



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:52 PM UTC

PDB ID : 6SCE / pdb_00006sce
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	:	4-5-2 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

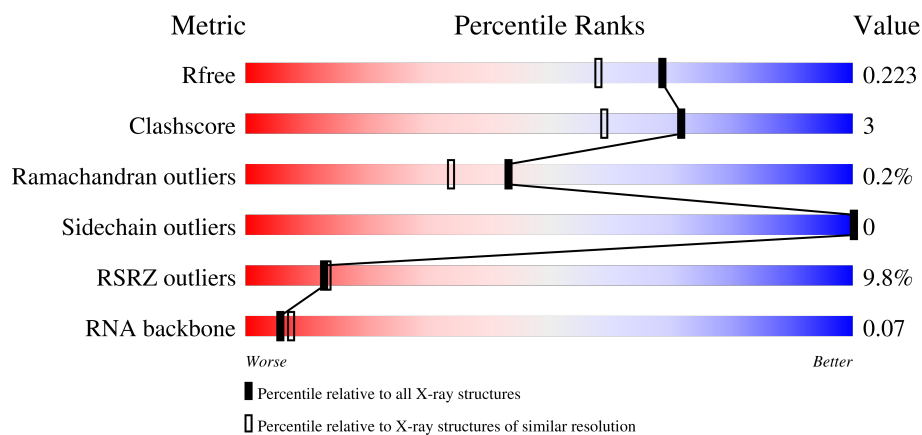
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)
RNA backbone	3983	1005 (2.24-1.44)

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	638	9% 89% 7% .
2	B	4	50% 50%

2 Entry composition

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
1	A	614	Total	C	N	O	S	Se	0	9	0
			4892	3165	883	834	3	7			

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
2	B	4	Total	C	N	O	P	0	0	0
			88	40	20	24	4			

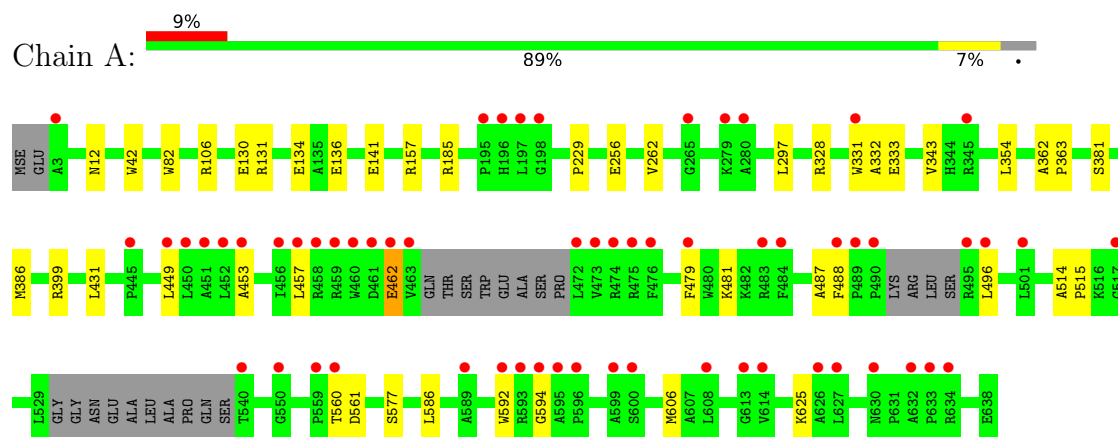
- Molecule 3 is water.

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

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



- Molecule 2: cyclic oligoadenylate



4 Data and refinement statistics

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 59.70 – 1.83	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.70-1.83) 100.0 (59.70-1.83)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.176 , 0.209 (Not available) , 0.223	Depositor DCC
R_{free} test set	3921 reflections (4.32%)	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)	0.34 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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.*

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](#)

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	0.72	0/5053	0.81	1/6849 (0.0%)
2	B	0.51	0/99	1.10	0/152
All	All	0.72	0/5152	0.82	1/7001 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	462	GLU	N-CA-C	5.80	119.01	109.85

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	4892	0	4846	33	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	33	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 (33) 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:354:LEU:C	1:A:354:LEU:HD23	2.36	0.50
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: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:256:GLU:O	1:A:577[B]:SER:OG	2.30	0.43
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:12:ASN:HD21	1:A:42:TRP:CG	2.39	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

5.3.1 Protein backbone

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%)	43	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	594	GLY

5.3.2 Protein sidechains ⓘ

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%)	475 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
1	A	512	HIS
1	A	548	HIS

5.3.3 RNA ⓘ

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 [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	607/638 (95%)	0.57	60 (9%) 13 13	13, 37, 71, 98	9 (1%)
2	B	4/4 (100%)	-1.19	0 100 100	24, 24, 26, 27	0
All	All	611/642 (95%)	0.56	60 (9%) 13 13	13, 37, 71, 98	9 (1%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	VAL	6.9
1	A	479	PHE	6.0
1	A	453	ALA	5.3
1	A	197	LEU	5.2
1	A	473	VAL	5.1
1	A	472	LEU	4.9
1	A	461	ASP	4.5
1	A	460	TRP	4.5
1	A	457	LEU	4.3
1	A	456	ILE	4.0
1	A	599	ALA	4.0
1	A	490	PRO	3.8
1	A	594	GLY	3.7
1	A	196	HIS	3.5
1	A	560	THR	3.5
1	A	559	PRO	3.4
1	A	517	GLY	3.3
1	A	452	LEU	3.3
1	A	198	GLY	3.3
1	A	476	PHE	3.3
1	A	632	ALA	3.2
1	A	462	GLU	3.2
1	A	450	LEU	3.1
1	A	600	SER	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	488	PHE	3.0
1	A	614	VAL	2.9
1	A	496	LEU	2.9
1	A	495	ARG	2.9
1	A	592	TRP	2.9
1	A	451	ALA	2.8
1	A	449	LEU	2.8
1	A	279	LYS	2.8
1	A	627	LEU	2.7
1	A	474	ARG	2.7
1	A	195	PRO	2.7
1	A	489	PRO	2.6
1	A	596	PRO	2.6
1	A	608	LEU	2.5
1	A	593	ARG	2.5
1	A	550	GLY	2.5
1	A	589	ALA	2.4
1	A	595	ALA	2.4
1	A	458	ARG	2.4
1	A	540	THR	2.4
1	A	280	ALA	2.4
1	A	634	ARG	2.3
1	A	3	ALA	2.2
1	A	345	ARG	2.2
1	A	501	LEU	2.2
1	A	265	GLY	2.2
1	A	613	GLY	2.2
1	A	633	PRO	2.2
1	A	459	ARG	2.1
1	A	445	PRO	2.1
1	A	483	ARG	2.1
1	A	630	ASN	2.0
1	A	331[A]	TRP	2.0
1	A	626	ALA	2.0
1	A	484	PHE	2.0
1	A	475	ARG	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 oligosaccharides 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.