(1408)-N(1))-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1540	979	274	284	3			
1	B	224	Total	C	N	O	S	0	0	0
			1670	1056	299	312	3			

There are 36 discrepancies between the modelled and reference sequences:

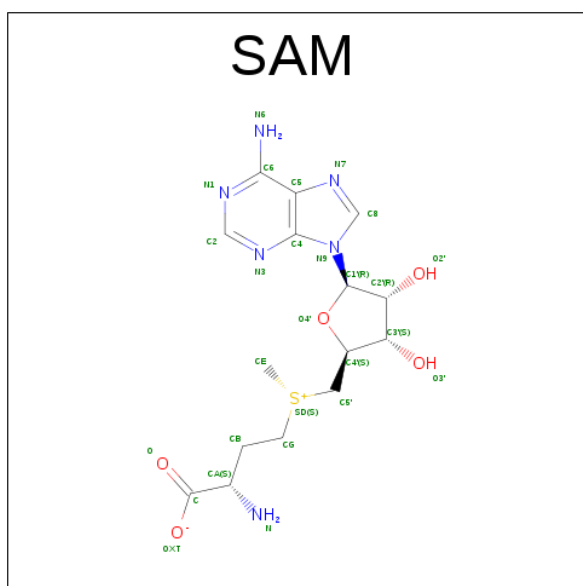
Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	expression tag	UNP C7Q5P8
A	-15	HIS	-	expression tag	UNP C7Q5P8
A	-14	HIS	-	expression tag	UNP C7Q5P8
A	-13	HIS	-	expression tag	UNP C7Q5P8
A	-12	HIS	-	expression tag	UNP C7Q5P8
A	-11	HIS	-	expression tag	UNP C7Q5P8
A	-10	HIS	-	expression tag	UNP C7Q5P8
A	-9	ALA	-	expression tag	UNP C7Q5P8
A	-8	SER	-	expression tag	UNP C7Q5P8
A	-7	GLY	-	expression tag	UNP C7Q5P8
A	-6	LEU	-	expression tag	UNP C7Q5P8
A	-5	VAL	-	expression tag	UNP C7Q5P8
A	-4	PRO	-	expression tag	UNP C7Q5P8
A	-3	ARG	-	expression tag	UNP C7Q5P8
A	-2	GLY	-	expression tag	UNP C7Q5P8
A	-1	SER	-	expression tag	UNP C7Q5P8
A	0	HIS	-	expression tag	UNP C7Q5P8
A	203	ALA	TRP	engineered mutation	UNP C7Q5P8
B	-16	MET	-	expression tag	UNP C7Q5P8
B	-15	HIS	-	expression tag	UNP C7Q5P8
B	-14	HIS	-	expression tag	UNP C7Q5P8
B	-13	HIS	-	expression tag	UNP C7Q5P8
B	-12	HIS	-	expression tag	UNP C7Q5P8
B	-11	HIS	-	expression tag	UNP C7Q5P8
B	-10	HIS	-	expression tag	UNP C7Q5P8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	ALA	-	expression tag	UNP C7Q5P8
B	-8	SER	-	expression tag	UNP C7Q5P8
B	-7	GLY	-	expression tag	UNP C7Q5P8
B	-6	LEU	-	expression tag	UNP C7Q5P8
B	-5	VAL	-	expression tag	UNP C7Q5P8
B	-4	PRO	-	expression tag	UNP C7Q5P8
B	-3	ARG	-	expression tag	UNP C7Q5P8
B	-2	GLY	-	expression tag	UNP C7Q5P8
B	-1	SER	-	expression tag	UNP C7Q5P8
B	0	HIS	-	expression tag	UNP C7Q5P8
B	203	ALA	TRP	engineered mutation	UNP C7Q5P8

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total	O	0	0
			35	35		
3	B	21	Total	O	0	0
			21	21		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.72Å 83.23Å 93.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.31 – 2.10 29.29 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.5 (29.31-2.10) 94.5 (29.29-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.183 , 0.230 0.192 , 0.236	Depositor DCC
R_{free} test set	1909 reflections (7.06%)	DCC
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 28935 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3320	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: SAM

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	1.00	2/1570 (0.1%)	1.02	6/2149 (0.3%)
1	B	0.90	1/1702 (0.1%)	0.95	2/2330 (0.1%)
All	All	0.95	3/3272 (0.1%)	0.99	8/4479 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	TRP	CE3-CZ3	-6.28	1.27	1.38
1	A	129	SER	CB-OG	-5.99	1.34	1.42
1	B	129	SER	CB-OG	-5.83	1.34	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	113	TRP	CA-CB-CG	5.66	124.46	113.70
1	A	113	TRP	CA-CB-CG	5.49	124.13	113.70
1	A	176	ASP	CB-CG-OD1	5.45	123.20	118.30
1	A	226	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	224	ASP	CB-CG-OD1	5.27	123.04	118.30
1	A	118	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	B	151	ARG	NE-CZ-NH1	5.01	122.80	120.30
1	A	43	ARG	NE-CZ-NH1	5.00	122.80	120.30

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	1540	0	1592	4	0
1	B	1670	0	1724	14	0
2	A	27	0	22	0	0
2	B	27	0	22	0	0
3	A	35	0	0	0	0
3	B	21	0	0	1	0
All	All	3320	0	3360	18	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 (18) 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:76:ARG:HB3	1:B:80:LYS:HG3	1.58	0.85
1:B:77:LYS:H	1:B:80:LYS:HE3	1.45	0.81
1:B:77:LYS:H	1:B:80:LYS:CE	2.07	0.66
1:B:149:ILE:HD12	1:B:158:ILE:HD13	1.79	0.65
1:B:148:SER:HA	1:B:151:ARG:HH11	1.63	0.62
1:A:108:MET:HB3	1:A:110:LEU:HD13	1.90	0.53
1:A:106:GLU:OE2	1:A:142:GLU:OE1	2.27	0.53
1:B:149:ILE:HD12	1:B:158:ILE:CD1	2.38	0.51
1:B:77:LYS:N	1:B:80:LYS:HE3	2.23	0.49
1:B:218:LEU:HD23	1:B:218:LEU:C	2.34	0.47
1:B:105:ASP:O	1:B:140:PRO:HD2	2.16	0.46
1:B:80:LYS:NZ	3:B:403:HOH:O	2.49	0.46
1:B:206:ARG:O	1:B:207:LEU:HG	2.16	0.45
1:B:77:LYS:HB3	1:B:78:PRO:CD	2.47	0.45
1:B:198:THR:O	1:B:200:SER:N	2.51	0.43
1:A:150:TRP:CE3	1:A:163:GLU:HA	2.54	0.42
1:A:15:LEU:HA	1:A:15:LEU:HD23	1.81	0.42
1:B:44:THR:O	1:B:48:GLN:HG3	2.20	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	201/267 (75%)	198 (98%)	2 (1%)	1 (0%)	34	30
1	B	222/267 (83%)	210 (95%)	7 (3%)	5 (2%)	8	3
All	All	423/534 (79%)	408 (96%)	9 (2%)	6 (1%)	14	7

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	199	ILE
1	B	205	ARG
1	B	200	SER
1	B	198	THR
1	B	206	ARG
1	A	192	PRO

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	161/211 (76%)	154 (96%)	7 (4%)	35	34
1	B	175/211 (83%)	170 (97%)	5 (3%)	50	53
All	All	336/422 (80%)	324 (96%)	12 (4%)	42	43

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
1	A	73	ARG
1	A	159	ARG
1	A	193	HIS
1	A	213	GLU
1	A	214	THR
1	A	227	ASP
1	B	176	ASP
1	B	195	ASP
1	B	202	SER
1	B	209	SER
1	B	229	VAL

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

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAM	A	301	-	23,29,29	1.44	2 (8%)	15,42,42	3.07	7 (46%)
2	SAM	B	301	-	23,29,29	1.61	1 (4%)	15,42,42	3.02	6 (40%)

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	SAM	A	301	-	-	0/8/33/33	0/3/3/3
2	SAM	B	301	-	-	0/8/33/33	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	SAM	CG-SD	-6.38	1.67	1.80
2	A	301	SAM	CG-SD	-5.36	1.69	1.80
2	A	301	SAM	O4'-C1'	2.31	1.44	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	SAM	N3-C2-N1	-8.06	122.54	128.87
2	A	301	SAM	C4'-O4'-C1'	-5.98	103.31	109.64
2	A	301	SAM	N3-C2-N1	-5.79	124.32	128.87
2	B	301	SAM	C4'-O4'-C1'	-5.06	104.28	109.64
2	B	301	SAM	C1'-N9-C4	-2.67	123.83	126.81
2	A	301	SAM	C1'-N9-C4	-2.65	123.84	126.81
2	A	301	SAM	C2'-C1'-N9	-2.55	106.64	113.47
2	B	301	SAM	C2'-C3'-C4'	2.38	107.50	102.64
2	A	301	SAM	O4'-C4'-C5'	2.40	115.28	108.90
2	B	301	SAM	N6-C6-N1	2.48	122.68	118.52
2	A	301	SAM	N6-C6-N1	2.98	123.51	118.52
2	B	301	SAM	O4'-C1'-N9	4.42	116.47	108.11
2	A	301	SAM	O4'-C1'-N9	5.97	119.38	108.11

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	A	205/267 (76%)	0.62	22 (10%) 8 11	27, 41, 69, 117	0
1	B	224/267 (83%)	1.03	38 (16%) 2 3	27, 46, 100, 120	0
All	All	429/534 (80%)	0.83	60 (13%) 4 5	27, 43, 93, 120	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	199	ILE	9.3
1	B	205	ARG	8.3
1	A	212	THR	8.1
1	B	196	LEU	7.1
1	B	202	SER	6.9
1	B	197	ASP	6.7
1	B	208	GLY	6.5
1	B	198	THR	6.0
1	B	206	ARG	5.9
1	B	209	SER	5.8
1	B	204	ALA	5.8
1	B	228	PRO	5.8
1	B	201	SER	5.7
1	B	226	ARG	5.5
1	B	210	GLY	5.4
1	B	203	ALA	5.3
1	A	193	HIS	5.1
1	B	207	LEU	4.9
1	B	200	SER	4.8
1	B	227	ASP	4.5
1	A	213	GLU	4.4
1	A	6	ALA	4.1
1	A	227	ASP	3.9
1	B	19	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	21	ASP	3.6
1	B	195	ASP	3.6
1	B	6	ALA	3.5
1	A	64	TRP	3.5
1	A	35	VAL	3.4
1	A	57	VAL	3.4
1	B	211	ALA	3.3
1	A	14	LYS	3.2
1	B	229	VAL	3.2
1	A	13	LYS	3.1
1	B	20	PRO	3.1
1	A	192	PRO	3.1
1	A	65	GLN	3.1
1	B	18	LEU	2.9
1	A	113	TRP	2.9
1	B	13	LYS	2.9
1	A	17	ASP	2.8
1	A	224	ASP	2.8
1	A	58	VAL	2.7
1	A	5	THR	2.6
1	B	128	LEU	2.6
1	B	7	LEU	2.6
1	B	17	ASP	2.5
1	B	109	VAL	2.5
1	B	152	GLU	2.5
1	A	34	LEU	2.4
1	A	56	LEU	2.4
1	B	120	VAL	2.4
1	B	117	LEU	2.4
1	B	116	LEU	2.3
1	B	153	PRO	2.3
1	A	107	VAL	2.3
1	B	121	VAL	2.2
1	A	214	THR	2.1
1	B	151	ARG	2.1
1	A	69	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
2	SAM	A	301	27/27	0.95	0.13	-0.24	32,43,75,81	0
2	SAM	B	301	27/27	0.95	0.14	-0.42	32,47,80,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.