Full wwPDB X-ray Structure Validation Report ⓘ

Jun 26, 2024 – 06:31 AM EDT

PDB ID	:	6SCE
Title	:	Structure of a Type III CRISPR defence DNA nuclease activated by cyclic oligoadenylate
Authors	:	McMahon, S.A.; Zhu, W.; Graham, S.; White, M.F.; Gloster, T.M.
Deposited on	:	2019-07-24
Resolution	:	1.83 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:

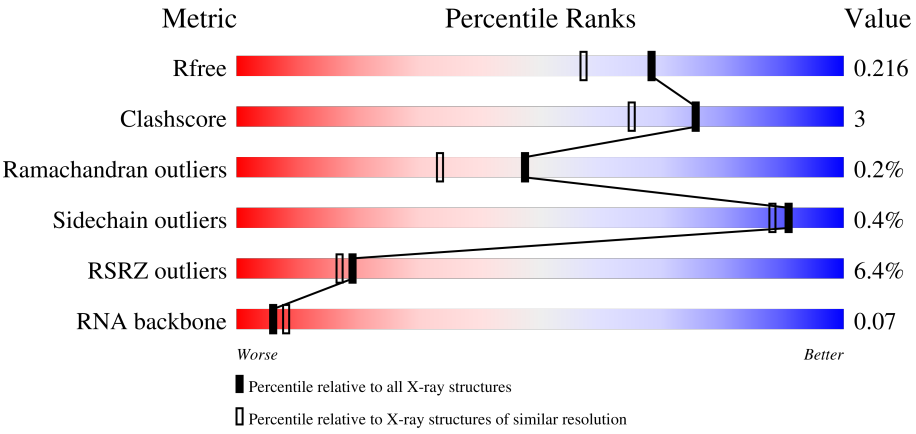
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.83 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}	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)
RNA backbone	3102	1038 (2.40-1.28)

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 chain
1	A	638	6% 89% 7% .
2	B	4	50% 50%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5394 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	614	4892	3165	883	834	3	7	0	9	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP Q53W14
A	2	GLU	GLN	conflict	UNP Q53W14
A	637	LEU	-	expression tag	UNP Q53W14
A	638	GLU	-	expression tag	UNP Q53W14

- Molecule 2 is a RNA chain called cyclic oligoadenylate.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	4	88	40	20	24	4	0	0	0

- Molecule 3 is water.

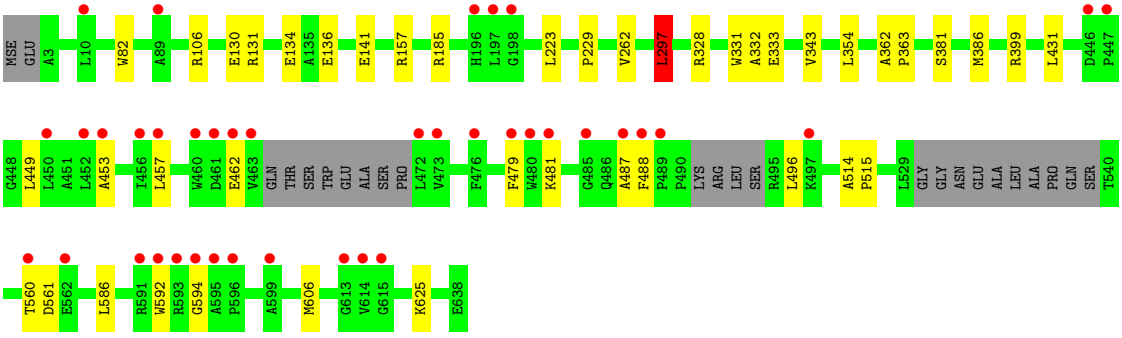
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	395	397	397	0	2
			Total	O		
3	B	17	17	17	0	0

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: Uncharacterized protein

Chain A:



• Molecule 2: cyclic oligoadenylate

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.37Å 84.52Å 123.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.70 – 1.83 59.71 – 1.83	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.70-1.83) 100.0 (59.71-1.83)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.05 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.176 , 0.209 0.185 , 0.216	Depositor DCC
R_{free} test set	3921 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	33.2	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5394	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.54	0/5053	0.70	2/6849 (0.0%)
2	B	0.64	0/99	1.30	0/152
All	All	0.54	0/5152	0.72	2/7001 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	297[A]	LEU	CA-CB-CG	-6.13	101.20	115.30
1	A	297[B]	LEU	CA-CB-CG	-6.13	101.20	115.30

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	4892	0	4846	31	0
2	B	88	0	44	0	0
3	A	397	0	0	4	0
3	B	17	0	0	0	0
All	All	5394	0	4890	31	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 (31) 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:A:106:ARG:NH1	3:A:945[B]:HOH:O	1.95	0.97
1:A:134:GLU:OE2	1:A:185:ARG:NH2	2.23	0.66
1:A:297[B]:LEU:HD13	1:A:386:MSE:HB3	1.79	0.63
1:A:399:ARG:HD3	3:A:962:HOH:O	2.04	0.57
1:A:297[A]:LEU:HD22	1:A:386:MSE:HB3	1.92	0.52
1:A:333:GLU:HG3	1:A:343:VAL:HG11	1.90	0.52
1:A:481:LYS:CD	1:A:487:ALA:HB2	2.41	0.51
1:A:297[B]:LEU:CD1	1:A:386:MSE:HB3	2.40	0.51
1:A:141:GLU:OE2	1:A:157:ARG:NH1	2.44	0.50
1:A:328:ARG:HD2	1:A:331[A]:TRP:CE3	2.47	0.50
1:A:332:ALA:HA	1:A:431:LEU:HD12	1.95	0.48
1:A:297[B]:LEU:HD13	1:A:386:MSE:CB	2.45	0.46
1:A:449:LEU:HD13	1:A:479:PHE:HB3	1.98	0.46
1:A:297[B]:LEU:HD12	1:A:381:SER:O	2.16	0.46
1:A:354:LEU:C	1:A:354:LEU:HD23	2.36	0.46
1:A:488:PHE:CG	1:A:496:LEU:HD21	2.51	0.45
1:A:462:GLU:HA	1:A:462:GLU:OE1	2.17	0.44
1:A:131[B]:ARG:NH1	1:A:136:GLU:OE2	2.41	0.44
1:A:625:LYS:HB2	3:A:922:HOH:O	2.18	0.44
1:A:560:THR:HG22	1:A:561:ASP:N	2.33	0.43
1:A:561:ASP:HB3	1:A:592:TRP:CD2	2.54	0.42
1:A:130:GLU:HG2	3:A:866:HOH:O	2.18	0.42
1:A:453:ALA:O	1:A:457:LEU:HG	2.20	0.42
1:A:586:LEU:HD11	1:A:606:MSE:SE	2.70	0.42
1:A:560:THR:HG22	1:A:561:ASP:OD1	2.20	0.42
1:A:514:ALA:HB3	1:A:515:PRO:HD3	2.01	0.41
1:A:331[B]:TRP:CE3	1:A:331[B]:TRP:HA	2.56	0.41
1:A:229:PRO:HA	1:A:262:VAL:O	2.21	0.41
1:A:82:TRP:CZ2	1:A:106:ARG:HD2	2.57	0.40
1:A:362:ALA:HB3	1:A:363:PRO:HD3	2.04	0.40
1:A:496:LEU:HD12	1:A:496:LEU:N	2.36	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	615/638 (96%)	606 (98%)	8 (1%)	1 (0%)	47 33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	594	GLY

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	475/495 (96%)	472 (99%)	3 (1%)	86 82

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	297[A]	LEU
1	A	297[B]	LEU

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

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	3/4 (75%)	2 (66%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	3	A
2	B	4	A

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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)	Q<0.9
1	A	607/638 (95%)	0.39	39 (6%) 19 17	24, 38, 71, 98	0
2	B	4/4 (100%)	-0.24	0 100 100	24, 24, 26, 27	0
All	All	611/642 (95%)	0.38	39 (6%) 19 17	24, 38, 71, 98	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	479	PHE	6.9
1	A	197	LEU	6.2
1	A	488	PHE	4.9
1	A	473	VAL	4.8
1	A	596	PRO	4.5
1	A	453	ALA	4.3
1	A	472	LEU	4.1
1	A	457	LEU	4.1
1	A	594	GLY	4.0
1	A	614	VAL	3.8
1	A	476	PHE	3.8
1	A	198	GLY	3.6
1	A	487	ALA	3.4
1	A	560	THR	3.3
1	A	463	VAL	3.2
1	A	562	GLU	2.9
1	A	485	GLY	2.9
1	A	613	GLY	2.9
1	A	481	LYS	2.9
1	A	460	TRP	2.8
1	A	456	ILE	2.7
1	A	480	TRP	2.7
1	A	450	LEU	2.6
1	A	592	TRP	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	462	GLU	2.6
1	A	489	PRO	2.6
1	A	196	HIS	2.6
1	A	461	ASP	2.5
1	A	447	PRO	2.5
1	A	446	ASP	2.5
1	A	595	ALA	2.4
1	A	452	LEU	2.4
1	A	591	ARG	2.4
1	A	593	ARG	2.3
1	A	615	GLY	2.3
1	A	10	LEU	2.1
1	A	599	ALA	2.1
1	A	497	LYS	2.1
1	A	89	ALA	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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.