



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Apr 24, 2017 – 07:31 PM EDT

PDB ID : 5XF8
EMDB ID: : EMD-6671
Title : Cryo-EM structure of the Cdt1-MCM2-7 complex in AMPPNP state
Authors : Zhai, Y.; Cheng, E.; Wu, H.; Li, N.; Yung, P.Y.; Gao, N.; Tye, B.K.
Deposited on : 2017-04-09
Resolution : 7.10 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-20029077

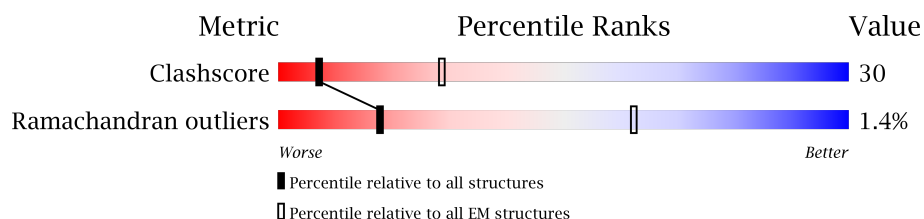
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


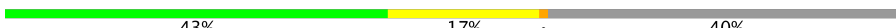





The reported resolution of this entry is 7.10 Å.

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

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	2	868	 47% 20% . 32%
2	3	997	 43% 17% . 40%
3	4	933	 52% 24% . 23%
4	5	775	 62% 19% 18%
5	6	1017	 38% 23% . 36%
6	7	845	 51% 22% 26%
7	C	604	 65% 12% 22%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 21215 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 DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	591	Total	C	N	O	0	0
			2924	1742	591	591		

- Molecule 2 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	601	Total	C	N	O	0	0
			2974	1772	601	601		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	-25	MET	-	initiating methionine	UNP P24279
3	-24	ASP	-	expression tag	UNP P24279
3	-23	TYR	-	expression tag	UNP P24279
3	-22	LYS	-	expression tag	UNP P24279
3	-21	ASP	-	expression tag	UNP P24279
3	-20	HIS	-	expression tag	UNP P24279
3	-19	ASP	-	expression tag	UNP P24279
3	-18	GLY	-	expression tag	UNP P24279
3	-17	ASP	-	expression tag	UNP P24279
3	-16	TYR	-	expression tag	UNP P24279
3	-15	LYS	-	expression tag	UNP P24279
3	-14	ASP	-	expression tag	UNP P24279
3	-13	HIS	-	expression tag	UNP P24279
3	-12	ASP	-	expression tag	UNP P24279
3	-11	ILE	-	expression tag	UNP P24279
3	-10	ASP	-	expression tag	UNP P24279
3	-9	TYR	-	expression tag	UNP P24279
3	-8	LYS	-	expression tag	UNP P24279
3	-7	ASP	-	expression tag	UNP P24279
3	-6	ASP	-	expression tag	UNP P24279
3	-5	ASP	-	expression tag	UNP P24279

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Chain	Residue	Modelled	Actual	Comment	Reference
3	-4	ASP	-	expression tag	UNP P24279
3	-3	LYS	-	expression tag	UNP P24279
3	-2	GLY	-	expression tag	UNP P24279
3	-1	GLY	-	expression tag	UNP P24279
3	0	ARG	-	expression tag	UNP P24279

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	4	716	Total	C	N	O	0	0
			3551	2119	716	716		

- Molecule 4 is a protein called Minichromosome maintenance protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	632	Total	C	N	O	0	0
			3130	1866	632	632		

- Molecule 5 is a protein called DNA replication licensing factor MCM6.

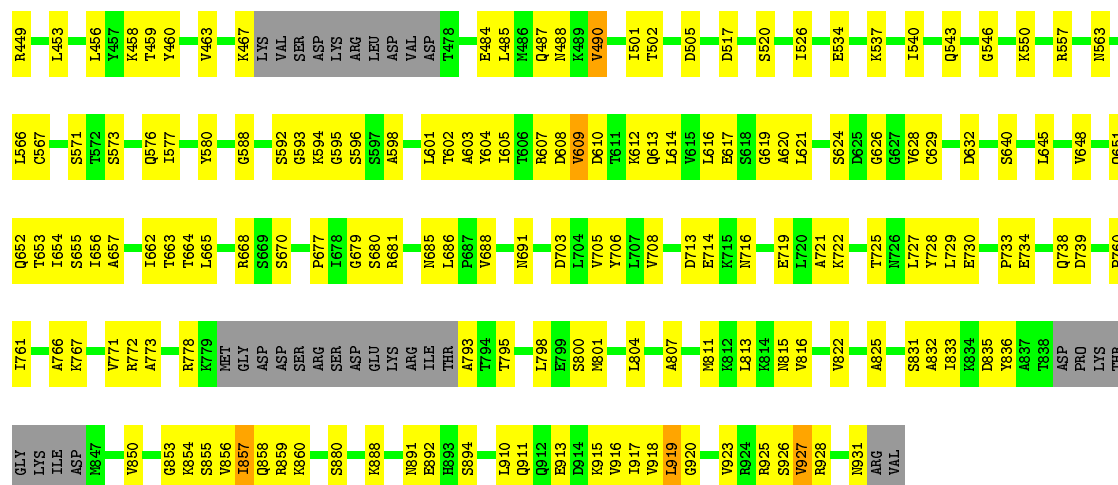
Mol	Chain	Residues	Atoms				AltConf	Trace
5	6	652	Total	C	N	O	0	0
			3230	1926	652	652		

- Molecule 6 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	7	622	Total	C	N	O	0	0
			3076	1832	622	622		

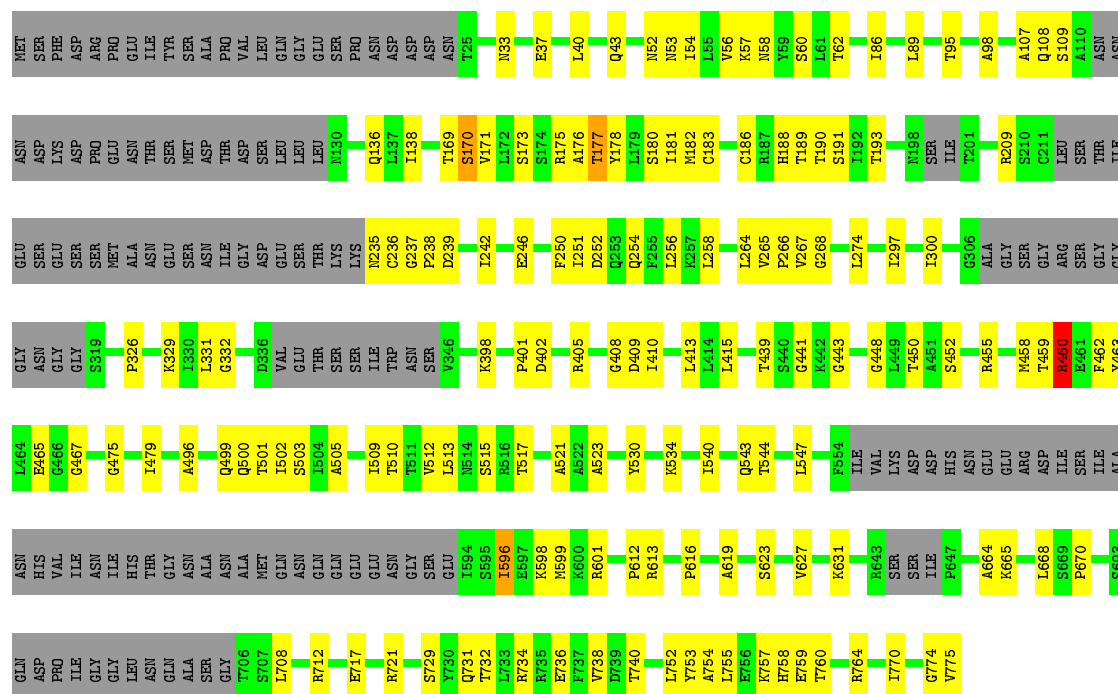
- Molecule 7 is a protein called Cell division cycle protein CDT1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	C	469	Total	C	N	O	0	0
			2330	1392	469	469		



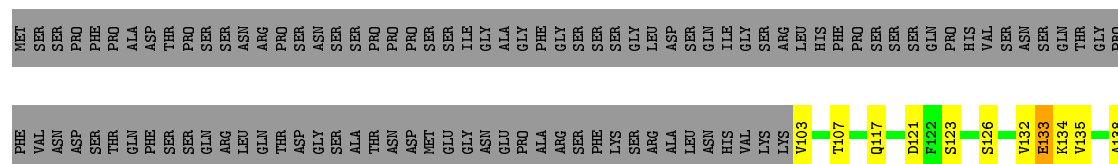
• Molecule 4: Minichromosome maintenance protein 5

Chain 5: 62% 19% 18%



• Molecule 5: DNA replication licensing factor MCM6

Chain 6: 38% 23% 36%



ILE	ASN	GLU	GLY	ASN	THR	LEU	LYS	PHE	VAL	ASP	ASP	GLY	THR	MET	ASP	THR	GLN	GLU	ASP	SER	LYS	VAL	SER	THR	PRO	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
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● Molecule 7: Cell division cycle protein CDT1



P528	Y529	Y533	S536	V539	S545	ASN	ASN	PRO	ILE	GLY	T551	H572	Q573	V574	D575	G576	G577	L578	K579	I597	H598	K599	S600	K601	D604																									
ALA	ASN	ALA	LEU	ASN	SER	SER	TYR	LEU	ALA	ASN	GLU	ASN	PHE	MET	LYS	GLU	MET	PRO	ASP	GLN	ALA	ASN	LEU	ARG	GLU	ARG	GLU	ARG	ARG	ARG	ARG	ALA	ALA	LEU	S499	L509	K512	I519	L520	F521	S522	L523	T524	R525	G526	Q527				
V372	V373	E374	L375	N376	S377	R378	G379	E380	L381	T382	M383	N384	L385	P386	K387	R388	A407	W410	S417	LYS	ASP	GLU	ILE	THR	ASP	VAL	PRO	ALA	PHE	LYS	ILE	ASN	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG					
GLY	ALA	THR	VAL	LEU	PRO	THR	GLY	ASP	PHE	GLN	TYR	LEU	PHE	E184	K203	A204	I205	S210	T211	M212	A213	A289	F290	R300	GLU	LEU	PRO	LEU	GLU	ASP	ASP	V87	E90	Q91	Y92	I93	M108	V134	M157	ASP	ASN	GLY	SER	THR	HIS	ASP	GLY	ALA	ASP	ALA

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	63000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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	2	0.52	0/2920	0.69	3/4063 (0.1%)
2	3	0.45	0/2968	0.62	0/4127
3	4	0.51	0/3546	0.69	4/4939 (0.1%)
4	5	0.39	0/3121	0.56	0/4337
5	6	0.54	0/3221	0.77	5/4477 (0.1%)
6	7	0.46	0/3071	0.64	0/4271
7	C	0.38	0/2324	0.60	0/3235
All	All	0.47	0/21171	0.66	12/29449 (0.0%)

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	2	0	6
2	3	0	5
3	4	0	6
4	5	0	2
5	6	0	19
6	7	0	6
7	C	0	4
All	All	0	48

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	6	626	GLY	N-CA-C	-6.63	96.52	113.10
5	6	561	GLU	N-CA-C	-6.51	93.41	111.00
1	2	334	LEU	N-CA-C	-6.49	93.48	111.00
1	2	570	GLY	N-CA-C	6.27	128.77	113.10
3	4	920	GLY	C-N-CA	-5.95	106.81	121.70

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	218	TYR	Peptide
1	2	298	SER	Peptide
1	2	367	CYS	Peptide
1	2	434	TYR	Peptide
1	2	588	GLU	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	2	2924	0	1308	146	0
2	3	2974	0	1349	134	0
3	4	3551	0	1537	162	0
4	5	3130	0	1369	97	0
5	6	3230	0	1449	202	0
6	7	3076	0	1381	157	0
7	C	2330	0	1004	47	0
All	All	21215	0	9397	908	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 30.

The worst 5 of 908 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)
1:2:386:GLN:N	1:2:410:LEU:O	1.57	1.36
1:2:224:ARG:CB	7:C:212:MET:HA	1.55	1.34
3:4:856:VAL:HA	3:4:860:LYS:CB	1.73	1.19
5:6:625:ALA:HB3	5:6:629:MET:H	1.04	1.13
2:3:190:SER:HA	2:3:456:ARG:HA	1.34	1.09

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 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	2	583/868 (67%)	503 (86%)	69 (12%)	11 (2%)	9	47
2	3	589/997 (59%)	516 (88%)	65 (11%)	8 (1%)	13	54
3	4	706/933 (76%)	603 (85%)	95 (14%)	8 (1%)	17	60
4	5	614/775 (79%)	564 (92%)	45 (7%)	5 (1%)	22	67
5	6	634/1017 (62%)	539 (85%)	80 (13%)	15 (2%)	7	42
6	7	612/845 (72%)	542 (89%)	62 (10%)	8 (1%)	14	56
7	C	457/604 (76%)	407 (89%)	46 (10%)	4 (1%)	20	63
All	All	4195/6039 (70%)	3674 (88%)	462 (11%)	59 (1%)	18	54

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2	305	SER
1	2	334	LEU
2	3	198	ARG
3	4	179	ILE
3	4	490	VAL

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.