



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 22, 2017 – 04:24 AM EDT

PDB ID : 5MZ6
EMDB ID: : EMD-3583
Title : Cryo-EM structure of a Separase-Securin complex from *Caenorhabditis elegans*
at 3.8 Å resolution
Authors : Boland, A.; Martin, T.G.; Zhang, Z.; Yang, J.; Bai, X.C.; Chang, L.; Scheres,
S.H.W.; Barford, D.
Deposited on : unknown
Resolution : 3.80 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

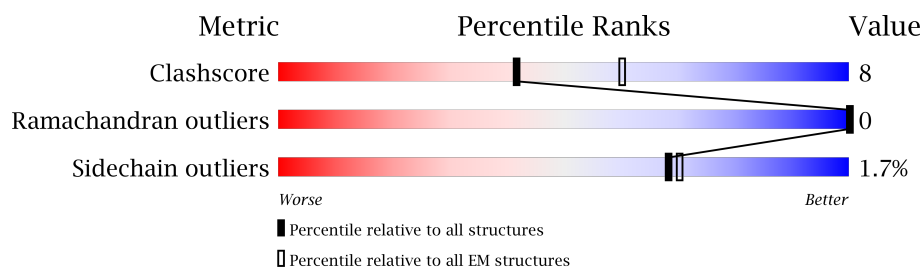
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

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	1	1262	
2	B	244	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8401 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 SEParase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1018	Total	C	N	O	S	0	0
			7968	5080	1379	1440	69		

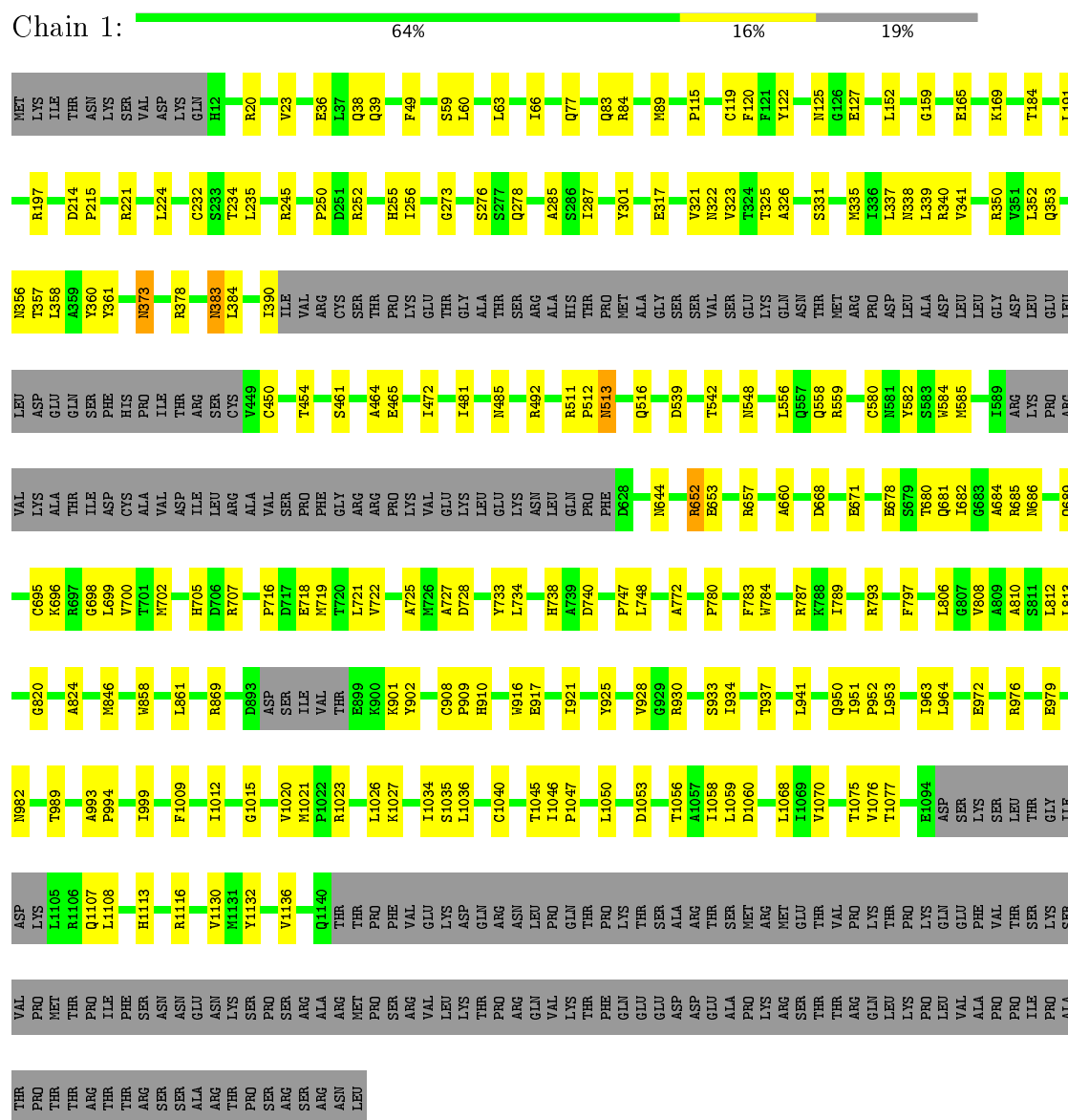
- Molecule 2 is a protein called Interactor of FizzY protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	74	Total	C	N	O	S	0	0
			433	259	78	95	1		

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 the various outlier classes 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: SEParase



- Molecule 2: Interactor of FizzY protein



ALA	ASP	ASP	LEU	ASP	SER	TYR	ASP	LEU	LEU	ALA	GLU	ALA	ASN	LEU	PRO	LEU	GLU	GLY	ASP	GLN	ILE	LYS	LEU	GLU	THR	ARG	HIS	THR	VAL	ILE	ALA	ASP	ASP	GLU	VAL	LYS	MET	SER	LYS	ALA	ARG	GLU	ARG	ASN	THR	PHE	LEU	SER	ASP	SER	LEU	ALA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	103696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	1	0.31	0/8132	0.54	2/10988 (0.0%)
2	B	0.33	0/434	0.82	5/597 (0.8%)
All	All	0.31	0/8566	0.56	7/11585 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	118	LEU	CA-CB-CG	6.75	130.82	115.30
2	B	148	PRO	N-CA-CB	6.03	110.53	103.30
2	B	168	PRO	N-CA-CB	5.81	110.27	103.30
2	B	172	PRO	N-CA-CB	5.67	110.10	103.30
2	B	169	PRO	N-CA-CB	5.57	109.99	103.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	951	ILE	Peptide

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	1	7968	0	7853	131	0
2	B	433	0	279	24	0
All	All	8401	0	8132	139	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 8.

The worst 5 of 139 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)
1:1:772:ALA:HB1	2:B:125:ASP:OD2	1.51	1.08
1:1:1040:CYS:HB3	1:1:1075:THR:HA	1.31	1.07
1:1:783:PHE:CG	2:B:122:ILE:HG22	2.12	0.84
2:B:122:ILE:HD12	2:B:122:ILE:O	1.78	0.84
1:1:1077:THR:CG2	2:B:123:GLU:HB3	2.10	0.82

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 PDB entries followed by that with respect to all EM entries.

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	1	1008/1262 (80%)	965 (96%)	43 (4%)	0	100	100
2	B	72/244 (30%)	59 (82%)	13 (18%)	0	100	100
All	All	1080/1506 (72%)	1024 (95%)	56 (5%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	1	842/1125 (75%)	830 (99%)	12 (1%)	71	87
2	B	21/212 (10%)	18 (86%)	3 (14%)	4	25
All	All	863/1337 (64%)	848 (98%)	15 (2%)	68	85

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	559	ARG
1	1	652	ARG
2	B	118	LEU
1	1	513	ASN
1	1	1027	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	1	373	ASN
1	1	383	ASN
1	1	968	ASN
1	1	353	GLN
1	1	705	HIS

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 [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.