wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 07:21 PM GMT

PDB ID	:	4ONQ
Title	:	Crystal structure of ntDRM E283S/R309S/F310S/Y590S/D591S mutant
Authors	:	Du, J.; Patel, D.J.
Deposited on	:	2014-01-28
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

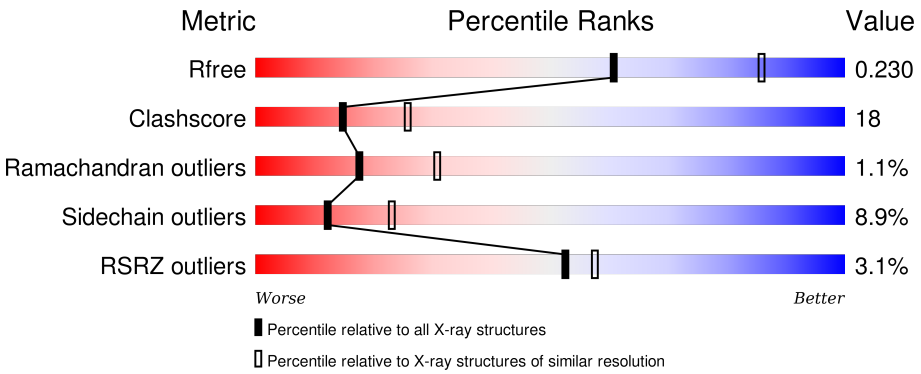
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 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 <=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	357	3%, 75%, 15%, •, 8%
1	B	357	3%, 61%, 23%, 5%, 11%

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
2	SFG	A	700	-	-	-	X
2	SFG	B	700	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5301 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.

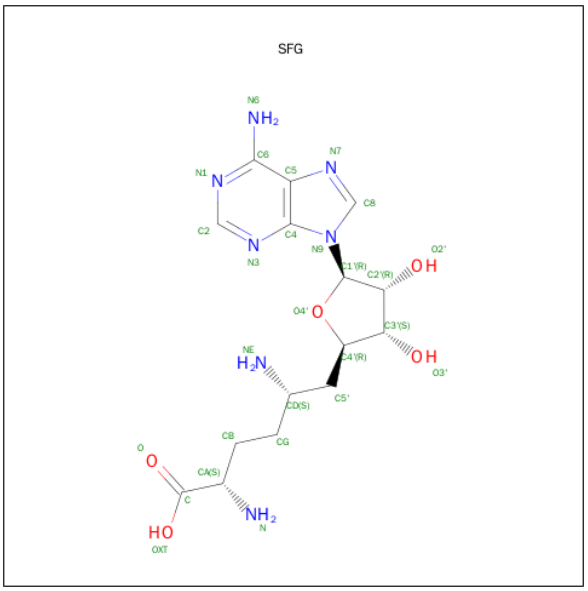
- Molecule 1 is a protein called DNA methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	327	2603	1676	454	465	8	0	0	0
1	B	317	2531	1630	441	453	7	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	252	SER	-	EXPRESSION TAG	UNP Q76KU6
A	253	GLU	-	EXPRESSION TAG	UNP Q76KU6
A	254	PHE	-	EXPRESSION TAG	UNP Q76KU6
A	283	SER	GLU	ENGINEERED MUTATION	UNP Q76KU6
A	309	SER	ARG	ENGINEERED MUTATION	UNP Q76KU6
A	310	SER	PHE	ENGINEERED MUTATION	UNP Q76KU6
A	590	SER	TYR	ENGINEERED MUTATION	UNP Q76KU6
A	591	SER	ASP	ENGINEERED MUTATION	UNP Q76KU6
B	252	SER	-	EXPRESSION TAG	UNP Q76KU6
B	253	GLU	-	EXPRESSION TAG	UNP Q76KU6
B	254	PHE	-	EXPRESSION TAG	UNP Q76KU6
B	283	SER	GLU	ENGINEERED MUTATION	UNP Q76KU6
B	309	SER	ARG	ENGINEERED MUTATION	UNP Q76KU6
B	310	SER	PHE	ENGINEERED MUTATION	UNP Q76KU6
B	590	SER	TYR	ENGINEERED MUTATION	UNP Q76KU6
B	591	SER	ASP	ENGINEERED MUTATION	UNP Q76KU6

- Molecule 2 is SINEFUNGIN (three-letter code: SFG) (formula: $C_{15}H_{23}N_7O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			27	15	7	5		
2	B	1	Total	C	N	O	0	0
			27	15	7	5		

- Molecule 3 is water.

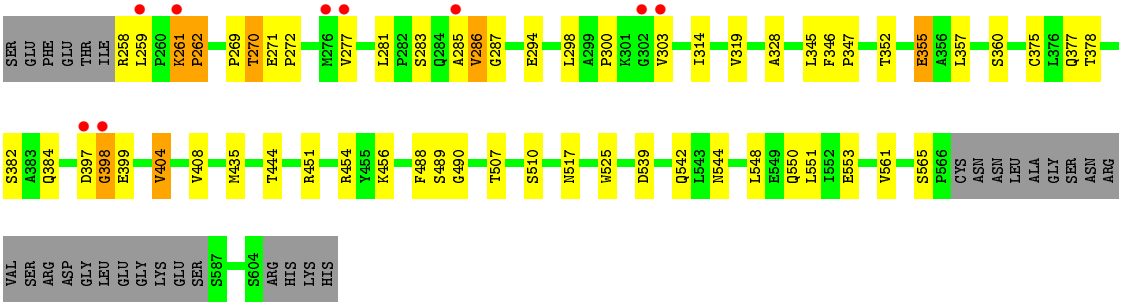
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	74	Total	O	0	0
			74	74		
3	B	39	Total	O	0	0
			39	39		

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.

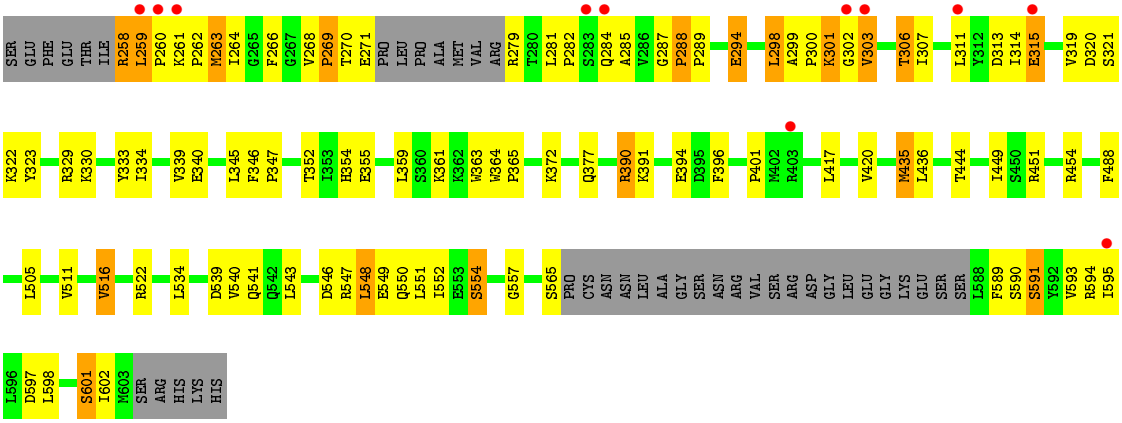
- Molecule 1: DNA methyltransferase

Chain A:



- Molecule 1: DNA methyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	131.50Å 131.50Å 88.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.88 – 2.50 43.04 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.88-2.50) 99.9 (43.04-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.44 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.185 , 0.230 0.193 , 0.230	Depositor DCC
R_{free} test set	1524 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	55.7	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.4	EDS
Estimated twinning fraction	0.036 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 30042 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5301	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: SFG

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	0.69	1/2673 (0.0%)	0.58	0/3632
1	B	0.74	2/2597 (0.1%)	0.64	0/3525
All	All	0.72	3/5270 (0.1%)	0.61	0/7157

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	269	PRO	N-CD	-5.93	1.39	1.47
1	A	525	TRP	NE1-CE2	-5.07	1.30	1.37
1	B	593	VAL	CA-CB	-5.01	1.44	1.54

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	2603	0	2607	37	0
1	B	2531	0	2528	146	0
2	A	27	0	22	3	0
2	B	27	0	22	3	0
3	A	74	0	0	1	0
3	B	39	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5301	0	5179	183	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 18.

The worst 5 of 183 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:281:LEU:CD2	1:B:285:ALA:HB3	1.25	1.58
1:B:352:THR:CG2	1:B:355:GLU:HG3	1.42	1.45
1:A:261:LYS:HG2	1:A:262:PRO:CD	1.57	1.34
1:B:281:LEU:HD21	1:B:285:ALA:CB	1.56	1.34
1:B:300:PRO:O	1:B:303:VAL:HG23	1.34	1.27

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	323/357 (90%)	315 (98%)	4 (1%)	4 (1%)	16 29
1	B	311/357 (87%)	296 (95%)	12 (4%)	3 (1%)	19 34
All	All	634/714 (89%)	611 (96%)	16 (2%)	7 (1%)	17 31

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	GLY
1	A	262	PRO
1	B	288	PRO
1	A	565	SER

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Mol	Chain	Res	Type
1	B	259	LEU

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	286/312 (92%)	266 (93%)	20 (7%)	19 34
1	B	277/312 (89%)	247 (89%)	30 (11%)	8 15
All	All	563/624 (90%)	513 (91%)	50 (9%)	12 23

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	270	THR
1	B	303	VAL
1	B	590	SER
1	B	279	ARG
1	B	298	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	GLN
1	A	506	ASN
1	A	541	GLN
1	B	335	HIS
1	B	354	HIS

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)

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	SFG	A	700	-	21,29,29	1.74	5 (23%)	19,42,42	6.15	8 (42%)
2	SFG	B	700	-	21,29,29	1.02	0	19,42,42	2.48	4 (21%)

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	SFG	A	700	-	-	0/9/33/33	0/3/3/3
2	SFG	B	700	-	-	0/9/33/33	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	700	SFG	C5-C4	-2.98	1.33	1.40
2	A	700	SFG	O4'-C1'	2.17	1.43	1.41
2	A	700	SFG	O4'-C4'	2.45	1.50	1.45
2	A	700	SFG	C2-N1	3.17	1.39	1.33
2	A	700	SFG	C2-N3	4.56	1.40	1.32

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	700	SFG	O4'-C4'-C5'	-19.72	80.46	109.36
2	A	700	SFG	N3-C2-N1	-14.10	118.10	128.89
2	A	700	SFG	O4'-C4'-C3'	-8.21	88.61	105.15
2	B	700	SFG	N3-C2-N1	-8.03	122.75	128.89
2	A	700	SFG	C5'-CD-CG	-3.84	100.28	114.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	700	SFG	3	0
2	B	700	SFG	3	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, 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	327/357 (91%)	-0.04	9 (2%)	56	61	27, 50, 95, 157	0
1	B	317/357 (88%)	0.11	11 (3%)	48	53	32, 65, 114, 165	0
All	All	644/714 (90%)	0.04	20 (3%)	52	57	27, 57, 107, 165	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	283	SER	4.2
1	B	303	VAL	4.1
1	B	261	LYS	3.8
1	B	315	GLU	3.5
1	A	398	GLY	3.5

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(Å^2)	Q<0.9
2	SFG	A	700	27/27	0.86	0.26	3.13	66,86,99,102	0
2	SFG	B	700	27/27	0.89	0.21	2.11	72,83,93,95	0

6.5 Other polymers (i)

There are no such residues in this entry.