



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:56 PM BST

PDB ID : 4C3G
EMDB ID: : EMD-2441
Title : cryo-EM structure of activated and oligomeric restriction endonuclease SgrAI
Authors : Lyumkis, D.; Talley, H.; Stewart, A.; Shah, S.; Park, C.K.; Tama, F.; Potter, C.S.; Carragher, B.; Horton, N.C.
Deposited on : 2013-08-23
Resolution : 8.60 Å(reported)
Based on PDB ID : 3DVO

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

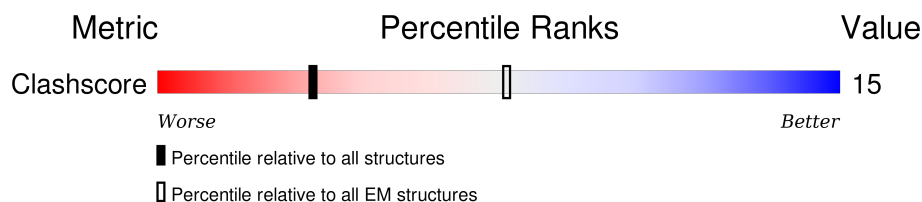
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.60 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)	EM structures (#Entries)
Clashscore	114402	924

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	337	 97% ..
1	B	337	 97% ..
2	C	18	 83% 17%
2	D	18	 67% 33%
3	E	22	 55% 41% 5%
3	F	22	 86% 14%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1534 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 SGRAIR RESTRICTION ENZYME.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	333	Total	C	0	333
			333	333		
1	B	333	Total	C	0	333
			333	333		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	ASP	ASN	CONFLICT	UNP Q9F6L0
B	63	ASP	ASN	CONFLICT	UNP Q9F6L0

- Molecule 2 is a DNA chain called 5'-D(*GP*AP*TP*GP*CP*GP*TP*GP*GP*GP*TP*C
P*TP*TP *CP*AP*CP*AP)-3'.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	18	Total	C	O	P	0	0
			195	90	88	17		
2	D	18	Total	C	O	P	0	0
			195	90	88	17		

- Molecule 3 is a DNA chain called 5'-D(*CP*CP*GP*GP*TP*GP*TP*GP*AP*AP*GP*A
P*CP*CP *CP*AP*CP*GP*CP*AP*TP*CP)-3'.

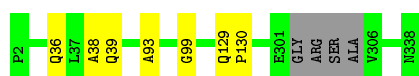
Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	22	Total	C	O	P	0	0
			239	110	108	21		
3	F	22	Total	C	O	P	0	0
			239	110	108	21		

3 Residue-property plots

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. 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. 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: SGRAIR RESTRICTION ENZYME

Chain A:  97% ..




- Molecule 1: SGRAIR RESTRICTION ENZYME

Chain B:  97% ..



- Molecule 2: 5'-D(*GP*AP*TP*GP*CP*GP*TP*GP*GP*GP*TP*CP*TP*TP *CP*AP*CP*AP)-3'

Chain C:  83% 17%



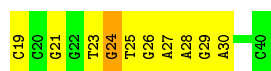
- Molecule 2: 5'-D(*GP*AP*TP*GP*CP*GP*TP*GP*GP*GP*TP*CP*TP*TP *CP*AP*CP*AP)-3'

Chain D:  67% 33%

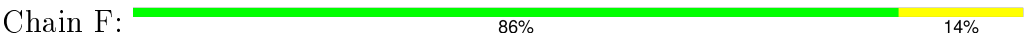


- Molecule 3: 5'-D(*CP*CP*GP*GP*TP*GP*TP*GP*AP*AP*GP*AP*CP*CP *CP*AP*CP*GP*CP*AP*TP*CP)-3'

Chain E:  55% 41% 5%



- Molecule 3: 5'-D(*CP*CP*GP*GP*TP*GP*TP*GP*AP*AP*GP*AP*CP*CP *CP*AP*CP*GP*CP*AP*TP*CP)-3'



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	60000	Depositor
Image detector	DE-12	Depositor

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	$\# Z > 2$	RMSZ	$\# Z > 2$
2	C	0.20	0/212	0.82	0/316
2	D	0.29	0/212	1.08	0/316
3	E	0.89	0/260	1.26	3/388 (0.8%)
3	F	0.31	0/260	1.15	0/388
All	All	0.52	0/944	1.10	3/1408 (0.2%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	21	DG	O4'-C4'-C3'	5.93	109.56	106.00
3	E	24	DG	O4'-C4'-C3'	5.83	109.50	106.00
3	E	19	DC	O4'-C4'-C3'	5.33	109.20	106.00

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	333	0	0	9	0
1	B	333	0	0	6	0
2	C	195	0	110	2	0
2	D	195	0	110	5	0
3	E	239	0	134	15	0
3	F	239	0	134	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	1534	0	488	30	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 15.

The worst 5 of 30 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:38:ALA:CA	3:E:25:DT:P	2.36	1.12
1:B:39:GLN:CA	3:F:25:DT:OP1	2.08	1.01
3:E:29:DG:H2''	3:E:30:DA:H5'	1.41	0.99
1:A:38:ALA:CA	3:E:25:DT:OP1	2.18	0.91
3:E:28:DA:H2''	3:E:29:DG:C5'	2.20	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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](#)

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.